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1 protein - protein search, using sw model

in on: May 24, 2004, 17:38:13 ; Search time 15 Seconds
(without alignments)
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File: US-09-594-978A-3

irect score: 20

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oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 389414 seqs, 51625971 residues

tal number of hits satisfying chosen parameters: 389414

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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SUMMARIES

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1	19	95.0	7	4	US-09-724-566A-78
2	19	95.0	8	4	US-09-724-566A-81
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4	19	95.0	9	4	US-08-197-484-145
5	19	95.0	9	4	US-09-724-566A-73
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7	19	95.0	9	5	PCT-US95-02121-145
8	19	95.0	14	4	US-09-724-566A-72
9	19	95.0	14	4	US-09-724-566A-97
10	19	95.0	28	2	US-08-733-825-3
11	19	95.0	35	1	US-08-487-890A-69
12	19	95.0	35	1	US-08-468-763-1
13	19	95.0	35	2	US-08-393-996A-1
14	19	95.0	35	2	US-08-478-435-69
15	19	95.0	35	2	US-08-337-483-69
16	19	95.0	35	2	US-08-478-373-69
17	19	95.0	35	3	US-08-474-671-69
18	19	95.0	35	3	US-08-483-577A-69
19	19	95.0	35	3	US-08-897-438-69
20	19	95.0	35	3	US-08-637-654-69
21	19	95.0	35	4	US-08-649-518-69
22	19	95.0	68	4	US-09-393-634-80
23	19	95.0	69	4	US-09-489-039A-13555
24	19	95.0	71	4	US-09-328-352-7111
25	19	95.0	73	1	US-08-321-071A-10
26	19	95.0	74	4	US-08-894-139-10
27	19	95.0	88	4	US-09-732-210-1412

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102	19	95.0	241	4	US-09-489-039A-7795	Sequence 7795, Ap	175	19	95.0	338	4	US-09-328-352-7151	Sequence 7151, Ap
103	19	95.0	243	4	US-09-134-001C-3587	Sequence 3587, Ap	176	19	95.0	339	3	US-09-345-468-3	Sequence 3, Appli
104	19	95.0	246	4	US-09-252-991A-30976	Sequence 30976, A	177	19	95.0	339	4	US-09-414-453A-3	Sequence 3, Appli
105	19	95.0	247	4	US-09-230-196-16	Sequence 16, Appl	178	19	95.0	339	4	US-09-134-000C-5209	Sequence 5209, Ap
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108	19	95.0	249	3	US-09-345-468-9	Sequence 9, Appli	181	19	95.0	346	4	US-09-266-965-107	Sequence 107, App
109	19	95.0	249	3	US-09-372-422A-22	Sequence 22, Appl	182	19	95.0	347	4	US-09-134-001C-3298	Sequence 3298, Ap
110	19	95.0	249	4	US-09-414-453A-9	Sequence 9, Appli	183	19	95.0	350	4	US-09-655-270A-17	Sequence 17, Appl
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115	19	95.0	250	3	US-08-654-025-7	Sequence 7, Appli	188	19	95.0	357	4	US-09-540-236-3808	Sequence 3808, Ap
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121	19	95.0	257	4	US-09-543-681A-6811	Sequence 6811, Ap	194	19	95.0	370	4	US-09-564-595D-53	Sequence 53, Appli
122	19	95.0	259	4	US-09-543-681A-6390	Sequence 6390, Ap	195	19	95.0	370	4	US-09-808-972-4	Sequence 4, Appli
123	19	95.0	259	4	US-09-489-039A-11936	Sequence 11936, A	196	19	95.0	371	2	US-08-837-593-6	Sequence 6, Appli
124	19	95.0	261	4	US-09-252-991A-23795	Sequence 23795, A	197	19	95.0	372	4	US-09-800-729-213	Sequence 213, App
125	19	95.0	262	4	US-09-252-991A-19738	Sequence 19738, A	198	19	95.0	374	4	US-09-489-039A-12678	Sequence 12678, A
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129	19	95.0	269	1	US-08-448-160-5	Sequence 5, Appli	202	19	95.0	390	4	US-09-543-681A-6415	Sequence 6415, Ap
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140	19	95.0	290	4	US-09-743-847-2	Sequence 2, Appli	213	19	95.0	403	4	US-09-540-236-2573	Sequence 2573, Ap
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142	19	95.0	291	4	US-09-489-039A-9578	Sequence 9578, Ap	215	19	95.0	405	4	US-09-232-197-63	Sequence 63, Appl
143	19	95.0	294	4	US-09-523-263B-20	Sequence 20, Appl	216	19	95.0	405	4	US-09-291-023A-20	Sequence 20, Appl
144	19	95.0	295	4	US-09-543-681A-5660	Sequence 5660, Ap	217	19	95.0	405	4	US-09-232-201-63	Sequence 63, Appl
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146	19	95.0	299	4	US-09-314-701-46	Sequence 46, Appl	219	19	95.0	405	4	US-09-232-195-63	Sequence 63, Appl
147	19	95.0	299	4	US-09-393-634-35	Sequence 35, Appl	220	19	95.0	406	4	US-09-543-681A-7962	Sequence 7962, Ap
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256	19	95.0	450	4	US-09-543-681A-7260	Sequence 7260, Ap	329	19	95.0	493	3	US-08-993-722A-70	Sequence 70, Appl
257	19	95.0	451	4	US-09-134-000C-6421	Sequence 6421, Ap	330	19	95.0	493	3	US-08-993-170A-70	Sequence 70, Appl
258	19	95.0	455	4	US-09-252-991A-19356	Sequence 19356, A	331	19	95.0	493	3	US-08-993-775B-70	Sequence 70, Appl
259	19	95.0	456	4	US-09-252-991A-31884	Sequence 31884, A	332	19	95.0	493	3	US-09-177-349-5	Sequence 5, Appl
260	19	95.0	457	4	US-09-252-991A-28824	Sequence 28824, A	333	19	95.0	493	4	US-09-328-352-6753	Sequence 6753, Ap
261	19	95.0	467	4	US-09-543-681A-6871	Sequence 6871, Ap	334	19	95.0	493	4	US-09-427-770-70	Sequence 70, Appl
262	19	95.0	468	4	US-09-252-991A-18608	Sequence 18608, A	335	19	95.0	493	4	US-09-427-769-70	Sequence 70, Appl
263	19	95.0	468	4	US-09-543-681A-5423	Sequence 5423, Ap	336	19	95.0	493	4	US-09-540-236-2869	Sequence 2869, Ap
264	19	95.0	474	4	US-09-252-991A-27524	Sequence 27524, A	337	19	95.0	495	3	US-09-179-966-1	Sequence 1, Appl
265	19	95.0	475	4	US-09-252-991A-32806	Sequence 32806, A	338	19	95.0	495	3	US-08-980-994-1	Sequence 1, Appl
266	19	95.0	479	4	US-09-328-352-5396	Sequence 5396, Ap	339	19	95.0	504	4	US-09-252-991A-20317	Sequence 20317, A
267	19	95.0	485	2	US-08-446-803-2	Sequence 1, Appl	340	19	95.0	506	3	US-09-232-191-9	Sequence 9, Appl
268	19	95.0	485	2	US-08-446-803-2	Sequence 2, Appl	341	19	95.0	506	3	US-09-232-200-9	Sequence 9, Appl
269	19	95.0	485	2	US-08-861-837-1	Sequence 1, Appl	342	19	95.0	506	3	US-09-232-200-95	Sequence 95, Appl
270	19	95.0	485	2	US-08-861-837-2	Sequence 2, Appl	343	19	95.0	506	4	US-09-232-197-9	Sequence 9, Appl
271	19	95.0	485	2	US-08-600-908A-12	Sequence 12, Appl	344	19	95.0	506	4	US-09-232-197-95	Sequence 95, Appl
272	19	95.0	485	3	US-08-683-838A-12	Sequence 12, Appl	345	19	95.0	506	4	US-09-232-201-9	Sequence 9, Appl
273	19	95.0	485	3	US-08-600-656-1	Sequence 1, Appl	346	19	95.0	506	4	US-09-232-201-95	Sequence 95, Appl
274	19	95.0	485	3	US-08-600-656-2	Sequence 2, Appl	347	19	95.0	506	4	US-09-232-195-9	Sequence 95, Appl
275	19	95.0	485	3	US-08-600-656-7	Sequence 7, Appl	348	19	95.0	506	4	US-09-232-195-95	Sequence 95, Appl
276	19	95.0	485	3	US-09-170-670-1	Sequence 1, Appl	349	19	95.0	516	4	US-09-986-676A-2	Sequence 2, Appl
277	19	95.0	485	3	US-09-170-670-2	Sequence 2, Appl	350	19	95.0	522	4	US-09-252-991A-30451	Sequence 30451, A
278	19	95.0	485	3	US-09-170-670-6	Sequence 6, Appl	351	19	95.0	524	2	US-08-928-692-12	Sequence 12, Appl
279	19	95.0	485	3	US-09-170-670-7	Sequence 7, Appl	352	19	95.0	524	2	US-08-957-302A-2	Sequence 2, Appl
280	19	95.0	485	3	US-09-170-670-8	Sequence 8, Appl	353	19	95.0	524	3	US-08-942-403-2	Sequence 2, Appl
281	19	95.0	485	3	US-09-133-068-1	Sequence 1, Appl	354	19	95.0	532	4	US-09-339-972-12	Sequence 12, Appl
282	19	95.0	485	3	US-09-133-068-2	Sequence 2, Appl	355	19	95.0	532	4	US-09-252-991A-27288	Sequence 27288, A
283	19	95.0	485	3	US-09-133-068-6	Sequence 6, Appl	356	19	95.0	536	4	US-09-107-532A-6930	Sequence 6930, Ap
284	19	95.0	485	3	US-09-133-068-7	Sequence 7, Appl	357	19	95.0	538	4	US-09-489-039A-13518	Sequence 13518, A
285	19	95.0	485	3	US-09-133-068-8	Sequence 8, Appl	358	19	95.0	540	4	US-09-621-451-2	Sequence 2, Appl
286	19	95.0	485	3	US-09-183-412-1	Sequence 1, Appl	359	19	95.0	540	4	US-10-233-355-2	Sequence 2, Appl
287	19	95.0	485	3	US-09-183-412-2	Sequence 2, Appl	360	19	95.0	544	4	US-09-328-352-4446	Sequence 4446, Ap
288	19	95.0	485	3	US-09-183-412-6	Sequence 6, Appl	361	19	95.0	547	3	US-08-483-577A-149	Sequence 149, App
289	19	95.0	485	3	US-09-183-412-7	Sequence 7, Appl	362	19	95.0	547	3	US-08-897-438-149	Sequence 149, App
290	19	95.0	485	3	US-09-183-412-8	Sequence 8, Appl	363	19	95.0	547	4	US-08-649-518-149	Sequence 149, App
291	19	95.0	485	3	US-09-264-097-5	Sequence 5, Appl	364	19	95.0	550	4	US-09-396-478A-2	Sequence 2, Appl
292	19	95.0	485	3	US-09-264-097-7	Sequence 7, Appl	365	19	95.0	552	4	US-09-489-039A-13735	Sequence 13735, A
293	19	95.0	485	3	US-09-354-191A-1	Sequence 1, Appl	366	19	95.0	557	4	US-09-134-001C-5569	Sequence 5569, Ap
294	19	95.0	485	3	US-09-354-191A-2	Sequence 2, Appl	367	19	95.0	557	4	US-09-489-039A-13795	Sequence 13795, A
295	19	95.0	485	3	US-09-354-191A-7	Sequence 7, Appl	368	19	95.0	557	4	US-09-134-000C-4354	Sequence 4354, Ap
296	19	95.0	485	4	US-09-291-023A-13	Sequence 13, Appl	369	19	95.0	558	4	US-09-252-991A-27678	Sequence 27678, A
297	19	95.0	485	4	US-09-291-023A-18	Sequence 18, Appl	370	19	95.0	566	4	US-09-513-783A-142	Sequence 142, App
298	19	95.0	485	4	US-09-291-023A-19	Sequence 19, Appl	371	19	95.0	567	2	US-08-504-459-4	Sequence 4, Appl
299	19	95.0	485	4	US-09-290-734-1	Sequence 1, Appl	372	19	95.0	567	2	US-08-504-459-6	Sequence 6, Appl
300	19	95.0	485	4	US-09-290-734-2	Sequence 2, Appl	373	19	95.0	571	3	US-08-809-326A-6	Sequence 6, Appl
301	19	95.0	485	4	US-09-290-734-6	Sequence 6, Appl	374	19	95.0	571	4	US-09-689-914A-6	Sequence 6, Appl
302	19	95.0	485	4	US-09-290-734-7	Sequence 7, Appl	375	19	95.0	571	4	US-09-689-916A-6	Sequence 6, Appl
303	19	95.0	485	4	US-09-290-734-8	Sequence 8, Appl	376	19	95.0	571	4	US-09-328-352-4675	Sequence 4675, Ap
304	19	95.0	485	4	US-09-290-734-24	Sequence 24, Appl	377	19	95.0	573	4	US-09-198-452A-332	Sequence 332, App
305	19	95.0	485	4	US-09-290-734-26	Sequence 26, Appl	378	19	95.0	580	4	US-09-635-552A-3	Sequence 3, Appl
306	19	95.0	485	4	US-09-636-352A-12	Sequence 12, Appl	379	19	95.0	587	4	US-08-675-499A-4	Sequence 4, Appl
307	19	95.0	485	4	US-09-417-359A-5	Sequence 5, Appl	380	19	95.0	587	4	US-08-812-008-4	Sequence 4, Appl
308	19	95.0	485	4	US-09-381-687-1	Sequence 1, Appl	381	19	95.0	587	4	US-09-643-657-14	Sequence 14, Appl
309	19	95.0	485	4	US-09-381-687-2	Sequence 2, Appl	382	19	95.0	589	4	US-08-736-770-5	Sequence 5, Appl
310	19	95.0	485	4	US-09-381-687-3	Sequence 3, Appl	383	19	95.0	591	2	US-09-643-657-5	Sequence 5, Appl
311	19	95.0	485	4	US-09-381-687-5	Sequence 5, Appl	384	19	95.0	591	4	US-09-643-657-15	Sequence 15, Appl
312	19	95.0	485	4	US-09-545-586-1	Sequence 1, Appl	385	19	95.0	591	4	US-09-252-991A-23152	Sequence 23152, A
313	19	95.0	485	4	US-09-545-586-2	Sequence 2, Appl	386	19	95.0	597	4	US-09-540-236-2805	Sequence 2805, Ap
314	19	95.0	485	4	US-09-545-586-6	Sequence 6, Appl	387	19	95.0	597	4	US-08-472-534-5	Sequence 5, Appl
315	19	95.0	485	4	US-09-545-586-7	Sequence 7, Appl	388	19	95.0	607	2	US-08-736-770-1	Sequence 1, Appl
316	19	95.0	485	4	US-09-545-586-8	Sequence 8, Appl	389	19	95.0	608	2	US-08-637-670-40	Sequence 40, Appl
317	19	95.0	485	4	US-09-545-586-24	Sequence 24, Appl	390	19	95.0	620	4	US-09-041-991A-6	Sequence 6, Appl
318	19	95.0	485	4	US-09-545-586-26	Sequence 26, Appl	391	19	95.0	623	3		
319	19	95.0	485	4	US-09-540-715A-13	Sequence 13, Appl	392	19	95.0				

393	19	95.0	623	4	US-09-608-533A-6	Sequence 6, Appli	466	19	95.0	651	3	US-08-993-170A-56	Sequence 56, Appl
394	19	95.0	625	4	US-09-661-322A-48	Sequence 48, Appl	467	19	95.0	651	3	US-08-993-170A-58	Sequence 58, Appl
395	19	95.0	626	4	US-09-252-991A-20268	Sequence 20268, A	468	19	95.0	651	3	US-08-993-775B-52	Sequence 52, Appl
396	19	95.0	631	1	US-08-487-890A-111	Sequence 111, App	469	19	95.0	651	3	US-08-993-775B-56	Sequence 56, Appl
397	19	95.0	631	2	US-08-478-435-111	Sequence 111, App	470	19	95.0	651	3	US-08-993-775B-58	Sequence 58, Appl
398	19	95.0	631	2	US-08-337-483-111	Sequence 111, App	471	19	95.0	651	4	US-08-427-770-52	Sequence 52, Appl
399	19	95.0	631	2	US-08-478-373-111	Sequence 111, App	472	19	95.0	651	4	US-08-427-770-56	Sequence 56, Appl
400	19	95.0	631	2	US-08-474-671-111	Sequence 111, App	473	19	95.0	651	4	US-08-427-770-58	Sequence 58, Appl
401	19	95.0	631	3	US-08-483-577A-111	Sequence 111, App	474	19	95.0	651	4	US-08-427-769-52	Sequence 52, Appl
402	19	95.0	631	3	US-08-897-438-111	Sequence 111, App	475	19	95.0	651	4	US-08-427-769-56	Sequence 56, Appl
403	19	95.0	631	4	US-08-637-654-111	Sequence 111, App	476	19	95.0	651	4	US-08-427-769-58	Sequence 58, Appl
404	19	95.0	631	4	US-08-649-518-111	Sequence 111, App	477	19	95.0	652	3	US-08-996-441B-2	Sequence 2, Appli
405	19	95.0	632	3	US-09-232-200-34	Sequence 34, Appl	478	19	95.0	652	3	US-08-996-441B-4	Sequence 4, Appli
406	19	95.0	632	3	US-09-232-200-35	Sequence 35, Appl	479	19	95.0	652	3	US-08-996-441B-6	Sequence 6, Appli
407	19	95.0	632	3	US-09-232-200-39	Sequence 39, Appl	480	19	95.0	652	3	US-08-996-441B-8	Sequence 8, Appli
408	19	95.0	632	4	US-09-232-197-34	Sequence 34, Appl	481	19	95.0	652	3	US-08-996-441B-10	Sequence 10, Appl
409	19	95.0	632	4	US-09-232-197-35	Sequence 35, Appl	482	19	95.0	652	3	US-08-996-441B-12	Sequence 12, Appl
410	19	95.0	632	4	US-09-232-197-39	Sequence 39, Appl	483	19	95.0	652	3	US-08-996-441B-14	Sequence 14, Appl
411	19	95.0	632	4	US-09-232-201-34	Sequence 34, Appl	484	19	95.0	652	3	US-08-996-441B-16	Sequence 16, Appl
412	19	95.0	632	4	US-09-232-201-35	Sequence 35, Appl	485	19	95.0	652	3	US-08-996-441B-18	Sequence 18, Appl
413	19	95.0	632	4	US-09-232-201-39	Sequence 39, Appl	486	19	95.0	652	3	US-08-996-441B-20	Sequence 20, Appl
414	19	95.0	632	4	US-09-232-195-34	Sequence 34, Appl	487	19	95.0	652	3	US-08-996-441B-22	Sequence 22, Appl
415	19	95.0	632	4	US-09-232-195-35	Sequence 35, Appl	488	19	95.0	652	3	US-08-996-441B-24	Sequence 24, Appl
416	19	95.0	632	4	US-09-232-195-39	Sequence 39, Appl	489	19	95.0	652	3	US-08-996-441B-26	Sequence 26, Appl
417	19	95.0	635	4	US-09-107-532A-7135	Sequence 7135, Ap	490	19	95.0	652	3	US-08-996-441B-28	Sequence 28, Appl
418	19	95.0	638	4	US-09-489-039A-8996	Sequence 8996, Ap	491	19	95.0	652	3	US-08-996-441B-30	Sequence 30, Appl
419	19	95.0	639	4	US-09-328-352-4379	Sequence 4379, Ap	492	19	95.0	652	3	US-08-996-441B-32	Sequence 32, Appl
420	19	95.0	641	4	US-09-543-681A-6258	Sequence 6258, Ap	493	19	95.0	652	3	US-08-996-441B-34	Sequence 34, Appl
421	19	95.0	641	4	US-09-232-200-27	Sequence 27, Appl	494	19	95.0	652	3	US-08-996-441B-36	Sequence 36, Appl
422	19	95.0	643	3	US-09-232-200-41	Sequence 41, Appl	495	19	95.0	652	3	US-08-996-441B-38	Sequence 38, Appl
423	19	95.0	643	3	US-09-232-200-42	Sequence 42, Appl	496	19	95.0	652	3	US-08-996-441B-40	Sequence 40, Appl
424	19	95.0	643	3	US-09-232-200-45	Sequence 45, Appl	497	19	95.0	652	3	US-08-996-441B-42	Sequence 42, Appl
425	19	95.0	643	3	US-09-232-200-53	Sequence 53, Appl	498	19	95.0	652	3	US-08-996-441B-44	Sequence 44, Appl
426	19	95.0	643	3	US-09-232-200-71	Sequence 71, Appl	499	19	95.0	652	3	US-08-996-441B-46	Sequence 46, Appl
427	19	95.0	643	4	US-09-232-197-27	Sequence 27, Appl	500	19	95.0	652	3	US-08-996-441B-48	Sequence 48, Appl
428	19	95.0	643	4	US-09-232-197-41	Sequence 41, Appl	501	19	95.0	652	3	US-08-996-441B-50	Sequence 50, Appl
429	19	95.0	643	4	US-09-232-197-42	Sequence 42, Appl	502	19	95.0	652	3	US-08-996-441B-54	Sequence 54, Appl
430	19	95.0	643	4	US-09-232-197-45	Sequence 45, Appl	503	19	95.0	652	3	US-08-996-441B-60	Sequence 60, Appl
431	19	95.0	643	4	US-09-232-197-53	Sequence 53, Appl	504	19	95.0	652	3	US-08-996-441B-62	Sequence 62, Appl
432	19	95.0	643	4	US-09-232-201-27	Sequence 27, Appl	505	19	95.0	652	3	US-08-996-441B-64	Sequence 64, Appl
433	19	95.0	643	4	US-09-232-201-41	Sequence 41, Appl	506	19	95.0	652	3	US-08-996-441B-66	Sequence 66, Appl
434	19	95.0	643	4	US-09-232-201-45	Sequence 45, Appl	507	19	95.0	652	3	US-08-996-441B-68	Sequence 68, Appl
435	19	95.0	643	4	US-09-232-201-45	Sequence 45, Appl	508	19	95.0	652	3	US-08-996-441B-98	Sequence 98, Appl
436	19	95.0	643	4	US-09-232-201-45	Sequence 45, Appl	509	19	95.0	652	3	US-08-996-441B-108	Sequence 108, App
437	19	95.0	643	4	US-09-232-201-53	Sequence 53, Appl	510	19	95.0	652	3	US-08-996-441B-110	Sequence 110, App
438	19	95.0	643	4	US-09-232-201-71	Sequence 71, Appl	511	19	95.0	652	3	US-08-996-441B-111	Sequence 111, App
439	19	95.0	643	4	US-09-343-681A-6345	Sequence 6345, Ap	512	19	95.0	652	3	US-08-993-722A-2	Sequence 2, Appli
440	19	95.0	643	4	US-09-232-195-27	Sequence 27, Appl	513	19	95.0	652	3	US-08-993-722A-4	Sequence 4, Appli
441	19	95.0	643	4	US-09-232-195-41	Sequence 41, Appl	514	19	95.0	652	3	US-08-993-722A-6	Sequence 6, Appli
442	19	95.0	643	4	US-09-232-195-42	Sequence 42, Appl	515	19	95.0	652	3	US-08-993-722A-8	Sequence 8, Appli
443	19	95.0	643	4	US-09-232-195-45	Sequence 45, Appl	516	19	95.0	652	3	US-08-993-722A-10	Sequence 10, Appl
444	19	95.0	643	4	US-09-232-195-55	Sequence 55, Appl	517	19	95.0	652	3	US-08-993-722A-12	Sequence 12, Appl
445	19	95.0	643	4	US-09-232-195-71	Sequence 71, Appl	518	19	95.0	652	3	US-08-993-722A-14	Sequence 14, Appl
446	19	95.0	643	4	US-09-232-195-71	Sequence 71, Appl	519	19	95.0	652	3	US-08-993-722A-16	Sequence 16, Appl
447	19	95.0	644	1	US-08-487-890A-6	Sequence 6, Appli	520	19	95.0	652	3	US-08-993-722A-18	Sequence 18, Appl
448	19	95.0	644	2	US-08-478-435-6	Sequence 6, Appli	521	19	95.0	652	3	US-08-993-722A-20	Sequence 20, Appl
449	19	95.0	644	2	US-08-337-483-6	Sequence 6, Appli	522	19	95.0	652	3	US-08-993-722A-22	Sequence 22, Appl
450	19	95.0	644	2	US-08-478-373-6	Sequence 6, Appli	523	19	95.0	652	3	US-08-993-722A-24	Sequence 24, Appl
451	19	95.0	644	3	US-08-474-671-6	Sequence 6, Appli	524	19	95.0	652	3	US-08-993-722A-26	Sequence 26, Appl
452	19	95.0	644	3	US-08-483-577A-6	Sequence 6, Appli	525	19	95.0	652	3	US-08-993-722A-28	Sequence 28, Appl
453	19	95.0	644	3	US-08-897-438-6	Sequence 6, Appli	526	19	95.0	652	3	US-08-993-722A-30	Sequence 30, Appl
454	19	95.0	644	4	US-08-637-654-6	Sequence 6, Appli	527	19	95.0	652	3	US-08-993-722A-32	Sequence 32, Appl
455	19	95.0	644	4	US-08-649-518-6	Sequence 6, Appli	528	19	95.0	652	3	US-08-993-722A-34	Sequence 34, Appl
456	19	95.0	644	4	US-08-483-577A-148	Sequence 148, App	529	19	95.0	652	3	US-08-993-722A-36	Sequence 36, Appl
457	19	95.0	647	3	US-08-897-438-148	Sequence 148, App	530	19	95.0	652	3	US-08-993-722A-38	Sequence 38, Appl
458	19	95.0	647	4	US-08-649-518-148	Sequence 148, App	531	19	95.0	652	3	US-08-993-722A-40	Sequence 40, Appl
459	19	95.0	651	3	US-08-996-441B-52	Sequence 52, Appl	532	19	95.0	652	3	US-08-993-722A-42	Sequence 42, Appl
460	19	95.0	651	3	US-08-996-441B-56	Sequence 56, Appl	533	19	95.0	652	3	US-08-993-722A-44	Sequence 44, Appl
461	19	95.0	651	3	US-08-996-441B-58	Sequence 58, Appl	534	19	95.0	652	3	US-08-993-722A-46	Sequence 46, Appl
462	19	95.0	651	3	US-08-993-722A-52	Sequence 52, Appl	535	19	95.0	652	3	US-08-993-722A-48	Sequence 48, Appl
463	19	95.0	651	3	US-08-993-722A-56	Sequence 56, Appl	536	19	95.0	652	3	US-08-993-722A-50	Sequence 50, Appl
464	19	95.0	651	3	US-08-993-722A-58	Sequence 58, Appl	537	19	95.0	652	3	US-08-993-722A-54	Sequence 54, Appl
465	19	95.0	651	3	US-08-993-170A-52	Sequence 52, Appl	538	19	95.0	652	3	US-08-993-722A-60	Sequence 60, Appl

685	19	95.0	652	4	US-09-427-769-68	Sequence 68, Appl	758	19	95.0	736	4	US-09-252-991A-27827	Sequence 27827, A
686	19	95.0	652	4	US-09-427-769-98	Sequence 98, Appl	759	19	95.0	748	4	US-09-252-991A-28449	Sequence 28449, A
687	19	95.0	652	4	US-09-427-769-108	Sequence 108, Appl	760	19	95.0	749	4	US-09-563-737-100	Sequence 100, Appl
688	19	95.0	652	4	US-09-427-769-110	Sequence 110, Appl	761	19	95.0	749	4	US-09-252-991A-16877	Sequence 16877, A
689	19	95.0	652	4	US-09-427-769-111	Sequence 111, Appl	762	19	95.0	753	4	US-09-328-352-5412	Sequence 5412, Appl
690	19	95.0	652	5	PCT-US92-00040-1	Sequence 2, Appl	763	19	95.0	771	4	US-09-252-991A-17243	Sequence 17243, A
691	19	95.0	652	6	5187091-2	Patent No. 5187091	764	19	95.0	788	2	US-08-907-166-6	Sequence 6, Appl
692	19	95.0	653	3	US-09-996-441B-100	Sequence 100, Appl	765	19	95.0	788	4	US-09-391-340-6	Sequence 6, Appl
693	19	95.0	653	3	US-08-993-722A-100	Sequence 100, Appl	766	19	95.0	789	4	US-09-390-234-16	Sequence 16, Appl
694	19	95.0	653	3	US-08-993-170A-100	Sequence 100, Appl	767	19	95.0	789	4	US-09-603-311-16	Sequence 16, Appl
695	19	95.0	653	3	US-08-993-775B-100	Sequence 100, Appl	768	19	95.0	791	4	US-09-107-532A-6065	Sequence 6065, Appl
696	19	95.0	653	4	US-09-377-466B-8	Sequence 8, Appl	769	19	95.0	812	4	US-09-513-783A-4	Sequence 4, Appl
697	19	95.0	653	4	US-09-377-466B-10	Sequence 10, Appl	770	19	95.0	812	4	US-09-513-783A-6	Sequence 6, Appl
698	19	95.0	653	4	US-09-377-466B-12	Sequence 12, Appl	771	19	95.0	816	4	US-09-489-039A-10520	Sequence 10520, A
699	19	95.0	653	4	US-09-377-466B-14	Sequence 14, Appl	772	19	95.0	819	4	US-09-651-656-15	Sequence 15, Appl
700	19	95.0	653	4	US-09-377-466B-16	Sequence 16, Appl	773	19	95.0	819	4	US-09-650-855-15	Sequence 15, Appl
701	19	95.0	653	4	US-09-377-466B-18	Sequence 18, Appl	774	19	95.0	821	3	US-09-423-869-24	Sequence 24, Appl
702	19	95.0	653	4	US-09-377-466B-20	Sequence 20, Appl	775	19	95.0	844	3	US-09-029-267-20	Sequence 20, Appl
703	19	95.0	653	4	US-09-377-466B-22	Sequence 22, Appl	776	19	95.0	846	4	US-09-328-352-6648	Sequence 6648, Appl
704	19	95.0	653	4	US-09-377-466B-24	Sequence 24, Appl	777	19	95.0	848	4	US-09-489-039A-13773	Sequence 13773, A
705	19	95.0	653	4	US-09-377-466B-37	Sequence 37, Appl	778	19	95.0	849	4	US-09-252-991A-17953	Sequence 17953, A
706	19	95.0	653	4	US-09-377-466B-39	Sequence 39, Appl	779	19	95.0	873	4	US-09-252-991A-30504	Sequence 30504, A
707	19	95.0	653	4	US-09-427-770-100	Sequence 100, Appl	780	19	95.0	925	4	US-09-252-991A-37057	Sequence 37057, A
708	19	95.0	653	4	US-09-427-769-100	Sequence 100, Appl	781	19	95.0	927	4	US-09-134-001C-4831	Sequence 4831, A
709	19	95.0	654	1	US-08-487-890A-12	Sequence 12, Appl	782	19	95.0	944	4	US-09-328-352-4401	Sequence 4401, Appl
710	19	95.0	654	2	US-08-478-435-12	Sequence 12, Appl	783	19	95.0	972	3	US-08-335-84A-24	Sequence 24, Appl
711	19	95.0	654	2	US-08-337-483-12	Sequence 12, Appl	784	19	95.0	972	4	US-09-129-366-24	Sequence 24, Appl
712	19	95.0	654	2	US-08-478-373-12	Sequence 12, Appl	785	19	95.0	975	4	US-09-543-681A-5755	Sequence 5755, Appl
713	19	95.0	654	2	US-08-474-671-12	Sequence 12, Appl	786	19	95.0	982	4	US-09-023-909A-7	Sequence 7, Appl
714	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	787	19	95.0	990	4	US-09-252-991A-22792	Sequence 22792, A
715	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	788	19	95.0	993	4	US-09-894-998A-50	Sequence 50, Appl
716	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	789	19	95.0	1009	4	US-09-693-146-4	Sequence 4, Appl
717	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	790	19	95.0	1037	4	US-09-894-998A-54	Sequence 54, Appl
718	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	791	19	95.0	1056	4	US-09-513-783A-22	Sequence 22, Appl
719	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	792	19	95.0	1061	4	US-09-252-991A-23691	Sequence 23691, A
720	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	793	19	95.0	1074	2	US-08-470-058-2	Sequence 2, Appl
721	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	794	19	95.0	1074	3	US-09-037-188-2	Sequence 2, Appl
722	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	795	19	95.0	1074	3	US-09-285-310-2	Sequence 2, Appl
723	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	796	19	95.0	1113	4	US-09-894-998A-51	Sequence 51, Appl
724	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	797	19	95.0	1114	4	US-09-975-413A-12	Sequence 12, Appl
725	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	798	19	95.0	1125	4	US-09-513-783A-152	Sequence 152, Appl
726	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	799	19	95.0	1125	4	US-09-513-783A-152	Sequence 152, Appl
727	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	800	19	95.0	1128	4	US-09-252-991A-19672	Sequence 19672, A
728	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	801	19	95.0	1155	4	US-09-543-681A-6286	Sequence 6286, Appl
729	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	802	19	95.0	1410	2	US-08-470-058-4	Sequence 4, Appl
730	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	803	19	95.0	1410	3	US-09-037-188-4	Sequence 4, Appl
731	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	804	19	95.0	1410	3	US-09-285-310-4	Sequence 4, Appl
732	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	805	19	95.0	1477	3	US-08-492-459-10	Sequence 10, Appl
733	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	806	19	95.0	1477	3	US-08-423-752-10	Sequence 10, Appl
734	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	807	19	95.0	1477	3	US-08-945-994-3	Sequence 3, Appl
735	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	808	19	95.0	1477	3	US-08-716-873-24	Sequence 24, Appl
736	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	809	19	95.0	1477	3	US-09-368-431-24	Sequence 24, Appl
737	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	810	19	95.0	1477	3	US-09-414-006-10	Sequence 10, Appl
738	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	811	19	95.0	1477	3	US-09-447-223-10	Sequence 10, Appl
739	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	812	19	95.0	1477	3	US-09-252-991A-28442	Sequence 28442, A
740	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	813	19	95.0	1477	3	US-09-513-783A-22	Sequence 22, Appl
741	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	814	19	95.0	1477	3	US-08-514-975B-2	Sequence 2, Appl
742	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	815	19	95.0	1477	3	PCT-US95-12507-2	Sequence 2, Appl
743	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	816	19	95.0	1477	3	US-08-475-886-2	Sequence 2, Appl
744	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	817	19	95.0	1477	3	US-08-475-886-6	Sequence 6, Appl
745	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	818	19	95.0	1477	3	US-08-397-233-2	Sequence 2, Appl
746	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	819	19	95.0	1477	3	US-08-397-233-2	Sequence 2, Appl
747	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	820	19	95.0	1477	3	US-09-171-387-2	Sequence 2, Appl
748	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	821	19	95.0	1477	3	US-09-653-499-2	Sequence 2, Appl
749	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	822	19	95.0	1477	3	US-09-653-499-4	Sequence 4, Appl
750	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	823	19	95.0	1477	3	US-09-653-499-6	Sequence 6, Appl
751	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	824	19	95.0	1477	3	US-10-104-966-12	Sequence 12, Appl
752	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	825	19	95.0	1477	3	US-10-135-988-2	Sequence 2, Appl
753	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	826	19	95.0	1477	3	US-10-135-988-4	Sequence 4, Appl
754	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	827	19	95.0	1477	3	US-10-135-988-6	Sequence 6, Appl
755	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	828	19	95.0	1477	3	US-10-135-988-6	Sequence 6, Appl
756	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	829	19	95.0	1477	3	US-08-015-973-1	Sequence 1, Appl
757	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	830	19	95.0	1477	3	US-08-448-164-1	Sequence 1, Appl

831	19	95.0	2314	4	US-09-816-703A-2	Sequence 2, Appli	904	18	90.0	149	1	US-08-100-874-2	Sequence 2, Appli
832	19	95.0	2629	2	US-08-751-189-4	Sequence 4, Appli	905	18	90.0	149	3	US-08-963-409-4	Sequence 4, Appli
833	19	95.0	2629	2	US-09-060-836-4	Sequence 4, Appli	906	18	90.0	149	3	US-08-641-873-20	Sequence 20, Appl
834	19	95.0	2629	3	US-09-184-445-4	Sequence 4, Appli	907	18	90.0	152	3	US-08-963-409-5	Sequence 5, Appli
835	19	95.0	5588	3	US-09-036-987A-6	Sequence 6, Appli	908	18	90.0	152	4	US-09-252-991A-18700	Sequence 18700, A
836	19	95.0	5588	3	US-09-370-700-6	Sequence 6, Appli	909	18	90.0	152	4	US-05-252-991A-31418	Sequence 31418, A
837	19	95.0	5588	4	US-09-603-207-6	Sequence 6, Appli	910	18	90.0	157	4	US-05-134-001C-2991	Sequence 2991, Ap
838	19	95.0	5588	4	US-08-714-741-32	Sequence 32, Appl	911	18	90.0	158	1	US-08-611-107-4	Sequence 4, Appli
839	18	90.0	9	4	US-09-372-338-6	Sequence 6, Appli	912	18	90.0	158	3	US-08-422-560A-4	Sequence 4, Appli
840	18	90.0	9	4	US-10-126-752-6	Sequence 6, Appli	913	18	90.0	158	3	US-08-468-793-4	Sequence 4, Appli
841	18	90.0	10	2	US-08-489-228-120	Sequence 120, App	914	18	90.0	160	2	US-08-602-941-1	Sequence 1, Appli
842	18	90.0	10	3	US-08-489-228-120	Sequence 120, App	915	18	90.0	160	2	US-08-961-264-1	Sequence 1, Appli
843	18	90.0	11	2	US-08-934-222-99	Sequence 99, Appl	916	18	90.0	160	4	US-09-442-099A-1	Sequence 1, Appli
844	18	90.0	11	2	US-08-934-222-99	Sequence 99, Appl	917	18	90.0	160	4	US-09-612-342-1	Sequence 1, Appli
845	18	90.0	11	2	US-09-207-621-99	Sequence 99, Appl	918	18	90.0	160	4	US-09-612-421A-1	Sequence 1, Appli
846	18	90.0	11	2	US-08-533-818-99	Sequence 99, Appl	919	18	90.0	160	4	US-09-744-401-1	Sequence 1, Appli
847	18	90.0	11	3	US-09-231-787-99	Sequence 99, Appl	920	18	90.0	162	3	US-09-108-020-50	Sequence 50, Appl
848	18	90.0	11	3	US-09-231-787-99	Sequence 99, Appl	921	18	90.0	172	4	US-09-107-532A-5847	Sequence 5847, Ap
849	18	90.0	11	3	US-08-934-224-99	Sequence 99, Appl	922	18	90.0	179	4	US-09-634-238-296	Sequence 296, App
850	18	90.0	11	3	US-08-933-843-99	Sequence 99, Appl	923	18	90.0	184	4	US-09-489-039A-11491	Sequence 11491, A
851	18	90.0	11	3	US-08-934-223-99	Sequence 99, Appl	924	18	90.0	185	1	US-07-741-940-6	Sequence 6, Appli
852	18	90.0	11	3	US-09-413-432-99	Sequence 99, Appl	925	18	90.0	185	1	US-08-289-548A-6	Sequence 6, Appli
853	18	90.0	19	4	US-08-833-281-10	Sequence 10, Appl	926	18	90.0	185	1	US-08-452-558B-6	Sequence 6, Appli
854	18	90.0	20	1	US-08-658-130-1	Sequence 1, Appli	927	18	90.0	185	1	US-08-452-558B-6	Sequence 6, Appli
855	18	90.0	20	2	US-08-793-825-22	Sequence 22, Appl	928	18	90.0	185	2	US-08-865-336-3	Sequence 3, Appli
856	18	90.0	20	4	US-09-092-000-5	Sequence 5, Appli	929	18	90.0	185	2	US-08-865-336-3	Sequence 3, Appli
857	18	90.0	20	4	US-09-280-068-22	Sequence 22, Appl	930	18	90.0	185	2	US-08-450-582-6	Sequence 6, Appli
858	18	90.0	20	4	US-08-833-281-12	Sequence 12, Appl	931	18	90.0	185	3	US-08-450-582-6	Sequence 6, Appli
859	18	90.0	20	4	US-09-481-593-18	Sequence 18, Appl	932	18	90.0	185	4	US-08-449-731-6	Sequence 6, Appli
860	18	90.0	20	5	PCT-US96-08723-1	Sequence 1, Appli	933	18	90.0	185	4	US-09-138-452A-858	Sequence 858 App
861	18	90.0	22	2	US-08-907-673-1	Sequence 1, Appli	934	18	90.0	187	4	US-09-138-452A-858	Sequence 858 App
862	18	90.0	22	3	US-08-803-397-6	Sequence 6, Appli	935	18	90.0	189	4	US-09-134-000C-4845	Sequence 4845, Ap
863	18	90.0	22	4	US-09-425-597-6	Sequence 6, Appli	936	18	90.0	199	1	US-08-602-262-2	Sequence 2, Appli
864	18	90.0	27	5	PCT-US95-12502-6	Sequence 6, Appli	937	18	90.0	199	3	US-09-004-716-2	Sequence 2, Appli
865	18	90.0	28	4	US-09-033-780A-82	Sequence 82, Appl	938	18	90.0	199	4	US-09-477-510-2	Sequence 2, Appli
866	18	90.0	30	4	US-09-033-780A-81	Sequence 81, Appl	939	18	90.0	199	5	US-03-543-681A-5219	Sequence 5219, Ap
867	18	90.0	38	4	US-09-033-780A-83	Sequence 104, App	940	18	90.0	201	1	PCT-US94-02889-2	Sequence 5, Appli
868	18	90.0	38	4	US-09-033-780A-84	Sequence 84, Appl	941	18	90.0	205	1	US-07-929-380B-5	Sequence 5, Appli
869	18	90.0	39	2	US-09-098-244-15	Sequence 15, Appl	942	18	90.0	208	1	US-08-631-607-3	Sequence 3, Appli
870	18	90.0	39	3	US-09-098-244-15	Sequence 15, Appl	943	18	90.0	208	1	US-09-098-358B-3	Sequence 3, Appli
871	18	90.0	39	4	US-09-375-314-15	Sequence 15, Appl	944	18	90.0	210	1	US-07-741-940-4	Sequence 4, Appli
872	18	90.0	39	4	US-09-767-335-15	Sequence 15, Appl	945	18	90.0	210	1	US-08-289-548A-4	Sequence 4, Appli
873	18	90.0	43	4	US-09-033-780A-89	Sequence 89, Appl	946	18	90.0	210	1	US-08-452-554-4	Sequence 4, Appli
874	18	90.0	44	4	US-09-033-780A-88	Sequence 88, Appl	947	18	90.0	210	1	US-08-452-558B-4	Sequence 4, Appli
875	18	90.0	44	4	US-09-033-780A-88	Sequence 88, Appl	948	18	90.0	210	3	US-08-450-582-4	Sequence 4, Appli
876	18	90.0	54	4	US-09-033-780A-90	Sequence 90, Appl	949	18	90.0	210	4	US-08-449-731-4	Sequence 4, Appli
877	18	90.0	56	4	US-09-033-780A-93	Sequence 93, Appl	950	18	90.0	214	4	US-09-328-352-5256	Sequence 5256, Ap
878	18	90.0	60	4	US-09-134-000C-4258	Sequence 4258, Ap	951	18	90.0	220	4	US-09-795-326-16	Sequence 16, Appl
879	18	90.0	61	4	US-09-107-532A-4993	Sequence 4993, Ap	952	18	90.0	220	4	US-09-107-532A-6803	Sequence 6803, Ap
880	18	90.0	66	4	US-09-543-681A-5898	Sequence 5898, Ap	953	18	90.0	223	1	US-07-708-885B-3	Sequence 3, Appli
881	18	90.0	69	4	US-09-328-352-5719	Sequence 5719, Ap	954	18	90.0	223	1	US-07-708-885B-3	Sequence 3, Appli
882	18	90.0	88	4	US-09-733-210-1423	Sequence 1423, Ap	955	18	90.0	223	1	US-07-708-888A-3	Sequence 3, Appli
883	18	90.0	90	4	US-09-393-634-76	Sequence 76, Appl	956	18	90.0	229	4	US-09-489-039A-9391	Sequence 9391, Ap
884	18	90.0	101	4	US-09-107-532A-6901	Sequence 6901, Ap	957	18	90.0	232	4	US-09-134-000C-3556	Sequence 3556, Ap
885	18	90.0	105	4	US-09-489-039A-10362	Sequence 10362, A	958	18	90.0	235	3	US-09-390-721-4	Sequence 4, Appli
886	18	90.0	113	4	US-09-614-912-186	Sequence 186, App	959	18	90.0	237	3	US-09-248-335-48	Sequence 48, Appl
887	18	90.0	116	4	US-09-489-039A-12512	Sequence 12512, A	960	18	90.0	243	4	US-09-134-000C-3733	Sequence 3733, Ap
888	18	90.0	118	4	US-09-540-236-3531	Sequence 3531, Ap	961	18	90.0	245	4	US-09-543-681A-5699	Sequence 5699, Ap
889	18	90.0	122	4	US-09-540-236-3531	Sequence 3531, Ap	962	18	90.0	247	4	US-09-328-352-7311	Sequence 7311, Ap
890	18	90.0	131	4	US-09-328-352-4806	Sequence 4806, Ap	963	18	90.0	249	4	US-09-252-991A-32233	Sequence 32233, A
891	18	90.0	132	4	US-09-134-000C-3642	Sequence 3642, Ap	964	18	90.0	251	4	US-09-648-004-20	Sequence 20, Appl
892	18	90.0	136	4	US-09-732-210-211	Sequence 211, App	965	18	90.0	251	4	US-09-286-981B-4	Sequence 4, Appli
893	18	90.0	142	1	US-07-951-715A-24	Sequence 24, Appl	966	18	90.0	252	4	US-09-489-039A-13690	Sequence 13690, A
894	18	90.0	142	3	US-08-459-448A-24	Sequence 24, Appl	967	18	90.0	254	4	US-09-138-452A-632	Sequence 632, App
895	18	90.0	142	3	US-08-459-595A-24	Sequence 24, Appl	968	18	90.0	257	2	US-08-637-759B-92	Sequence 92, Appl
896	18	90.0	142	3	US-08-459-504B-24	Sequence 24, Appl	969	18	90.0	257	3	US-08-871-355A-92	Sequence 92, Appl
897	18	90.0	142	3	US-08-459-444-24	Sequence 24, Appl	970	18	90.0	257	4	US-09-201-945-92	Sequence 9, Appl
898	18	90.0	142	3	US-09-547-422-24	Sequence 24, Appl	971	18	90.0	262	1	US-08-622-353-9	Sequence 9, Appli
899	18	90.0	143	3	US-08-946-329A-52	Sequence 52, Appl	972	18	90.0	262	2	US-08-622-352A-11	Sequence 11, Appl
900	18	90.0	143	3	US-09-328-352-7008	Sequence 7008, Ap	973	18	90.0	262	3	US-08-826-390-11	Sequence 11, Appl
901	18	90.0	143	4	US-09-134-000C-4544	Sequence 4544, Ap	974	18	90.0	265	4	US-09-795-326-5	Sequence 6, Appli
902	18	90.0	144	4	US-09-543-681A-5427	Sequence 5427, Ap	975	18	90.0	265	4	US-09-134-000C-5370	Sequence 5370, Ap
903	18	90.0	145	3	US-08-720-625-5	Sequence 5, Appli	976	18	90.0	267	4	US-09-543-681A-6389	Sequence 6389, Ap

977 18 90.0 268 4 US-09-489-039A-7310 Sequence 7310, Ap
978 18 90.0 269 4 US-09-540-236-2149 Sequence 2149, Ap
979 18 90.0 270 4 US-09-489-039A-9313 Sequence 9313, Ap
980 18 90.0 273 4 US-09-489-039A-12815 Sequence 12815, A
981 18 90.0 280 4 US-09-252-991A-23529 Sequence 23529, A
982 18 90.0 281 3 US-09-053-702-2 Sequence 2, Appl
983 18 90.0 281 4 US-09-540-236-2349 Sequence 2349, Ap
984 18 90.0 284 4 US-09-372-422A-8 Sequence 8, Appl
985 18 90.0 284 4 US-09-372-448A-4 Sequence 4, Appl
986 18 90.0 285 4 US-09-314-701-30 Sequence 30, Appl
987 18 90.0 286 4 US-09-489-039A-13264 Sequence 13264, A
988 18 90.0 288 4 US-09-372-422A-12 Sequence 12, Appl
989 18 90.0 288 4 US-09-372-422A-16 Sequence 16, Appl
990 18 90.0 288 4 US-09-372-422A-18 Sequence 18, Appl
991 18 90.0 288 4 US-09-372-448A-2 Sequence 2, Appl
992 18 90.0 289 4 US-09-372-422A-2 Sequence 2, Appl
993 18 90.0 289 4 US-09-372-422A-14 Sequence 14, Appl
994 18 90.0 292 4 US-09-372-422A-4 Sequence 4, Appl
995 18 90.0 292 4 US-09-372-422A-10 Sequence 10, Appl
996 18 90.0 292 4 US-09-489-039A-9431 Sequence 9431, Ap
997 18 90.0 295 4 US-09-134-000C-3576 Sequence 3576, Ap
998 18 90.0 296 4 US-09-372-422A-20 Sequence 20, Appl
999 18 90.0 296 4 US-09-328-352-6437 Sequence 6437, Ap
1000 18 90.0 296 4 US-09-540-236-2843 Sequence 2843, Ap

ALIGNMENTS

RESULT 1
US-09-724-566A-78
Sequence 78, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
NAME/KEY: MOD_RES
LOCATION: 3
OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-81
Query Match 95.0%; Score 19; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 5 VAEF 8
RESULT 3
US-08-197-484-86
Sequence 86, Application US/08197484
Patent No. 641931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Eteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco

STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-86

Query Match 95.0%; Score 19; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 2 VAEF 5

RESULT 4
US-08-197-484-145
Sequence 145, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-145

Query Match 95.0%; Score 19; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 2 VAEF 5

RESULT 5
US-09-724-566A-73
Sequence 73, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 73
LENGTH: 9

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P4-P4'staD-V peptide inhibitor
NAME/KEY: MOD_RES
LOCATION: 5
OTHER INFORMATION: Xaa is statine moiety
US-09-724-566A-73

Query Match 95.0%; Score 19; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 6 VAEF 9

RESULT 6
PCT-US93-02121-86
; Sequence 86, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-86

Query Match 95.0%; Score 19; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 6 VAEF 9

Db 2 VAEF 5

RESULT 7
PCT-US95-02121-145
; Sequence 145, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-145

Query Match 95.0%; Score 19; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 2 VAEF 5

RESULT 8
US-09-724-566A-72
; Sequence 72, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen

APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P10-P4'stad-V peptide inhibitor
FEATURE:
NAME/KEY: MOD_RES
LOCATION: 10
OTHER INFORMATION: Xaa is statine moiety
US-09-724-566A-72

Query Match 95.0%; Score 19; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 11 VAEF 14

RESULT 9
US-09-724-566A-97
Sequence 97, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guripal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: APP-derived fragment P10-P4' (D-V)
US-09-724-566A-97

Query Match 95.0%; Score 19; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 11 VAEF 14
RESULT 10
US-08-733-825-3
Sequence 3, Application US/08733825
Patent No. 5837839
GENERAL INFORMATION:
APPLICANT: Toth, Matthew J.
APPLICANT: Huwylar, Leslie R.
TITLE OF INVENTION: Coding Sequences for Mevalonate
TITLE OF INVENTION: Pyrophosphate Decarboxylase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5837839artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,825
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,652
FILING DATE: 18-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5837839ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-20615/P1/CGC 1834
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4606
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-825-3

Query Match 95.0%; Score 19; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 20 VAEF 23

RESULT 11
US-08-487-890A-69
Sequence 69, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mordin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 69:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-69
Query Match 95.0%; Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 VAEF 5
Db 14 VAEF 17
RESULT 12
US-08-468-763-1
Sequence 1, Application US/08468763
Patent No. 5741671
GENERAL INFORMATION:
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of
TITLE OF INVENTION: Transmembrane Water Channel Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: US
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,996A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-393-996A-1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,763
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,996
FILING DATE: 24-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-763-1
Query Match 95.0%; Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 VAEF 5
Db 14 VAEF 17
RESULT 13
US-08-393-996A-1
Sequence 1, Application US/08393996A
Patent No. 5854702
GENERAL INFORMATION:
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of
TITLE OF INVENTION: Transmembrane Water Channel Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: US
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,996A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-393-996A-1

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 14

US-08-478-435-69
; Sequence 69, Application US/08478435
; Patent No. 5923323
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-462 MIS:V9
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-478-435-69

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VAEF 5
Db 14 VAEF 17

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 15

US-08-337-483-69
; Sequence 69, Application US/08337483
; Patent No. 5923562
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-337-483-69

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 16

US-08-478-373-69
; Sequence 69, Application US/08478373
; Patent No. 5923841
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney

US-08-478-373-69

```

; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-373-69

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 14 VAEF 17

RESULT 17
; US-08-474-671-69
; Sequence 69, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-474-671-69

Query Match 95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 14 VAEF 17

RESULT 18
; US-08-483-577A-69
; Sequence 69, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483

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;; FILING DATE: 08-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/175,116
;; FILING DATE: 29-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/148,968
;; FILING DATE: 08-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-511
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 69:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
JS-08-483-577A-69

Query Match 95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
DB 14 VAEF 17
|||||

RESULT 19
JS-08-897-438-69
; Sequence 69, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968

;; FILING DATE: 08-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-720
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 69:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 35 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-897-438-69

Query Match 95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 14 VAEF 17
|||||

RESULT 20
US-08-637-654-69
; Sequence 69, Application US/08637654
; Patent No. 6358727
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Harkness, Robin E
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew D
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,654
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA94/00616
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-595
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-637-654-69

Query Match 95.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 21

US-08-649-518-69
; Sequence 69, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/649,518

FILING DATE: 17-MAY-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,483

FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/483,577

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-608

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-649-518-69

Query Match 95.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

Db 14 VAEF 17

RESULT 22

US-09-393-634-80
; Sequence 80, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SP, a No. 6558910e1 Family of Taste Receptors
; FILE REFERENCE: 023075-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 80
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR24
US-09-393-634-80

Query Match 95.0%; Score 19; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

Db 14 VAEF 17

RESULT 23

US-09-489-039A-13555
; Sequence 13555, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 13555
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13555

Query Match 95.0%; Score 19; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

Db 5 VAEF 8

RESULT 24

US-09-328-352-7111
; Sequence 7111, Application US/09328352

Qy

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7111
LENGTH: 71
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7111

Query Match 95.0%; Score 19; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
26 VAEF 29

RESULT 25
US-08-321-071A-10
Sequence 10, Application US/08321071A
Patent No. 5672866
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bcl-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,071A
FILING DATE: 11-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10103
FILING DATE: 09-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.121CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-321-071A-10

Query Match 95.0%; Score 19; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
26 VAEF 29

RESULT 26
US-08-894-139-10
Sequence 10, Application US/08894139
Patent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJWANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-139-10

Query Match 95.0%; Score 19; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
23 VAEF 26

RESULT 27
US-09-732-210-1412
Sequence 1412, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1412
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-732-210-1412

Query Match 95.0%; Score 19; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|
|
|
|
Db 11 VAEF 14

RESULT 28
US-07-612-674-12
; Sequence 12, Application US/07612674
; Patent No. 5658792
; GENERAL INFORMATION:
; APPLICANT: NUEL, MARK J.
; APPLICANT: MCCLUNG, J. KEITH
; APPLICANT: STEWART, DAVID A.
; APPLICANT: DANNER, DAVID B.
; TITLE OF INVENTION: AN ANTIPROLIFERATIVE PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/612,674
; FILING DATE: 19901114
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/82332
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3027
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-612-674-12

Query Match 95.0%; Score 19; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|
|
|
|
Db 18 VAEF 21

RESULT 29
US-09-543-681A-5816

; Sequence 5816, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB1
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5816
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5816

Query Match 95.0%; Score 19; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|
|
|
|
Db 21 VAEF 24

RESULT 30
US-08-464-517-8
; Sequence 8, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

JS-08-464-517-8

Query Match 95.0%; Score 19; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 13 VAEF 16

RESULT 31

JS-08-246-361A-8
; Sequence 8, Application US/08246361A
; Patent No. 5998582

GENERAL INFORMATION:

APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/246.361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-246-361A-8

Query Match 95.0%; Score 19; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 13 VAEF 16

RESULT 32

US-08-463-772-8
; Sequence 8, Application US/08463772
; Patent No. 6066501

GENERAL INFORMATION:

APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-MAY-1991
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-772-8

Query Match 95.0%; Score 19; DB 3; Length 100;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 13 VAEF 16

RESULT 33

PCT-US93-05000-8

; Sequence 8, Application PC/TUS9305000

GENERAL INFORMATION:

APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/889,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-8

Query Match 95.0%; Score 19; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 13 VAEF 16

RESULT 34
US-08-580-988A-21
Sequence 21, Application US/08590988A
Patent No. 5856161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE:

DESCRIPTION: protein
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-580-988A-21

Query Match 95.0%; Score 19; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 70 VAEF 73

RESULT 35
US-09-540-236-3612
Sequence 3612, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT?
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3612
LENGTH: 103
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-3612

Query Match 95.0%; Score 19; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 65 VAEF 68

RESULT 36
US-08-464-517-25
Sequence 25, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-25

Query Match 95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
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|
|
|
Db 66 VAEF 69

RESULT 37
US-08-246-361A-25
Sequence 25, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-246-361A-25
Query Match 95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|
|
|
|
Db 66 VAEF 69

RESULT 38
US-08-463-772-25
Sequence 25, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-772-25

Query Match 95.0%; Score 19; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|
|
|
|
Db 66 VAEF 69

RESULT 39
US-09-489-039A-8721
Sequence 8721, Application US/09489039A
Patent No. 6610836

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; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8721
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8721

Query Match          95.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      43 VAEF 46

RESULT 40
PCT-US93-05000-25
; Sequence 25, Application PC/TUS9305000
; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL91-02A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 616-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-25

Query Match          95.0%; Score 19; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      66 VAEF 69

```

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RESULT 41
US-09-489-039A-9915
; Sequence 9915, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9915
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9915

Query Match          95.0%; Score 19; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      50 VAEF 53

RESULT 42
US-09-252-991A-21614
; Sequence 21614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21614
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21614

Query Match          95.0%; Score 19; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      85 VAEF 88

RESULT 43
US-09-489-039A-7200
; Sequence 7200, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27

```

PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7200

Query Match 95.0%; Score 19; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 61 VAEF 64

RESULT 44
US-08-529-055-53
Sequence 53, Application US/08529055
Patent No. 6592876
GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yotter, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-53

Query Match 95.0%; Score 19; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 7 VAEF 10

RESULT 45
US-09-489-039A-12835
Sequence 12835, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12835
LENGTH: 143
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12835

Query Match 95.0%; Score 19; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 138 VAEF 141

RESULT 46
US-09-198-452A-167
Sequence 167, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Grifais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 167
LENGTH: 145
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-167

Query Match 95.0%; Score 19; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 31 VAEF 34

RESULT 47
US-09-134-000C-4292
Sequence 4292, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1

SEQ ID NO 4292
LENGTH: 145
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4292

Query Match 95.0%; Score 19; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 113 VAEF 116

RESULT 48

US-08-460-694-3
Sequence 3, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-694-3

Query Match 95.0%; Score 19; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 66 VAEF 69

RESULT 49

US-08-460-744-3
Sequence 3, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-3

Query Match 95.0%; Score 19; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 66 VAEF 69

RESULT 50

US-07-667-711B-3
Sequence 3, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

```
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-07-667-711B-3
Query Match          95.0%; Score 19; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      66 VAEF 69

RESULT 51
US-08-679-493A-208
; Sequence 208, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 152
; TYPE: PRT
; ORGANISM: blueshark
US-08-679-493A-208

Query Match          95.0%; Score 19; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      92 VAEF 95

RESULT 52
US-09-134-000C-4087
; Sequence 4087, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4087
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4087

Query Match          95.0%; Score 19; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5

; LENGTH: 101 VAEF 104

RESULT 53
US-09-252-991A-20805
; Sequence 20805, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196,136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20805
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20805

Query Match          95.0%; Score 19; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      84 VAEF 87

RESULT 54
US-09-370-838-203
; Sequence 203, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 203
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-203

Query Match          95.0%; Score 19; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      100 VAEF 103

RESULT 55
US-09-540-236-2222
; Sequence 2222, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
```

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2222
LENGTH: 166
TYPE: PRT
ORGANISM: M. catarrhalis
US-09-540-236-2222

Query Match 95.0%; Score 19; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 97 VAEF 100

RESULT 56
US-08-471-058-16
Sequence 16, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-16

Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-594-978a-3.ra1

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2222
LENGTH: 166
TYPE: PRT
ORGANISM: M. catarrhalis
US-09-540-236-2222

Query Match 95.0%; Score 19; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 97 VAEF 100

RESULT 56
US-08-471-058-16
Sequence 16, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-16

Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 122 VAEF 125

RESULT 57
US-08-690-095-3
Sequence 3, Application US/08690095
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Yang, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 293274
US-08-690-095-3

Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 122 VAEF 125

RESULT 58
US-08-471-057-16
Sequence 16, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-16

Query Match 95.0%; Score 19; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 122 VAEF 125

RESULT 59
US-09-113-789-3
Sequence 3, Application US/09113789
Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Yang, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 293274
US-09-113-789-3

Query Match 95.0%; Score 19; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 122 VAEF 125

RESULT 60
US-08-470-865-16
Sequence 16, Application US/08470865
Patent No. 6586395
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,865
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-865-16

Query Match 95.0%; Score 19; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
100.0%	100.0%	95.0%	DB 4	174	0	0	0
Matches	Matches	Conservative			0	0	0
QY	QY	2 VAEF 5					
DB	DB	77 VAEF 80					
<p>US-08-193-977-4</p> <p>Sequence 4, Application US/08193977</p> <p>Patent No. 5625031</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: WEBSTER, KEVIN R.</p> <p>APPLICANT: COLEMAN, KEVIN G.</p> <p>TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND</p> <p>TITLE OF INVENTION: P34CDK2 CELL CYCLE REGULATORY KINASES AND HUMAN</p> <p>TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN</p> <p>NUMBER OF SEQUENCES: 34</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: REED & ROBINS</p> <p>STREET: 635 BRYANT STREET</p> <p>CITY: PALO ALTO</p> <p>STATE: CALIFORNIA</p> <p>COUNTRY: UNITED STATES OF AMERICA</p> <p>ZIP: 94301</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent in Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/193,977</p> <p>FILING DATE: 08-FEB-1994</p> <p>CLASSIFICATION: 530</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: ROBINS, ROBERTA L.</p> <p>REGISTRATION NUMBER: 33,208</p> <p>REFERENCE/DOCKET NUMBER: 5998-0016</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (415) 617-8999</p> <p>TELEFAX: (415) 327-3231</p> <p>INFORMATION FOR SEQ ID NO: 4:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 173 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: peptide</p> <p>US-08-193-977-4</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
100.0%	100.0%	95.0%	DB 1	173	0	0	0
Matches	Matches	Conservative			0	0	0
QY	QY	2 VAEF 5					
DB	DB	100 VAEF 103					
<p>US-09-489-039A-9869</p> <p>Sequence 9869, Application US/09489039A</p> <p>Patent No. 6610836</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Gary Breton et. al</p> <p>TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA</p> <p>TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS</p> <p>FILE REFERENCE: 2709.2004001</p> <p>CURRENT APPLICATION NUMBER: US/09/489,039A</p> <p>CURRENT FILING DATE: 2000-01-27</p> <p>PRIOR APPLICATION NUMBER: US 60/117,747</p> <p>PRIOR FILING DATE: 1999-01-29</p> <p>NUMBER OF SEQ ID NOS: 14342</p> <p>SEQ ID NO 9869</p> <p>LENGTH: 174</p> <p>TYPE: PRT</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
100.0%	100.0%	95.0%	DB 19	174	0	0	0
Matches	Matches	Conservative			0	0	0
QY	QY	2 VAEF 5					
DB	DB	122 VAEF 125					
<p>US-09-328-352-6739</p> <p>Sequence 6739, Application US/09328352</p> <p>Patent No. 6562958</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Gary L. Breton et al.</p> <p>TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER</p> <p>TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS</p> <p>FILE REFERENCE: GTC99-03PA</p> <p>CURRENT APPLICATION NUMBER: US/09/328,352</p> <p>CURRENT FILING DATE: 1999-06-04</p> <p>NUMBER OF SEQ ID NOS: 8252</p> <p>SEQ ID NO 6739</p> <p>LENGTH: 180</p> <p>TYPE: PRT</p> <p>ORGANISM: Acinetobacter baumannii</p> <p>US-09-328-352-6739</p>							
Query Match	Best Local Similarity	Score	DB	Length	Indels	Mismatches	Gaps
100.0%	100.0%	95.0%	DB 4	180	0	0	0
Matches	Matches	Conservative			0	0	0
QY	QY	2 VAEF 5					
DB	DB	8 VAEF 11					
<p>US-09-489-039A-9869</p> <p>Sequence 9869, Application US/09489039A</p> <p>Patent No. 6610836</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Gary Breton et. al</p> <p>TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA</p> <p>TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS</p> <p>FILE REFERENCE: 2709.2004001</p> <p>CURRENT APPLICATION NUMBER: US/09/489,039A</p> <p>CURRENT FILING DATE: 2000-01-27</p> <p>PRIOR APPLICATION NUMBER: US 60/117,747</p> <p>PRIOR FILING DATE: 1999-01-29</p> <p>NUMBER OF SEQ ID NOS: 14342</p> <p>SEQ ID NO 9869</p> <p>LENGTH: 174</p> <p>TYPE: PRT</p>							

RESULT 65
US-09-252-991A-24341
Sequence 24341, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24341
LENGTH: 185
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24341

Query Match 95.0%; Score 19; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
|||
4 VAEF 7

RESULT 66
US-09-543-681A-7313
Sequence 7313, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7313
LENGTH: 189
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7313

Query Match 95.0%; Score 19; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
73 VAEF 76

RESULT 67
US-08-816-241-1
Sequence 1, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/816,241
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646823
US-08-816-241-1

Query Match 95.0%; Score 19; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
104 VAEF 107

RESULT 68
US-09-128-395-1
Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/128,395
APPLICATION NUMBER: US/09/128,395
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0239 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 190 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: PROSTUT09
 ; CLONE: 1646823
 ; US-09-128-395-1

Query Match 95.0%; Score 19; DB 3; Length 190;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 104 VAEF 107

RESULT 69

; US-09-134-000C-3800
 ; Sequence 3800, Application US/09134000C
 ; Patent No. 6617156

; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3800
 ; LENGTH: 194
 ; TYPE: PRT

; ORGANISM: Enterococcus faecalis
 ; US-09-134-000C-3800

Query Match 95.0%; Score 19; DB 4; Length 194;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 115 VAEF 118

RESULT 70

; US-09-232-200-85
 ; Sequence 85, Application US/09232200A
 ; Patent No. 6288213

; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.

; APPLICANT: Gimeno, Ruth E.
 ; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
 ; FILE REFERENCE: WH197-21P3MB

; CURRENT APPLICATION NUMBER: US/09/232,200A
 ; CURRENT FILING DATE: 1999-01-14

; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15

; EARLIER APPLICATION NUMBER: 60/093,491

; EARLIER FILING DATE: 1998-07-20
 ; EARLIER APPLICATION NUMBER: 60/110,941
 ; EARLIER FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 105
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 85
 ; LENGTH: 199
 ; TYPE: PRT
 ; ORGANISM: Aspergillus nidulans
 ; US-09-232-200-85

Query Match 95.0%; Score 19; DB 3; Length 199;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 99 VAEF 102

RESULT 71

; US-09-232-197-85
 ; Sequence 85, Application US/09232197A
 ; Patent No. 6300096

; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.

; APPLICANT: Gimeno, Ruth E.
 ; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
 ; FILE REFERENCE: WH197-21P3MA

; CURRENT APPLICATION NUMBER: US/09/232,197A
 ; CURRENT FILING DATE: 1999-01-14

; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15

; EARLIER APPLICATION NUMBER: 60/093,491
 ; EARLIER FILING DATE: 1998-07-20

; EARLIER APPLICATION NUMBER: 60/110,941
 ; EARLIER FILING DATE: 1998-12-04

; NUMBER OF SEQ ID NOS: 105
 ; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 85
 ; LENGTH: 199

; TYPE: PRT
 ; ORGANISM: Aspergillus nidulans

; US-09-232-197-85

Query Match 95.0%; Score 19; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 99 VAEF 102

RESULT 72

; US-09-232-201-85
 ; Sequence 85, Application US/09232201A
 ; Patent No. 6348321

; GENERAL INFORMATION:
 ; APPLICANT: Stahl, Andreas

; APPLICANT: Hirsch, David J.
 ; APPLICANT: Lodish, Harvey F.

; APPLICANT: Gimeno, Ruth E.
 ; APPLICANT: Tartaglia, Louis A.

; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
 ; FILE REFERENCE: WH197-21P3MC

; CURRENT APPLICATION NUMBER: US/09/232,201A
 ; CURRENT FILING DATE: 1999-01-14

; EARLIER APPLICATION NUMBER: 60/071,374
 ; EARLIER FILING DATE: 1998-01-15

EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
TYPE: PRT
ORGANISM: Aspergillus nidulans
US-09-232-201-85

Query Match 95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 99 VAEF 102

RESULT 73
US-09-232-195-85
; Sequence 85, Application US/09232195A
; Patent No. 6657049
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21D3MD
; CURRENT APPLICATION NUMBER: US/09/232,195A
; CURRENT FILING DATE: 1998-01-04
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-232-195-85

Query Match 95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 99 VAEF 102

RESULT 74
US-09-107-532A-4612
; Sequence 4612, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4612:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...203
SEQUENCE DESCRIPTION: SEQ ID NO: 4612:
US-09-107-532A-4612
Query Match 95.0%; Score 19; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VAEF 5
Db 63 VAEF 66
RESULT 75
US-08-684-024-1
; Sequence 1, Application US/08684024
; Patent No. 5834298
; GENERAL INFORMATION:
; APPLICANT: Beneza, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-584-024-1

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Query Match          95.0%; Score 19; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 VAEF 5
Db      20 VAEF 23

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M protein - protein search, using sw model

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(without alignments)
35.179 Million cell updates/sec

title: US-09-594-978A-3

effect score: 20

sequence: 1 XVAEF 5

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total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Published Applications AA:*
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12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
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2	19	95.0	8	10	US-09-791-393-206	Sequence 206, App
3	19	95.0	8	10	US-09-791-393-206	Sequence 206, App
4	19	95.0	8	14	US-10-128-711-86	Sequence 86, App
5	19	95.0	9	14	US-10-128-711-145	Sequence 145, App
6	19	95.0	10	12	US-09-908-943A-197	Sequence 197, App
7	19	95.0	12	12	US-09-908-943A-196	Sequence 196, App
8	19	95.0	12	14	US-10-032-818-34	Sequence 34, App
9	19	95.0	13	14	US-10-239-313A-379	Sequence 379, App
10	19	95.0	15	14	US-10-119-528-7	Sequence 7, Appli
11	19	95.0	20	10	US-09-171-432A-62	Sequence 62, Appl
12	19	95.0	20	10	US-09-171-432A-63	Sequence 63, Appl
13	19	95.0	25	10	US-09-171-432A-65	Sequence 65, Appl
14	19	95.0	28	9	US-09-864-761-47201	Sequence 47201, A
15	19	95.0	28	12	US-10-424-599-216297	Sequence 216297,

Sequence 69, Appl
Sequence 570, App
Sequence 49, Appl
Sequence 45, Appl
Sequence 71, Appl
Sequence 37202, A
Sequence 183032,
Sequence 183032,
Sequence 171318,
Sequence 38166, A
Sequence 205632,
Sequence 192247,
Sequence 233502,
Sequence 63, Appl
Sequence 67, Appl
Sequence 4, Appl
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Sequence 215734,
Sequence 260762,
Sequence 75, Appl
Sequence 214930,
Sequence 45291, A
Sequence 80, Appl
Sequence 40, Appl
Sequence 80, Appl
Sequence 80, Appl
Sequence 45716, A
Sequence 5596, Ap
Sequence 185385,
Sequence 28645, A
Sequence 202605,
Sequence 274981, A
Sequence 3348, A
Sequence 2320, A
Sequence 10, Appl
Sequence 9071, Ap
Sequence 156128,
Sequence 261424,
Sequence 23204,
Sequence 211908,
Sequence 7493, A
Sequence 32709, A
Sequence 162039,
Sequence 262701,
Sequence 368, App
Sequence 216097,
Sequence 14, Appl
Sequence 5282, Ap
Sequence 125, App
Sequence 155636,
Sequence 201853,
Sequence 11224, A
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Sequence 58489, A
Sequence 58530, A
Sequence 66960, A
Sequence 68774, A
Sequence 180307,
Sequence 360, App
Sequence 245830,
Sequence 200533,
Sequence 204269,
Sequence 79, Appl
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Sequence 7494, Ap
Sequence 196121,
Sequence 245993,
Sequence 30, Appl
Sequence 90, Appl
Sequence 4520, Ap
Sequence 357, App
Sequence 1338, Ap

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90	19	95.0	110	12	US-10-424-599-257728,	Sequence 257728,	163	19	95.0	189	14	US-10-238-075-1037	Sequence 1037, Ap
91	19	95.0	111	12	US-10-424-599-192406,	Sequence 192406,	164	19	95.0	191	12	US-10-282-122A-77681	Sequence 77681, A
92	19	95.0	112	12	US-10-424-599-189066	Sequence 189066,	165	19	95.0	192	12	US-10-424-599-269537	Sequence 269537,
93	19	95.0	115	12	US-10-424-599-222263,	Sequence 222263,	166	19	95.0	193	9	US-09-888-911-4	Sequence 4, Appli
94	19	95.0	117	12	US-10-424-599-206883	Sequence 206883,	167	19	95.0	193	12	US-10-425-114-43750	Sequence 43750, A
95	19	95.0	117	12	US-10-424-599-221584	Sequence 221584,	168	19	95.0	193	14	US-10-156-761-13355	Sequence 13355, A
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98	19	95.0	119	12	US-10-424-599-240644	Sequence 240644,	170	19	95.0	195	12	US-10-424-599-238939	Sequence 238939,
99	19	95.0	119	14	US-10-563-568-12	Sequence 12, Appl	171	19	95.0	195	12	US-10-424-599-238939	Sequence 238939,
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101	19	95.0	120	12	US-10-424-599-276785	Sequence 276785,	173	19	95.0	197	15	US-09-366-880A-2	Sequence 2, Appli
102	19	95.0	122	11	US-09-864-408A-526	Sequence 526, App	174	19	95.0	198	12	US-10-425-114-47425	Sequence 47425, A
103	19	95.0	122	11	US-10-424-599-173522	Sequence 173522,	175	19	95.0	199	12	US-10-405-877-85	Sequence 85, Appl
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105	19	95.0	129	15	US-10-259-636-68	Sequence 68, Appl	177	19	95.0	200	12	US-10-424-599-220990	Sequence 220990,
106	19	95.0	130	12	US-10-424-599-184879	Sequence 184879,	178	19	95.0	201	12	US-10-276-162-2	Sequence 2, Appli
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108	19	95.0	131	9	US-09-738-636-5204	Sequence 5204, Ap	180	19	95.0	201	15	US-10-282-122A-60863	Sequence 60863, A
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113	19	95.0	135	12	US-10-424-599-53378	Sequence 53378, A	185	19	95.0	205	12	US-10-634-548-31	Sequence 31, Appl
114	19	95.0	138	12	US-10-112-944-912	Sequence 912, App	186	19	95.0	205	9	US-09-922-217-1108	Sequence 1108, Ap
115	19	95.0	138	12	US-10-156-761-8842	Sequence 8842, Ap	187	19	95.0	205	12	US-10-296-115-1330	Sequence 1330, Ap
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117	19	95.0	140	15	US-10-108-260A-3390	Sequence 3390, Ap	189	19	95.0	205	12	US-10-335-977-7980	Sequence 7980, Ap
118	19	95.0	143	15	US-10-385-415-119	Sequence 119, App	190	19	95.0	205	12	US-10-025-380-1108	Sequence 1108, Ap
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124	19	95.0	148	12	US-10-424-599-219032	Sequence 219032,	196	19	95.0	213	9	US-09-943-671-17	Sequence 17, Appl
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126	19	95.0	152	13	US-10-016-157A-151	Sequence 151, App	198	19	95.0	213	14	US-10-043-487-364	Sequence 164, App
127	19	95.0	156	12	US-10-424-599-254161	Sequence 254161,	199	19	95.0	213	14	US-10-405-877-17	Sequence 17, Appl
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131	19	95.0	164	9	US-09-738-973-203	Sequence 203, App	203	19	95.0	215	14	US-10-326-671-69	Sequence 69, Appl
132	19	95.0	164	9	US-09-854-133-203	Sequence 203, App	204	19	95.0	215	12	US-10-424-599-162041	Sequence 162041,
133	19	95.0	164	11	US-09-864-408A-1148	Sequence 1148, Ap	205	19	95.0	220	12	US-10-384-060-76	Sequence 76, Appl
134	19	95.0	164	14	US-10-144-649A-203	Sequence 203, App	206	19	95.0	221	12	US-10-424-599-266598	Sequence 266598,
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137	19	95.0	167	9	US-09-925-300-981	Sequence 981, App	209	19	95.0	222	9	US-09-925-300-1639	Sequence 157122,
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142	19	95.0	175	12	US-10-335-977-5868	Sequence 12575, A	214	19	95.0	224	12	US-10-424-599-151189	Sequence 1944, Ap
143	19	95.0	175	14	US-10-156-761-12575	Sequence 12, Appl	215	19	95.0	224	15	US-10-094-749-1944	Sequence 262650,
144	19	95.0	175	14	US-10-247-671-184	Sequence 184, App	216	19	95.0	225	12	US-10-351-334-155	Sequence 14916, A
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146	19	95.0	178	9	US-09-925-301-914	Sequence 914, App	218	19	95.0	225	12	US-10-424-599-262650	Sequence 14289, A
147	19	95.0	178	9	US-09-925-297-532	Sequence 532, App	219	19	95.0	225	15	US-10-369-493-14989	Sequence 14859, A
148	19	95.0	178	15	US-10-264-049-3578	Sequence 3578, Ap	220	19	95.0	226	9	US-09-738-626-4027	Sequence 5, Appli
149	19	95.0	180	12	US-10-424-599-170244	Sequence 170244,	221	19	95.0	226	12	US-10-424-599-239616	Sequence 7, Appli
150	19	95.0	180	14	US-10-156-761-12228	Sequence 12228, A	222	19	95.0	227	16	US-10-275-505-7	Sequence 47426, A
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152	19	95.0	184	12	US-10-335-977-7979	Sequence 17, Appl	224	19	95.0	228	13	US-10-051-325-8	Sequence 143683,
153	19	95.0	187	9	US-09-804-156-17	Sequence 9, Appli	225	19	95.0	229	12	US-10-424-599-143683	Sequence 4027, Ap
154	19	95.0	187	13	US-10-125-459-9	Sequence 9, Appli	226	19	95.0	230	9	US-09-738-626-4027	Sequence 51174, A
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160	19	95.0	188	12	US-10-282-122A-78177	Sequence 78177, A	232	19	95.0	231	12	US-10-425-114-5374	Sequence 57318, A
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236	19	95.0	232	15	US-10-340-792-40	Sequence 40, Appl	309	19	95.0	270	12	US-10-262-511-148	Sequence 148, App
237	19	95.0	234	12	US-10-425-114-45098	Sequence 45098, A	310	19	95.0	270	15	US-10-369-494-10566	Sequence 10566, A
238	19	95.0	234	12	US-10-425-114-63330	Sequence 63330, A	311	19	95.0	271	15	US-10-264-237-2658	Sequence 2658, Ap
239	19	95.0	234	12	US-10-425-114-64490	Sequence 64490, A	312	19	95.0	272	10	US-09-764-891-2960	Sequence 2960, Ap
240	19	95.0	236	9	US-09-815-242-11738	Sequence 11738, A	313	19	95.0	272	12	US-10-282-122A-70355	Sequence 70355, A
241	19	95.0	236	12	US-10-412-699B-1410	Sequence 1410, Ap	314	19	95.0	273	14	US-10-182-447-3	Sequence 3, Appl1
242	19	95.0	236	15	US-10-421-138A-308	Sequence 308, App	315	19	95.0	274	12	US-10-282-122A-51559	Sequence 51559, A
243	19	95.0	236	15	US-10-374-780A-1221	Sequence 1221, Ap	316	19	95.0	274	12	US-10-282-122A-74371	Sequence 74371, A
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252	19	95.0	243	10	US-09-870-406A-44	Sequence 44, Appl	325	19	95.0	281	14	US-10-314-639-58	Sequence 58, Appl
253	19	95.0	243	12	US-10-424-599-257488	Sequence 257488, A	326	19	95.0	281	14	US-10-156-761-9102	Sequence 9102, Ap
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258	19	95.0	246	9	US-09-771-161A-129	Sequence 129, App	331	19	95.0	283	12	US-10-425-114-43988	Sequence 43988, A
259	19	95.0	246	14	US-10-156-761-13663	Sequence 13663, A	332	19	95.0	283	12	US-10-329-624-5203	Sequence 5203, Ap
260	19	95.0	246	15	US-10-421-138A-311	Sequence 311, App	333	19	95.0	284	12	US-10-425-114-58685	Sequence 58685, A
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265	19	95.0	249	14	US-10-156-761-9204	Sequence 9204, Ap	338	19	95.0	286	12	US-10-262-511-144	Sequence 144, App
266	19	95.0	249	15	US-10-409-701-15	Sequence 15, Appl	339	19	95.0	287	12	US-10-424-599-147161	Sequence 147161, A
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272	19	95.0	254	12	US-10-262-511-150	Sequence 150, App	345	19	95.0	289	12	US-10-425-114-47186	Sequence 47186, A
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275	19	95.0	255	14	US-10-260-539-40	Sequence 40, Appl	348	19	95.0	290	15	US-10-369-493-15865	Sequence 15865, A
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278	19	95.0	256	15	US-10-374-780A-1247	Sequence 1247, Ap	351	19	95.0	291	15	US-10-292-798-2070	Sequence 2070, Ap
279	19	95.0	257	9	US-09-738-626-6642	Sequence 6642, Ap	352	19	95.0	291	15	US-10-564-237-2770	Sequence 2770, Ap
280	19	95.0	257	14	US-10-106-698-5221	Sequence 5221, Ap	353	19	95.0	292	15	US-10-369-493-5341	Sequence 5341, Ap
281	19	95.0	257	15	US-10-139-794-16	Sequence 16, Appl	354	19	95.0	292	15	US-10-369-493-15494	Sequence 15494, A
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283	19	95.0	258	12	US-10-282-122A-66426	Sequence 66426, A	356	19	95.0	293	14	US-10-156-761-14726	Sequence 14726, A
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285	19	95.0	258	14	US-10-424-599-248969	Sequence 303, App	358	19	95.0	294	14	US-10-336-699-12	Sequence 12, Appl
286	19	95.0	260	12	US-10-425-114-46566	Sequence 46566, A	359	19	95.0	294	14	US-10-306-762-155	Sequence 155, App
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289	19	95.0	261	14	US-10-011-364-10	Sequence 10, Appl	362	19	95.0	295	14	US-10-282-122A-50243	Sequence 50243, A
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293	19	95.0	263	9	US-09-800-729-88	Sequence 88, Appl	366	19	95.0	299	10	US-09-310-332-1	Sequence 1, Appli
294	19	95.0	263	10	US-09-746-783-2	Sequence 2, Appli	367	19	95.0	299	10	US-09-832-522-73	Sequence 73, Appl
295	19	95.0	263	11	US-09-833-245-2213	Sequence 2213, Ap	368	19	95.0	299	12	US-10-364-861-35	Sequence 35, Appl
296	19	95.0	264	14	US-10-182-447-1	Sequence 1, Appli	369	19	95.0	299	13	US-10-059-964-46	Sequence 46, Appl
297	19	95.0	265	12	US-10-282-122A-52414	Sequence 52414, A	370	19	95.0	299	14	US-10-314-639-46	Sequence 46, Appl
298	19	95.0	265	12	US-10-425-114-41437	Sequence 41437, A	371	19	95.0	299	14	US-10-383-982-35	Sequence 35, Appl
299	19	95.0	265	12	US-10-425-114-62005	Sequence 62005, A	372	19	95.0	299	9	US-09-738-626-3734	Sequence 3734, Ap
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587	19	95.0	379	14	US-10-157-223-6	Sequence 6, Appl	660	19	95.0	408	9	US-10-081-816-14	Sequence 14, Appl
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ALIGNMENTS

RESULT 1
 US-09-791-378-343
 ; Sequence 343, Application US/09791378
 ; Patent No. US20020142303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Parekh, Rajesh
 ; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
 ; FILE REFERENCE: 9195-061-999
 ; CURRENT APPLICATION NUMBER: US/09/791,378
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-02-23
 ; NUMBER OF SEQ ID NOS: 677
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 343
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens

Query Match 95.0%; Score 19; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 2 VAEF 5

RESULT 2
 US-09-791-393-206

Sequence 206, Application US/09791393
 ; Publication No. US20030032200A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Rohlff, Christian
 ; TITLE OF INVENTION: Proteins, Genes and Their Use for
 ; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 ; TITLE OF INVENTION: and Unipolar Depression
 ; FILE REFERENCE: 2543-1-001 N1
 ; CURRENT APPLICATION NUMBER: US/09/791,393
 ; CURRENT FILING DATE: 2002-01-02
 ; EARLIER FILING DATE: 2000-02-24
 ; EARLIER FILING DATE: 2000-02-24
 ; EARLIER FILING DATE: 2000-12-08
 ; EARLIER FILING DATE: 2000-12-08
 ; EARLIER FILING DATE: 2000-12-12
 ; NUMBER OF SEQ ID NOS: 308
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 ; TYPE: PRT
 ; ORGANISM: homo sapien

Query Match 95.0%; Score 19; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
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Qy 2 VAEF 5
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RESULT 3

US-09-791-389-206
 ; Sequence 206, Application US/09791389
 ; Publication No. US20030032773A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Rohlff, Christian
 ; APPLICANT: Terrett, Jonathan Alexander
 ; APPLICANT: Tyson, Kerry Louise
 ; TITLE OF INVENTION: Proteins, Genes and Their Use for
 ; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
 ; TITLE OF INVENTION: and Unipolar Depression
 ; FILE REFERENCE: 2543-1-001 N2
 ; CURRENT APPLICATION NUMBER: US/09/791,389
 ; CURRENT FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2001-02-23
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR FILING DATE: 2000-12-12
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 206
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: homo sapien

Query Match 95.0%; Score 19; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 2 VAEF 5

RESULT 4

S-10-128-711-86

Sequence 86, Application US/10128711

Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.

CHESTNUT, Robert W.

SETTE, Alessandro D.

CELIS, Esteban

GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Stuart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10128,711

FILING DATE: 22-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 86:

S-10-128-711-86

Query Match 95.0%; Score 19; DB 14; Length 9;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5

b 2 VAEF 5

RESULT 5

S-10-128-711-145

Sequence 145, Application US/10128711

Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.

RESULT 6

US-09-908-943A-197

Sequence 197, Application US/09908943A

Publication No. US20030017991A1

GENERAL INFORMATION:

APPLICANT: Yan, Riqiang

APPLICANT: Tomasselli, Alfredo G.

APPLICANT: Gurney, Mark E.

APPLICANT: Emmons, Thomas L.

APPLICANT: Bienkowski, Mike J.

APPLICANT: Heinrichson, Robert L.

TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY

FILE REFERENCE: 29915/00281A.US1

CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-10-128-711-145

Query Match 95.0%; Score 19; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 2 VAEF 5

```

; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 10
; TYPE: PRT
; ORGANISM: synthetic peptide sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(4)
; OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
JS-09-908-943A-197

Query Match          95.0%; Score 19; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 5 VAEF 8

RESULT 7
US-09-908-943A-196
; Sequence 196, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riciang
; APPLICANT: Tomasselli, Alfredo G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowski, Mike J.
; APPLICANT: Heinrichson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908,943A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,795
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: synthetic peptide sequence
; NAME/KEY: SITE
; LOCATION: (4)..(4)
; OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
US-09-908-943A-196

Query Match          95.0%; Score 19; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 5 VAEF 8

RESULT 8
US-10-032-818-34
; Sequence 34, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.

```

```

; APPLICANT: Koelsch, Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 2932.1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-032-818-34

Query Match          95.0%; Score 19; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 5 VAEF 8

RESULT 9
US-10-239-313A-379
; Sequence 379, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: BECK, Alain
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 379
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-239-313A-379

Query Match          95.0%; Score 19; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 4 VAEF 7

RESULT 10
US-10-119-528-7
; Sequence 7, Application US/10119528
; Publication No. US20030175722A1
; GENERAL INFORMATION:
; APPLICANT: Mann, M.
; APPLICANT: Mortensen, P.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES

```

FILE REFERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,551
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/285,362
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: Arabidopsis thaliana
-10-119-528-7

Query Match 95.0%; Score 19; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
10 VAEF 13

RESULT 11
3-09-171-432A-62
Sequence 62, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yuri E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polypeptide
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171.432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /label=YK-1368

3-09-171-432A-62
US-09-171-432A-62

Query Match 95.0%; Score 19; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
13 VAEF 16

RESULT 12
US-09-171-432A-63
Sequence 63, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
APPLICANT: Khudyakov, Yuri E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polypeptide
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171.432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /label=YK-1369

US-09-171-432A-63

Query Match 95.0%; Score 19; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
4 VAEF 7

RESULT 13
US-09-171-432A-65
Sequence 65, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.

APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polypeptide
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /label=YK-1832

JS-09-171-432A-65
Query Match 95.0%; Score 19; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 3 VAEF 6

RESULT 14
US-09-864-761-47201
; Sequence 47201, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Ches, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47201
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005772.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
US-09-864-761-47201

Query Match 95.0%; Score 19; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 4 VAEF 7

RESULT 15
US-10-424-599-216297
; Sequence 216297, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 216297
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37345C.1.pap
US-10-424-599-216297

Query Match 95.0%; Score 19; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
10 VAEF 13

US-10-242-355-570
Sequence 69, Application US/10043344
Publication No. US20030088086A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Harkness, Robin E.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Murdin, Andrew D.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
FILE REFERENCE: 1038-1221 MIS
CURRENT APPLICATION NUMBER: US/10/043,344
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/649,518
PRIOR FILING DATE: 1996-05-17
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 35
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-043-344-69

Query Match 95.0%; Score 19; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
14 VAEF 17

US-10-242-355-570
Sequence 570, Application US/10242355
Publication No. US20030235831A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC003C1
CURRENT APPLICATION NUMBER: US/10/242,355
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,897
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14

PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 570
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens
US-10-242-355-570

Query Match 95.0%; Score 19; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
14 VAEF 17

US-10-430-752A-49
Sequence 49, Application US/10430752A
Publication No. US20040005669A1
GENERAL INFORMATION:
APPLICANT: Stahl, Stefan
APPLICANT: Jonasson, Per
APPLICANT: Nygren, Per-Ake
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
FILE REFERENCE: 11541-003001
CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/485,286
PRIOR FILING DATE: 2000-02-07
PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: GB 9716790.2
PRIOR FILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 37
TYPE: PRT
ORGANISM: Verasper moseri
US-10-430-752A-49

Query Match 95.0%; Score 19; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
24 VAEF 27

US-10-430-752A-45
Sequence 45, Application US/10430752A
Publication No. US20040005669A1
GENERAL INFORMATION:
APPLICANT: Stahl, Stefan
APPLICANT: Jonasson, Per
APPLICANT: Nygren, Per-Ake
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
FILE REFERENCE: 11541-003001
CURRENT APPLICATION NUMBER: US/10/430,752A
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 09/485,286
PRIOR FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: GB 9716790.2
PRIOR FILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 38
TYPE: PRT
ORGANISM: Lophius piscatorius
US-10-430-752A-45

Query Match 95.0%; Score 19; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
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|
|
b 25 VAEF 28

RESULT 20
US-10-372-003A-71
Sequence 71, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRI40.001CPI
CURRENT APPLICATION NUMBER: US/10/372.003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic clone BGf13 with first open reading
OTHER INFORMATION: frame

Query Match 95.0%; Score 19; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
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|
|
b 28 VAEF 31

RESULT 21
US-09-864-761-37202
Sequence 37202, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/508,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37202
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035530.11
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95
OTHER INFORMATION: SWISSPROT HIT: P33485, EVALUE 3.60e-00
OTHER INFORMATION: EST_HUMAN HIT: AI765888.1, EVALUE 3.00e-18
US-09-864-761-37202

Query Match 95.0%; Score 19; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
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|
|
b 40 VAEF 43

RESULT 22
US-10-424-599-183032
Sequence 183032, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 183032
LENGTH: 43
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_136291C.1.pap
1-10-424-599-183032

Query Match 95.0%; Score 19; DB 12; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
25 VAEF 28

3-10-424-599-171318
Sequence 171318, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 171318
LENGTH: 45
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_125715C.1.pap
3-10-424-599-171318

Query Match 95.0%; Score 19; DB 12; Length 45;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
20 VAEF 23

3-09-864-761-38166
Sequence 38166, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205632
LENGTH: 52

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38166
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049833.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: SWISSPROT HIT: P11298, EVALUATE 7.90e+00
US-09-864-761-38166

Query Match 95.0%; Score 19; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
3 VAEF 6

RESULT 25
US-10-424-599-205632
Sequence 205632, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205632
LENGTH: 52

TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep
JS-10-424-599-205632

Query Match 95.0%; Score 19; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
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|
|
b 26 VAEF 29

RESULT 26

JS-10-424-599-192247
; Sequence 192247, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 192247
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1561C.1.pep
JS-10-424-599-192247

Query Match 95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
|
|
|
|
b 50 VAEF 53

RESULT 27

JS-10-424-599-233502
; Sequence 233502, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233502
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52879C.1.pep
JS-10-424-599-233502

Query Match 95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|
|
|
|
Db 24 VAEF 27

RESULT 28

US-10-372-003A-63
; Sequence 63, Application US/10372003A
; Publication No. US20030215846A1
; GENERAL INFORMATION:
; APPLICANT: Watt, Paul
; APPLICANT: Thomas, Wayne
; APPLICANT: Hopkins, Richard
; TITLE OF INVENTION: Methods of constructing and screening
; FILE REFERENCE: FBIC40.001CPI
; CURRENT APPLICATION NUMBER: US/10/372,003A
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/568,229
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,711
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic clone BGF05 with first open reading
; OTHER INFORMATION: frame
US-10-372-003A-63

Query Match 95.0%; Score 19; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
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|
|
Db 28 VAEF 31

RESULT 29

US-10-372-003A-67
; Sequence 67, Application US/10372003A
; Publication No. US20030215846A1
; GENERAL INFORMATION:
; APPLICANT: Watt, Paul
; APPLICANT: Thomas, Wayne
; APPLICANT: Hopkins, Richard
; TITLE OF INVENTION: Methods of constructing and screening
; FILE REFERENCE: FBIC40.001CPI
; CURRENT APPLICATION NUMBER: US/10/372,003A
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/568,229
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,711
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic clone BGF06 with first open reading
; OTHER INFORMATION: frame
US-10-372-003A-67

Query Match 95.0%; Score 19; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 28 VAEF 31
;
RESULT 30
S-10-219-329-4
Sequence 4, Application US/10219329
Publication No. US20030096757A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Weart, Ilona f
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US/10/219,329
PRIOR FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
S-10-219-329-4
Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 31 VAEF 34
;
RESULT 31
S-10-153-185-4
Sequence 4, Application US/10153185
Publication No. US2003014859A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.034U81
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
S-10-153-185-4
Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 31 VAEF 34
;
RESULT 32
S-10-219-561-4
Sequence 4, Application US/10219561
Publication No. US20030166567A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
APPLICANT: Villanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.008U52
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/153,185
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-561-4
Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 31 VAEF 34
;
RESULT 33
US-10-424-599-215734
Sequence 215734, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215734
LENGTH: 57
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep
US-10-424-599-215734
Query Match 95.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 48 VAEF 51
;
RESULT 34
US-10-424-599-260762
Sequence 260762, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
```

```
Sequence 4, Application US/10219561
Publication No. US20030166567A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
APPLICANT: Villanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.008U52
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/153,185
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-561-4
Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 31 VAEF 34
;
RESULT 33
US-10-424-599-215734
Sequence 215734, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215734
LENGTH: 57
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pep
US-10-424-599-215734
Query Match 95.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 2 VAEF 5
; ||||
; 48 VAEF 51
;
RESULT 34
US-10-424-599-260762
Sequence 260762, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
```

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260762
LENGTH: 57
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_77490C.1.pep
US-10-424-599-260762

Query Match 95.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 4 VAEF 7

RESULT 35
US-10-372-003A-75
Sequence 75, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
FILE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75
LENGTH: 57
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic clone BGF24 with first open reading
US-10-372-003A-75

Query Match 95.0%; Score 19; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 28 VAEF 31

RESULT 36
US-10-424-599-214930
Sequence 214930, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep
US-10-424-599-214930

Query Match 95.0%; Score 19; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 13 VAEF 16

RESULT 37
US-09-864-761-45291
Sequence 45291, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45291

```

LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EST_HUMAN HIT: AV756022.1, EVALUE 6.00e-28
OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
3-09-864-761-45291

Query Match          95.0%; Score 19; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f      2 VAEF 5
      ||||
      8 VAEF 11

RESULT 38
3-09-393-634-80
Sequence 80, Application US/09393634
Patent No. US20020051997A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
FILE REFERENCE: 02307E-0980000US
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GR24
S-09-393-634-80

Query Match          95.0%; Score 19; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      ||||
      14 VAEF 17

RESULT 39
S-09-864-408A-40
Sequence 40, Application US/09864408A
Publication No. US2004000947A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US2004000947A1el Human Polynucleotides and Polypeptides Encod
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24

LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EST_HUMAN HIT: AV756022.1, EVALUE 6.00e-28
OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
3-09-864-761-45291

Query Match          95.0%; Score 19; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f      2 VAEF 5
      ||||
      8 VAEF 11

RESULT 38
3-09-393-634-80
Sequence 80, Application US/09393634
Patent No. US20020051997A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
FILE REFERENCE: 02307E-0980000US
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GR24
S-09-393-634-80

Query Match          95.0%; Score 19; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      ||||
      14 VAEF 17

RESULT 39
S-09-864-408A-40
Sequence 40, Application US/09864408A
Publication No. US2004000947A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US2004000947A1el Human Polynucleotides and Polypeptides Encod
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24

LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EST_HUMAN HIT: AV756022.1, EVALUE 6.00e-28
OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
3-09-864-761-45291

Query Match          95.0%; Score 19; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
      3 VAEF 6

RESULT 40
US-10-364-861-80
Sequence 80, Application US/10364861
Publication No. US20040038312A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Hoon, Mark
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: T2R, a No. US20040038312A1el Family of Taste Receptors
FILE REFERENCE: 02307E-0980300US
CURRENT APPLICATION NUMBER: US/10/364,861
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human T2R24, GR24 or SF24
US-10-364-861-80

Query Match          95.0%; Score 19; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
      14 VAEF 17

RESULT 41
US-10-383-982-80
Sequence 80, Application US/10383982
Publication No. US20030157568A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20030157568A1el Family of Taste Receptors
FILE REFERENCE: 02307E-0980000US
CURRENT APPLICATION NUMBER: US/10/383,982
```

; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 80
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR24
US-10-383-982-80

Query Match 95.0%; Score 19; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 42
US-09-864-761-45716
; Sequence 45716, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Cherp, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45716
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL162171.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EST HUMAN HIT: BE55987.1, EVALUATE 2.00e-03
; OTHER INFORMATION: SWISSPROT HIT: P56093, EVALUATE 2.00e-00
US-09-864-761-45716

Query Match 95.0%; Score 19; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 15 VAEF 18

RESULT 43
US-09-738-626-5596
; Sequence 5596, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OKAZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5596
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5596

Query Match 95.0%; Score 19; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 23 VAEF 26

RESULT 44
US-10-424-599-185385
; Sequence 185385, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 185385
LENGTH: 69
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pap
US-10-424-599-185385

Query Match 95.0%; Score 19; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 24 VAEF 27

RESULT 45
US-10-029-386-28645
Sequence 28645, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28645
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR17.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7
OTHER INFORMATION: SWISSPROT HIT: P78716, EVALUE 3.00e-04
US-10-029-386-28645

Query Match 95.0%; Score 19; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 43 VAEF 46

RESULT 46
US-10-424-599-202605
Sequence 202605, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202605
LENGTH: 71
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pap
US-10-424-599-202605

Query Match 95.0%; Score 19; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 17 VAEF 20

RESULT 47
US-10-424-599-274981
Sequence 274981, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274981
LENGTH: 71
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_90329C.1.pap
US-10-424-599-274981

Query Match 95.0%; Score 19; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 39 VAEF 42

RESULT 48
US-10-029-386-30348
Sequence 30348, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1

SEQ ID NO 30348

LENGTH: 71

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHR7.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1

OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUATE 5.00e-22

JS-10-029-386-30348

Query Match 95.0%; Score 19; DB 14; Length 71;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

60 VAEF 63

DB

RESULT 49

JS-10-029-386-29320

Sequence 29320, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: AECOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annonax Sequence Listing Engine vers. 1.1

SEQ ID NO 29320

LENGTH: 72

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO CHR2.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81

OTHER INFORMATION: SWISSPROT HIT: P14650, EVALUATE 6.00e-14

US-10-029-386-29320

Query Match

Best Local Similarity 95.0%; Score 19; DB 14; Length 72;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

45 VAEF 48

DB

RESULT 50

US-10-214-188-10

Sequence 10, Application US/10214188

Publication No. US20030022260A1

GENERAL INFORMATION:

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

APPLICANT: LA THANGUE, NICHOLAS B.

BERNARDS, RENE

HIOMANS, ELEANORE M.

TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/10/214,188

APPLICATION NUMBER: US/10/214,188

FILING DATE: 08-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/894,139

FILING DATE: 13-Aug-1997

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 620-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 74 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-214-188-10

Query Match

Best Local Similarity 95.0%; Score 19; DB 14; Length 74;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

23 VAEF 26

DB

RESULT 51

US-10-156-761-9071

Sequence 9071, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 9071

LENGTH: 74

TYPE: PRT

```
ORGANISM: Streptomyces avermitilis
3-10-156-761-9071

Query Match          95.0%; Score 19; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      36 VAEF 39

RESULT 52
US-10-424-599-156128
; Sequence 156128, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156128
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(75)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112004C.1.pep
US-10-424-599-156128

Query Match          95.0%; Score 19; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      2 VAEF 5

RESULT 53
3-10-424-599-261424
; Sequence 261424, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 261424
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_78089C.1.pep
US-10-424-599-261424

Query Match          95.0%; Score 19; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      2 VAEF 5

RESULT 54
US-10-424-599-253204
; Sequence 253204, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 253204
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(76)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70669C.1.pep
US-10-424-599-253204

Query Match          95.0%; Score 19; DB 12; Length 76;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      64 VAEF 67

RESULT 55
US-10-424-599-211908
; Sequence 211908, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 211908
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3337C.1.pep
US-10-424-599-211908

Query Match          95.0%; Score 19; DB 12; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      16 VAEF 19
```

```
RESULT 56
US-10-335-977-7493
; Sequence 7493, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 7493:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3) LOCATION 1...77
; SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
US-10-335-977-7493
Query Match 95.0%; Score 19; DB 12; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 40 VAEF 43

RESULT 57
US-10-029-386-32709
; Sequence 32709, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/029,386
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 7493:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3) LOCATION 1...77
; SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
US-10-335-977-7493
Query Match 95.0%; Score 19; DB 12; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 40 VAEF 43

RESULT 58
US-10-424-599-162039
; Sequence 162039, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162039
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117339C.1.pap
US-10-424-599-162039
Query Match 95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 28 VAEF 31

RESULT 59
US-10-424-599-262701
; Sequence 262701, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 262701
; LENGTH: 78
US-10-424-599-262701
Query Match 95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 28 VAEF 31

RESULT 59
US-10-424-599-262701
; Sequence 262701, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 262701
; LENGTH: 78
US-10-424-599-262701
Query Match 95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 28 VAEF 31
```

```
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pep
3-10-424-599-262701

Query Match          95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      5 VAEF 8

RESULT 60
3-10-363-616-368
Sequence 368, Application US/10363616
Publication No. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 368
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
3-10-363-616-368

Query Match          95.0%; Score 19; DB 12; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      24 VAEF 27

RESULT 61
3-10-424-599-216097
Sequence 216097, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216097
LENGTH: 80
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37165C.1.pep
3-10-424-599-216097

Query Match          95.0%; Score 19; DB 12; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      35 VAEF 38

RESULT 62
US-10-367-980A-14
Sequence 14, Application US/10367980A
Publication No. US2003022852A1
GENERAL INFORMATION:
APPLICANT: St Vincent's Institute of Medical Research
APPLICANT: Rogers, Suzanne D
APPLICANT: Best, James D
TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8
FILE REFERENCE: VS:AJH:FP17928
CURRENT APPLICATION NUMBER: US/10/367,980A
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: 09/509,731
PRIOR FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 82
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: GLUT2
US-10-367-980A-14

Query Match          95.0%; Score 19; DB 15; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      13 VAEF 16

RESULT 63
US-09-864-408A-5282
Sequence 5282, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5282
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
US-09-864-408A-5282

Query Match          95.0%; Score 19; DB 11; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      52 VAEF 55

RESULT 64
US-10-078-090-125
Sequence 125, Application US/10078090
Publication No. US20030044815A1
GENERAL INFORMATION:
APPLICANT: Saiceda, Susana
APPLICANT: Macina, Roberto
```

```

; APPLICANT: Hu, Ping
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kaipana
; APPLICANT: Cafferey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Peptides
; CURRENT APPLICATION NUMBER: US/10/078,090
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/268,999
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapien
JS-10-078-090-125

Query Match          95.0%; Score 19; DB 14; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      38 VAEF 41

RESULT 65
US-10-424-599-155636
; Sequence 155636, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155636
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
US-10-424-599-155636

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      46 VAEF 49

RESULT 66
US-10-424-599-201853
; Sequence 201853, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155636
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
US-10-424-599-155636

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      46 VAEF 49

RESULT 67
US-09-815-242-11224
; Sequence 11224, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITFA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11224
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-11224

Query Match          95.0%; Score 19; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      12 VAEF 15
```

```

; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201853
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(85)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24299C.1.pep
US-10-424-599-201853

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VAEF 5
Db      58 VAEF 61
```

ESULT 68

S-09-815-242-11245
 Sequence 11245, Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11245
 LENGTH: 89
 TYPE: PRT
 ORGANISM: Haemophilus influenzae

Query Match 95.0%; Score 19; DB 9; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 12 VAEF 15

ESULT 69

S-10-282-122A-58489
 Sequence 58489, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 58489
 LENGTH: 89
 TYPE: PRT
 ORGANISM: Haemophilus influenzae

Query Match 95.0%; Score 19; DB 12; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Db 12 VAEF 15

RESULT 70

US-10-282-122A-58530
 Sequence 58530, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636

;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 58530
;; LENGTH: 89
;; TYPE: PRT
;; ORGANISM: Haemophilus influenzae
JS-10-282-122A-58530

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VAEF 5
Db 12 VAEF 15

RESULT 71
US-10-282-122A-66960
;; Sequence 66960, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 66960
;; LENGTH: 89
;; TYPE: PRT
;; ORGANISM: Pasteurella multocida
US-10-282-122A-66960

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 VAEF 5
Db 12 VAEF 15

RESULT 72
US-10-282-122A-68774
;; Sequence 68774, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68774
;; LENGTH: 89
;; TYPE: PRT
;; ORGANISM: Proteus mirabilis
US-10-282-122A-68774

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 VAEF 5
Db 12 VAEF 15

RESULT 73
US-10-424-599-180307
;; Sequence 180307, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa Thomas J
;; APPLICANT: Kovalic David K


```
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180307
LENGTH: 89
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_133832C.1.pap
-10-424-599-180307

Query Match          95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      24 VAEF 27

;SULT 74
-10-097-111-360
Sequence 360, Application US/10097111
Publication No. US2003013877A1
GENERAL INFORMATION:
APPLICANT: PELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: DUBOW, MICHAEL
TITLE OF INVENTION: DNA SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE EPI THAT
FILE REFERENCE: 073406-0603
CURRENT APPLICATION NUMBER: US/10/097,111
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 09/676,412
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,218
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 360
LENGTH: 89
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
-10-097-111-360

Query Match          95.0%; Score 19; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      11 VAEF 14

;SULT 75
-10-424-599-245830
Sequence 245830, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245830
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64015C.1.pap
US-10-424-599-245830

Query Match          95.0%; Score 19; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      60 VAEF 63

Search completed: May 24, 2004, 17:42:35
Job time : 41.6429 secs
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GenCore version 5.1.6
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M protein - protein search, using sw model

un on: May 24, 2004, 17:31:37 ; Search time 51.7857 Seconds
(without alignments)
27.280 Million cell updates/sec

title: US-09-594-978A-1
perfect score: 20
sequence: 1 XVAEF 5

coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1586107 seqs, 282547505 residues

total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length	ID	Description
1	19	95.0	6	5	AAM47151	Aam47151 S chrysom
2	19	95.0	7	3	AAB07871	Aab07871 A beta-se
3	19	95.0	8	3	AAB07872	Aab07872 A beta-se
4	19	95.0	8	4	ABB56241	Abb56241 Vascular
5	19	95.0	8	4	AAU28720	Aau28720 DPI trypt
6	19	95.0	8	4	AAU25114	Aau25114 Schizophr
7	19	95.0	8	4	AAU26368	Aau26368 Depressio
8	19	95.0	8	4	AAU15458	Aau15458 Schizophr
9	19	95.0	9	2	AAR78909	Aar78909 MAGE 3 10
10	19	95.0	9	5	ABB77871	Abb77871 A beta-am
11	19	95.0	10	5	ABB06593	Abb06593 Beta-secr
12	19	95.0	12	5	ABB06592	Abb06592 Beta-secr
13	19	95.0	12	5	ABG78404	Abg78404 Memapsin
14	19	95.0	12	7	ADD35467	Add35467 Escherich
15	19	95.0	13	3	AAB07889	Aab07889 A beta-se
16	19	95.0	13	4	AAM92276	Aam92276 Vaccine r
17	19	95.0	14	3	AAM97888	Aam97888 A peptide
18	19	95.0	14	4	AAM97460	Aam97460 Human pep
19	19	95.0	15	6	AAE32223	Aae32223 Arabidops
20	19	95.0	20	2	AAW42944	Aaw42944 Immunogen
21	19	95.0	20	2	AAW42943	Aaw42943 Immunogen
22	19	95.0	21	4	AAB69462	Aab69462 Synthetic
23	19	95.0	21	4	AAB69463	Aab69463 Synthetic
24	19	95.0	25	2	AAW42946	Aaw42946 Immunogen
25	19	95.0	25	4	AAB69465	Aab69465 Synthetic

26	19	95.0	28	2	AAW17832	Aaw17832 Human mev
27	19	95.0	28	4	AAW33910	Aam33910 Peptide #
28	19	95.0	28	4	ABG55464	Abg55464 Human liv
29	19	95.0	28	4	ABG43601	Abg43601 Human pep
30	19	95.0	30	2	AAW62760	Aaw62760 Streptoco
31	19	95.0	32	4	AAW82654	Aam82654 Human imm
32	19	95.0	33	4	AAO09024	Aao09024 Human pol
33	19	95.0	35	2	AAW77953	Aar77953 Antigenic
34	19	95.0	35	2	AAW46146	Aaw46146 Predicted
35	19	95.0	35	2	AAW51751	Aay51751 H. influe
36	19	95.0	35	2	AAW55788	Aaw55788 Human aqu
37	19	95.0	35	2	AAW54505	Aaw54505 Tbp2 anti
38	19	95.0	35	2	AAW54320	Aaw54320 Human aqu
39	19	95.0	35	3	AAW80448	Aay80448 H. influe
40	19	95.0	36	2	AAW27782	Aaw27782 UDP-N-ace
41	19	95.0	37	4	AAW99833	Aam99833 Human exc
42	19	95.0	37	4	AAW42648	Aam42648 Human kid
43	19	95.0	43	4	AAW17544	Aam17544 Peptide #
44	19	95.0	43	4	ABB31362	Abb31362 Peptide #
45	19	95.0	43	4	ABB21904	Abb21904 Protein #
46	19	95.0	43	4	ABG51414	Abg51414 Human liv
47	19	95.0	43	4	AAW05214	Aam05214 Peptide #
48	19	95.0	47	3	AAW27178	Aab27178 RSV parti
49	19	95.0	48	4	AAW18541	Aam18541 Peptide #
50	19	95.0	48	4	ABW37578	Abw37578 Peptide #
51	19	95.0	48	4	AAW30996	Aam30996 Peptide #
52	19	95.0	48	4	ABW22868	Abw22868 Protein #
53	19	95.0	48	4	AAW70687	Aam70687 Human bon
54	19	95.0	48	4	ABG52389	Abg52389 Human liv
55	19	95.0	48	4	AAW06107	Aam06107 Peptide #
56	19	95.0	53	4	AAO10565	Aao10565 Human pol
57	19	95.0	53	4	AAO05247	Aao05247 Human pol
58	19	95.0	56	4	AAW87390	Aam87390 Human imm
59	19	95.0	56	6	ABP97126	Abp97126 Human mat
60	19	95.0	56	6	ABG76312	Abg76312 Human mat
61	19	95.0	58	2	AAW55888	Aaw55888 Rat PC12.
62	19	95.0	58	5	ABP04854	Abp04854 Human ORF
63	19	95.0	59	3	AAW60085	Aag60085 Arabidops
64	19	95.0	59	3	AAW60683	Aag60683 Arabidops
65	19	95.0	60	4	ABB42044	Abb42044 Peptide #
66	19	95.0	60	4	AAW35846	Aam35846 Peptide #
67	19	95.0	60	4	AAW75737	Aam75737 Human bon
68	19	95.0	60	4	AAW62925	Aam62925 Human bra
69	19	95.0	60	4	ABG57475	Abg57475 Human liv
70	19	95.0	62	2	AAW17262	Aay17262 H1H domai
71	19	95.0	62	4	AAW91247	Aam91247 Human imm
72	19	95.0	62	6	ABW65667	Abw65667 Propionib
73	19	95.0	64	4	AAO09517	Aao09517 Human pol
74	19	95.0	67	2	AAW48352	Aay48352 Human pro
75	19	95.0	68	5	ABP31047	Abp31047 Human ORF
76	19	95.0	68	3	AAW32809	Aag32809 Zea mays
77	19	95.0	69	3	AAW21161	Aag21161 Zea mays
78	19	95.0	69	4	ABB42591	Abb42591 Peptide #
79	19	95.0	69	4	AAW36821	Aam36821 Peptide #
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81	19	95.0	69	4	AAW63900	Aam63900 Human bra
82	19	95.0	69	4	ABG58405	Abg58405 Human liv
83	19	95.0	69	4	AAW91842	Aag91842 C glutami
84	19	95.0	71	5	ABW08064	Abw08064 Human ORF
85	19	95.0	71	5	AAW15877	Aaaw15877 Hepatitis
86	19	95.0	71	6	ADA35824	Ada35824 Acinetoba
87	19	95.0	73	4	AAW53554	Aau53554 Propionib
88	19	95.0	73	4	AAW66465	Aau66465 Propionib
89	19	95.0	73	5	ABP06455	Abp06455 Human ORF
90	19	95.0	73	6	ABW50073	Abw50073 Propionib
91	19	95.0	73	6	ABW62984	Abw62984 Propionib
92	19	95.0	74	5	AAW15876	Aaaw15876 Hepatitis
93	19	95.0	75	4	ABG00769	Abg00769 Novel hum
94	19	95.0	76	4	AAW45469	Aau45469 Propionib
95	19	95.0	76	6	ABW41988	Abw41988 Propionib
96	19	95.0	79	5	ABP62931	Abp62931 Human pol
97	19	95.0	83	6	ABP79418	Abp79418 N. gonorr
98	19	95.0	84	5	ABP66623	Abp66623 Human bre

99	19	95.0	84	5	ABP33668	Human ORF	172	19	95.0	133	4	ABB27760	Human pep
100	19	95.0	86	4	AU50485	Propionib	173	19	95.0	133	4	ABB18410	Protein #
101	19	95.0	86	6	AM47004	Propionib	174	19	95.0	133	4	AM66115	Human bon
102	19	95.0	87	4	AAO05209	Human pol	175	19	95.0	133	4	AM53732	Human bra
103	19	95.0	87	4	AAU43264	Propionib	176	19	95.0	133	4	ABG47783	Human liv
104	19	95.0	87	4	AU466125	Propionib	177	19	95.0	133	4	AM01727	Peptide #
105	19	95.0	87	6	ABM62644	Propionib	178	19	95.0	133	5	ABP10781	Human ORF
106	19	95.0	87	6	ABM39783	Propionib	179	19	95.0	133	5	ABG35765	Human pep
107	19	95.0	88	4	AU56968	Propionib	180	19	95.0	134	4	AU34920	Novel hum
108	19	95.0	88	6	ABM53487	Propionib	181	19	95.0	134	4	ABG02560	Novel hum
109	19	95.0	88	7	ADC89159	Ribosomal	182	19	95.0	135	5	ABP07711	Human ORF
110	19	95.0	89	3	AB16761	Bacterioph	183	19	95.0	135	6	ABM69996	Phototriab
111	19	95.0	89	4	AU35652	Haemophil	184	19	95.0	136	2	AAW55889	Rat plasim
112	19	95.0	89	4	AU35631	Haemophil	185	19	95.0	139	3	AA10817	Methanoba
113	19	95.0	89	5	ABM54895	Lactococc	186	19	95.0	139	3	AAG41153	Zea may
114	19	95.0	89	6	ABU40860	Protein e	187	19	95.0	139	4	ABM64375	Amino aci
115	19	95.0	89	6	ABU30365	Protein e	188	19	95.0	141	3	AAG02426	Human sec
116	19	95.0	89	6	ABU30606	Protein e	189	19	95.0	141	4	AAU50269	Propionib
117	19	95.0	89	6	ABU39036	Protein e	190	19	95.0	141	4	ABG30243	Novel hum
118	19	95.0	93	3	AAG48060	Arabisdops	191	19	95.0	141	4	ABG07245	Novel hum
119	19	95.0	95	3	ABG34249	Arabisdops	192	19	95.0	141	6	ABM46788	Propionib
120	19	95.0	96	4	ABG07485	Novel hum	193	19	95.0	142	2	AAW10208	Canola co
121	19	95.0	97	5	AB248132	Listeria	194	19	95.0	142	6	ABP79097	N. gonorr
122	19	95.0	97	6	ABP75366	Human sec	195	19	95.0	143	3	AB10816	Archaeogl
123	19	95.0	99	5	ABP41643	Human ova	196	19	95.0	143	5	AAO14828	Human ste
124	19	95.0	100	3	AAG02653	Human sec	197	19	95.0	144	3	AAG05007	Arabisdops
125	19	95.0	100	4	AU62265	Propionib	198	19	95.0	144	2	AA134749	Chlamydia
126	19	95.0	100	6	ABM58784	Propionib	199	19	95.0	145	4	AAU27872	Human con
127	19	95.0	105	3	ABG32808	Zea may	200	19	95.0	145	5	ABG98409	Haloarcul
128	19	95.0	106	3	ABG32572	Arabisdops	201	19	95.0	145	5	ABJ11020	Yeast sel
129	19	95.0	106	5	ABM82190	P. multoc	202	19	95.0	145	5	ABJ11020	Yeast sel
130	19	95.0	107	3	ABM61315	Arabisdops	203	19	95.0	146	6	ABP57361	Anti-TRAI
131	19	95.0	107	3	AAG10318	Arabisdops	204	19	95.0	146	6	ABP57363	Anti-TRAI
132	19	95.0	107	4	AAG90766	C glutami	205	19	95.0	146	6	ABU42336	Protein e
133	19	95.0	108	3	AAG00023	Human sec	206	19	95.0	146	6	ABP56635	Ascaris s
134	19	95.0	109	4	ABG09614	Novel hum	207	19	95.0	146	7	AD26750	Human adi
135	19	95.0	109	5	ABM89162	Human pol	208	19	95.0	147	6	ABU07050	Maize SSI
136	19	95.0	109	5	ABP62930	Human pol	209	19	95.0	147	6	AAG41152	Zea may
137	19	95.0	109	7	ABP99534	Mut-IL-4	210	19	95.0	148	3	ABP78900	N. gonorr
138	19	95.0	111	2	AA137827	Amino aci	211	19	95.0	148	7	ABM74182	DNA clone
139	19	95.0	111	3	AA137827	Zea may	212	19	95.0	149	4	ABG05510	Novel hum
140	19	95.0	112	4	AA137827	Zea may	213	19	95.0	149	5	ABM74889	Listeria
141	19	95.0	112	4	AA137827	N-termina	214	19	95.0	150	3	AAG01131	Human sec
142	19	95.0	113	1	AA137827	N-termina	215	19	95.0	150	5	ABM49109	Listeria
143	19	95.0	113	3	AAG00866	Human sec	216	19	95.0	152	5	AAW52496	Superoxid
144	19	95.0	113	3	AAG03428	Arabisdops	217	19	95.0	152	5	ABP51829	Human col
145	19	95.0	114	1	AA137827	N-termina	218	19	95.0	153	3	ABM40336	Human ORF
146	19	95.0	114	6	ABP97830	Amino aci	219	19	95.0	153	4	ABG07294	Novel hum
147	19	95.0	115	5	ABM62790	Human RS3	220	19	95.0	153	4	ABG10037	Novel hum
148	19	95.0	116	6	ABM64780	Propionib	221	19	95.0	153	4	ABG05309	Novel hum
149	19	95.0	117	5	ABP05042	Human ORF	222	19	95.0	154	3	AAG41151	Zea may
150	19	95.0	119	3	ABG33308	Pinus rad	223	19	95.0	154	3	AAG38111	Arabisdops
151	19	95.0	119	6	ABM69462	Drosophil	224	19	95.0	154	3	AAG42939	Arabisdops
152	19	95.0	119	6	ABP70942	Drosophil	225	19	95.0	154	3	AAG19886	Arabisdops
153	19	95.0	122	5	ABM16105	Human ner	226	19	95.0	154	5	ABP43836	Riken 170
154	19	95.0	122	5	ABP31290	Human ORF	227	19	95.0	155	5	ABG80423	Haemophil
155	19	95.0	125	4	AAW1641	Human imm	228	19	95.0	156	4	ABM70411	Drosophil
156	19	95.0	125	4	AAW1641	Human imm	229	19	95.0	156	4	ABG24856	Novel hum
157	19	95.0	125	6	ABM63584	Propionib	230	19	95.0	157	4	ABM52504	Escherich
158	19	95.0	129	2	AAW14573	Streptoco	231	19	95.0	157	4	ABG26258	Novel hum
159	19	95.0	129	3	AAG30409	Arabisdops	232	19	95.0	159	2	AAW11201	S. pneumo
160	19	95.0	131	4	AAG91450	C glutami	233	19	95.0	162	3	AAG06266	Arabisdops
161	19	95.0	131	4	AAG30335	Novel hum	234	19	95.0	162	6	ABM70110	Phototriab
162	19	95.0	132	3	AAG01937	Human sec	235	19	95.0	163	3	AAG12749	Arabisdops
163	19	95.0	132	4	AAW41985	Human pol	236	19	95.0	163	3	AAG06265	Arabisdops
164	19	95.0	132	4	AAW41986	Human pol	237	19	95.0	163	4	ABM63381	Drosophil
165	19	95.0	132	4	AAW41984	Human pol	238	19	95.0	163	5	ABP97879	Human sec
166	19	95.0	132	4	ABG27027	Novel hum	239	19	95.0	164	2	AA129556	Human lun
167	19	95.0	133	3	AAW41454	Human ORF	240	19	95.0	164	3	AA13821	Human lun
168	19	95.0	133	4	AAW13986	Peptide #	241	19	95.0	164	4	AA13821	Listeria
169	19	95.0	133	4	AAU23379	Novel hum	242	19	95.0	164	5	ABM48330	Listeria
170	19	95.0	133	4	ABM22931	Peptide #	243	19	95.0	164	5	ABP31601	Human ORF
171	19	95.0	133	4	AAW26392	Peptide #	244	19	95.0	164	7	AD66511	Human lun

245	19	95.0	164	7	ADE87765	Ade87765 Human lun	318	19	95.0	199	4	AAB68971	Aab68971 Sheep mit
246	19	95.0	167	3	AAB56403	Aab56403 Human pro	319	19	95.0	199	4	AAB68972	Aab68972 Human mit
247	19	95.0	168	6	ABP79188	Abp79188 N. gonorr	320	19	95.0	199	4	AAB31894	Aab31894 Amino aci
248	19	95.0	169	3	AAG38110	Aag38110 Arabidops	321	19	95.0	199	4	AAB31892	Aab31892 Amino aci
249	19	95.0	170	4	ABG26260	Abg26260 Novel hum	322	19	95.0	199	4	AAB31893	Aab31893 Amino aci
250	19	95.0	171	2	AAW40216	Aaw40216 Mouse Al.	323	19	95.0	199	4	AAB83265	Aab83265 A nidulan
251	19	95.0	172	2	AAW05531	Aaw05531 Human foe	324	19	95.0	199	4	AAB60183	Aab60183 Human sec
252	19	95.0	173	2	AAW31531	Aaw31531 Human ant	325	19	95.0	199	4	AAB60185	Aab60185 Murine se
253	19	95.0	174	2	AAW20421	Aaw20421 H. pylori	326	19	95.0	199	5	AAW47317	Aam47317 Human nuc
254	19	95.0	175	5	AAU12115	Aau12115 Human bcl	327	19	95.0	199	7	ADD46946	Add46946 Human pro
255	19	95.0	176	6	ABU89728	Abu89728 Protein d	328	19	95.0	199	7	ADD46942	Add46942 Human pro
256	19	95.0	177	7	ADE25780	Ade25780 Human pro	329	19	95.0	200	4	AAB79735	Aab79735 Coryneb
257	19	95.0	178	4	AAW14209	Aam14209 Peptide #	330	19	95.0	200	4	AAB79757	Aab79757 Coryneb
258	19	95.0	179	4	ABB33156	Abb33156 Peptide #	331	19	95.0	201	3	AAG31750	Aag31750 Arabidops
259	19	95.0	180	4	AAW26619	Aam26619 Peptide #	332	19	95.0	201	3	AAG31750	Aag31750 Arabidops
260	19	95.0	181	4	ABB27984	Abb27984 Human pep	333	19	95.0	201	5	AAE15548	Aae15548 Human pro
261	19	95.0	182	4	ABB18621	Abb18621 Protein #	334	19	95.0	201	5	AAE15548	Aae15548 Human pro
262	19	95.0	183	4	AAW66340	Aam66340 Human bon	335	19	95.0	201	7	ADE57400	Ade57400 Human pro
263	19	95.0	184	4	AAW53952	Aam53952 Human bra	336	19	95.0	201	7	ADE57400	Ade57400 Human pro
264	19	95.0	185	4	ABG48006	Abg48006 Human liv	337	19	95.0	201	7	ADE56860	Ade56860 Human pro
265	19	95.0	186	4	AAW01941	Aam01941 Peptide #	338	19	95.0	202	3	AAG06264	Aag06264 Arabidops
266	19	95.0	187	5	ABG35988	Abg35988 Human pep	339	19	95.0	202	5	ABW47473	Abw47473 Listeria
267	19	95.0	188	6	ABP80373	Abp80373 N. gonorr	340	19	95.0	202	6	ABU32939	Abu32939 Protein e
268	19	95.0	189	6	ABP79196	Abp79196 N. gonorr	341	19	95.0	203	7	ADC94985	Adc94985 E. faeciu
269	19	95.0	190	7	ABW43469	Abw43469 Human can	342	19	95.0	203	7	ADC94985	Adc94985 E. faeciu
270	19	95.0	191	3	ABW54140	Abw54140 Human pan	343	19	95.0	204	5	ABG61835	Abg61835 Prostate
271	19	95.0	192	3	ABW44526	Abw44526 Virulence	344	19	95.0	205	2	AAW13020	Aaw13020 Human MAD
272	19	95.0	193	4	ABW62070	Abw62070 Drosophil	345	19	95.0	205	4	AAW27824	Aaw27824 Human ful
273	19	95.0	194	5	ABP41446	Abp41446 Human ova	346	19	95.0	205	4	AAW25815	Aam25815 Human pro
274	19	95.0	195	5	ABP54478	Abp54478 Pasteurel	347	19	95.0	205	5	ABP65838	Abp65838 Bifidobac
275	19	95.0	196	3	AAW10317	Aag10317 Arabidops	348	19	95.0	205	6	ABR58559	AbR58559 Human can
276	19	95.0	197	3	AAW61314	Aag61314 Arabidops	349	19	95.0	205	6	ABP55379	Abp55379 Human col
277	19	95.0	198	3	ADA35452	Ada35452 Acinetoba	350	19	95.0	205	6	ABP55379	Abp55379 Human col
278	19	95.0	199	3	AAW59111	Aag59111 Arabidops	351	19	95.0	206	7	ABM73792	Abm73792 DNA clone
279	19	95.0	200	4	ABW31895	Aab31895 Amino aci	352	19	95.0	206	7	ABU16876	Abu16876 Protein e
280	19	95.0	201	4	ABW85327	Aag85327 S. epider	353	19	95.0	208	6	ABU16876	Abu16876 Protein e
281	19	95.0	202	4	ABW85327	Aag85327 S. epider	354	19	95.0	209	6	ABU44637	Abu44637 Protein e
282	19	95.0	203	7	ADC08043	Adc08043 Enterohae	355	19	95.0	210	6	AAU23550	Aau23550 Novel hum
283	19	95.0	204	7	ABW99995	Abw99995 Enterohae	356	19	95.0	210	6	AAU23550	Aau23550 Novel hum
284	19	95.0	205	4	AAU42124	Aau42124 Propionib	357	19	95.0	212	6	ABJ18781	Abj18781 Pseudomon
285	19	95.0	206	6	ABW38643	Abm38643 Propionib	358	19	95.0	213	2	AAU14938	Aau14938 Amino aci
286	19	95.0	207	4	AAU59747	Aau59747 Propionib	359	19	95.0	213	3	AAG30715	Aag30715 Arabidops
287	19	95.0	208	6	ABW56266	Abm56266 Propionib	360	19	95.0	213	3	AAG30715	Aag30715 Arabidops
288	19	95.0	209	6	ABW56266	Abm56266 Propionib	361	19	95.0	213	3	AAG30715	Aag30715 Arabidops
289	19	95.0	210	6	ABW56266	Abm56266 Propionib	362	19	95.0	213	3	AAG30715	Aag30715 Arabidops
290	19	95.0	211	5	ABG30791	Abg30791 Human ser	363	19	95.0	213	3	AAG30715	Aag30715 Arabidops
291	19	95.0	212	5	AAE17922	Aae17922 Human gen	364	19	95.0	213	3	AAG30715	Aag30715 Arabidops
292	19	95.0	213	5	AAW00088	Aam00088 Alpha-glu	365	19	95.0	214	4	AAU48893	Aau48893 Propionib
293	19	95.0	214	6	ABW50253	Abu50253 Protein e	366	19	95.0	214	4	AAU48893	Aau48893 Propionib
294	19	95.0	215	6	ABU48662	Abu48662 Protein e	367	19	95.0	214	6	ABM45412	Abm45412 Propionib
295	19	95.0	216	6	ABW52817	Abw52817 Escherich	368	19	95.0	215	4	ABM45412	Abm45412 Propionib
296	19	95.0	217	2	AAW77092	Aaw77092 Human RNA	369	19	95.0	215	4	ABM45412	Abm45412 Propionib
297	19	95.0	218	3	AAW11973	Aam11973 Human RNA	370	19	95.0	216	6	ABU35052	Abu35052 Protein e
298	19	95.0	219	3	AAW38905	Aam38905 Human pol	371	19	95.0	217	3	AAW90786	Aaw90786 A. fulgid
299	19	95.0	220	6	AAW41183	Aab41183 Human ORF	372	19	95.0	217	6	ABO00751	AbO00751 Polypepti
300	19	95.0	221	6	ABU49757	Abu49757 Protein e	373	19	95.0	218	3	AAG20462	Aag20462 Arabidops
301	19	95.0	222	3	AAW10316	Aag10316 Arabidops	374	19	95.0	218	3	AAG20462	Aag20462 Arabidops
302	19	95.0	223	3	AAW61313	Aag61313 Arabidops	375	19	95.0	218	6	ABU50613	Abu50613 Protein e
303	19	95.0	224	3	AAW79736	Aab79736 Coryneb	376	19	95.0	218	6	ABU50613	Abu50613 Protein e
304	19	95.0	225	4	AAW72563	Aag72563 Coryneb	377	19	95.0	219	3	AAU74257	Aay74257 Neisseria
305	19	95.0	226	5	AAU732164	Aay732164 Corn Dp-2	378	19	95.0	219	3	AAU74257	Aay74257 Neisseria
306	19	95.0	227	4	AAW63330	Aab63330 Human bre	379	19	95.0	220	7	ADD27359	Add27359 Human adi
307	19	95.0	228	4	AAW63330	Aab63330 Human bre	380	19	95.0	220	7	ADD27359	Add27359 Human adi
308	19	95.0	229	6	AAW70654	Aam70654 Photorhab	381	19	95.0	221	4	AAW40691	Aam40691 Human pol
309	19	95.0	230	6	ABW19885	Abw19885 Arabidops	382	19	95.0	221	4	ABG29763	Abg29763 Novel hum
310	19	95.0	231	3	AAW42938	Aag42938 Arabidops	383	19	95.0	222	4	AAU23537	Aau23537 Novel hum
311	19	95.0	232	3	AAW42938	Aag42938 Arabidops	384	19	95.0	222	4	AAU23537	Aau23537 Novel hum
312	19	95.0	233	3	ABG11065	Abg11065 Novel hum	385	19	95.0	223	6	ADA36818	Ada36818 Acinetoba
313	19	95.0	234	4	ABG11065	Abg11065 Novel hum	386	19	95.0	223	6	ADA36818	Ada36818 Acinetoba
314	19	95.0	235	5	ABW54303	Abw54303 Lactococc	387	19	95.0	224	7	ADD27209	Add27209 Human adi
315	19	95.0	236	5	ABW54303	Abw54303 Lactococc	388	19	95.0	224	3	AAW91479	Aay91479 Human sec
316	19	95.0	237	3	AAW24197	Aab24197 Mouse act	389	19	95.0	224	3	AAW91479	Aay91479 Human sec
317	19	95.0	238	2	AAW17561	Aay17561 Protein i	390	19	95.0	224	4	AAG90867	Aag90867 C glutami
	19	95.0	239	2	AAW14965	Aay14965 Partial a							
	19	95.0	240	4	AAU27704	Aau27704 Human ful							

391	19	95.0	224	6	ADA54376	Adas4376 Human pro	464	19	95.0	257	2	AAR97285	Aar97285 Human 265
392	19	95.0	224	6	ADA56787	Adas6787 Human sec	465	19	95.0	257	2	AAR21729	Aar21729 Nuclear m
393	19	95.0	224	7	ADC74046	Adc74046 Human sec	466	19	95.0	257	3	AAW59110	Aaw59110 Arabidops
394	19	95.0	224	7	ADD37843	Add37843 Human sec	467	19	95.0	257	4	AAW74447	Aaw74447 Human col
395	19	95.0	226	4	AAW79581	Aaw79581 Human pro	468	19	95.0	257	4	AAG92888	Aag92888 C glutami
396	19	95.0	226	4	ABG03398	Abg03398 Novel hum	469	19	95.0	257	7	ADD27694	Add27694 Human adi
397	19	95.0	226	6	ABG09001	Abg09001 Novel hum	470	19	95.0	257	7	ADD26681	Add26681 Human adi
398	19	95.0	226	6	ADA36076	Ada36076 Acinetoba	471	19	95.0	257	7	ADD27489	Add27489 Human adi
399	19	95.0	227	5	AAE14342	Aae14342 Human pro	472	19	95.0	258	3	AAW16704	Aaw16704 Bacteriop
400	19	95.0	227	5	AAE14793	Aae14793 Neisseria	473	19	95.0	258	4	AAU36296	Aau36296 Pseudomon
401	19	95.0	228	3	ABA74793	Abv74793 Neisseria	474	19	95.0	258	6	ABU38502	Abu38502 Protein e
402	19	95.0	228	6	ABP78081	Abp78081 N. gonorr	475	19	95.0	260	4	AAW78433	Aaw78433 Human pro
403	19	95.0	228	6	ABP80081	Abp80081 N. gonorr	476	19	95.0	260	4	AAU58456	Aau58456 Propionib
404	19	95.0	228	6	ABG75884	Abg75884 Mycobacte	477	19	95.0	260	4	ABG30334	Abg30334 Novel hum
405	19	95.0	229	4	AAW1949	Aaw1949 S. epider	478	19	95.0	260	6	ABG54975	Abg54975 Propionib
406	19	95.0	229	4	AAU04888	Aau04888 Micromono	479	19	95.0	261	4	AAU00701	Aau00701 Mouse FCT
407	19	95.0	229	5	ABW1524	Abw1524 Herbicida	480	19	95.0	261	5	ABR79646	Abw79646 Mouse FCT
408	19	95.0	230	4	AAW80078	Aaw80078 Corynebac	481	19	95.0	261	5	ABG78505	Abg78505 Murine FC
409	19	95.0	230	4	AAW90273	Aaw90273 C glutami	482	19	95.0	261	5	ABG78505	Abg78505 Human hom
410	19	95.0	231	2	AAW60988	Aaw60988 Streptoco	483	19	95.0	261	6	ABU41453	Abu41453 Protein e
411	19	95.0	231	5	ABW50143	Abw50143 Listeria	484	19	95.0	261	7	ADW54842	Adw54842 Rat Prote
412	19	95.0	231	6	ADA36637	Ada36637 Acinetoba	485	19	95.0	261	7	ADW54844	Adw54844 Human pro
413	19	95.0	232	2	AAW27368	Aaw27368 Group B S	486	19	95.0	262	4	ABG04663	Abg04663 Novel hum
414	19	95.0	232	3	AAW11258	Aaw11258 Arabidops	487	19	95.0	262	5	AAU72572	Aau72572 Arabidops
415	19	95.0	233	3	AAW22116	Aaw22116 Maize glu	488	19	95.0	263	4	AAW95344	Aaw95344 Human adu
416	19	95.0	234	3	AAW36676	Aaw36676 Arabidops	489	19	95.0	263	4	AAW90550	Aaw90550 Human sec
417	19	95.0	234	5	ABW1390	Abw1390 Herbicida	490	19	95.0	263	5	ABG65464	Abg65464 Human alb
418	19	95.0	234	7	ADC96886	Adc96886 E. faeciu	491	19	95.0	263	5	ADW44959	Adw44959 Human pol
419	19	95.0	236	3	AAW42087	Aaw42087 Human ORF	492	19	95.0	264	3	AAW15729	Aaw15729 Arabidops
420	19	95.0	236	4	AAW36145	Aaw36145 Klebsiell	493	19	95.0	264	4	ABG86363	Abg86363 Human cer
421	19	95.0	236	4	AAW61537	Aaw61537 DegP prot	494	19	95.0	264	4	ABG18250	Abg18250 Novel hum
422	19	95.0	236	4	ABG27447	Abg27447 Novel hum	495	19	95.0	265	2	AAW08269	Aaw08269 Mouse neu
423	19	95.0	238	3	ABW11695	Abw11695 Mouse ser	496	19	95.0	265	2	AAW70534	Aaw70534 Mouse neu
424	19	95.0	238	3	AAW28132	Aaw28132 Glycerald	497	19	95.0	266	6	ABU24490	Abu24490 Protein e
425	19	95.0	238	4	AAW61538	Aaw61538 DegP prot	498	19	95.0	266	6	AAW79417	Aaw79417 Human pro
426	19	95.0	238	4	AAW83029	Aaw83029 S. epider	499	19	95.0	267	2	AAW85606	Aaw85606 Secreted
427	19	95.0	238	4	AAW83016	Aaw83016 S. epider	500	19	95.0	267	2	ABU50254	Abu50254 Protein e
428	19	95.0	238	5	ABW3557	Abw3557 Lactococc	501	19	95.0	268	5	AAE15256	Aae15256 Human RNA
429	19	95.0	238	5	AAU80750	Aau80750 Eucalyptu	502	19	95.0	268	5	ABP61845	Abp61845 Human pol
430	19	95.0	238	6	AAU44475	Aau44475 Protein e	503	19	95.0	269	2	AAW55786	Aaw55786 Human aqu
431	19	95.0	238	6	ABU42738	Abu42738 Protein e	504	19	95.0	269	2	AAW94322	Aaw94322 Human aqu
432	19	95.0	238	6	ABM72778	Abm72778 Staphyloc	505	19	95.0	269	4	ABG26217	Abg26217 Novel hum
433	19	95.0	239	3	AAW74795	Aaw74795 Neisseria	506	19	95.0	269	6	ABP53586	Abp53586 Protein s
434	19	95.0	239	3	AAW11257	Aaw11257 Arabidops	507	19	95.0	269	6	ABP58050	Abp58050 Human aqu
435	19	95.0	239	3	AAW74794	Aaw74794 Arabidops	508	19	95.0	269	6	ADW64028	Adw64028 Human pro
436	19	95.0	239	3	AAW96778	Aaw96778 Putative	509	19	95.0	270	6	ADA05788	Ada05788 C glutami
437	19	95.0	240	3	AAW19884	Aaw19884 Arabidops	510	19	95.0	270	6	ADA05788	Ada05788 Human NOV
438	19	95.0	240	3	AAW42937	Aaw42937 Arabidops	511	19	95.0	270	6	ADC08133	Adc08133 Rice prot
439	19	95.0	240	7	ADE25064	Ade25064 Plant gro	512	19	95.0	271	2	AAW15227	Aaw15227 Human rec
440	19	95.0	241	5	ABP40753	Abp40753 Staphyloc	513	19	95.0	271	3	AAW28205	Aaw28205 Novel hum
441	19	95.0	241	6	ABU28310	Abu28310 Protein e	514	19	95.0	271	3	AAW31287	Aaw31287 Arabidops
442	19	95.0	241	6	AAW96089	Aaw96089 S. pneumo	515	19	95.0	271	3	AAW22050	Aaw22050 Arabidops
443	19	95.0	243	5	ABP38742	Abp38742 Staphyloc	516	19	95.0	271	4	AAW92851	Aaw92851 Human pro
444	19	95.0	243	5	ABW33337	Abw33337 Human TSA	517	19	95.0	271	4	AAW88446	Aaw88446 Human mem
445	19	95.0	244	6	ABU4263	Abu4263 Protein e	518	19	95.0	271	4	AAW64357	Aaw64357 Human sig
446	19	95.0	244	6	ABU4263	Abu4263 Protein e	519	19	95.0	271	5	ABW90282	Abw90282 Human pol
447	19	95.0	245	7	ADC08337	Adc08337 Rice prot	520	19	95.0	271	7	ADW5444	Adw5444 E. faeciu
448	19	95.0	247	7	ADE86966	Ade86966 Human pan	521	19	95.0	272	4	AAW23799	Aaw23799 Novel hum
449	19	95.0	248	2	AAW11160	Aaw11160 S. pneumo	522	19	95.0	272	4	AAW94302	Aaw94302 Human rep
450	19	95.0	249	4	ABW1261	Abw1261 Human TAN	523	19	95.0	272	4	ABU16020	Abu16020 Novel hum
451	19	95.0	249	4	ABW19896	Abw19896 Polyketid	524	19	95.0	272	6	ABU42431	Abu42431 Protein e
452	19	95.0	249	6	ABU11227	Abu11227 Human TAN	525	19	95.0	272	6	ABW71001	Abw71001 Staphyloc
453	19	95.0	249	7	ABW1593	Abw1593 Z. mays a	526	19	95.0	272	6	ABW11696	Abw11696 Mouse ser
454	19	95.0	250	2	AAW33913	Aaw33913 Sequence	527	19	95.0	273	3	AAW15728	Aaw15728 Arabidops
455	19	95.0	250	2	AAW60153	Aaw60153 Nematode-	528	19	95.0	273	3	AAW86365	Aaw86365 Human cer
456	19	95.0	250	2	AAW77082	Aaw77082 Tobacco r	529	19	95.0	273	6	ABW42553	Abw42553 Simocycli
457	19	95.0	250	3	AAW42541	Aaw42541 Human ORF	530	19	95.0	273	7	ABW08633	Abw08633 Novel pro
458	19	95.0	250	3	AAW47372	Aaw47372 Propionib	531	19	95.0	274	3	AAW00020	Aaw00020 Putative
459	19	95.0	250	6	ABW43891	Abw43891 Propionib	532	19	95.0	274	3	AAW00211	Aaw00211 Potential
460	19	95.0	253	4	AAW34686	Aaw34686 E. coli c	533	19	95.0	274	4	AAW63322	Aaw63322 Human bre
461	19	95.0	253	7	ADC95445	Adc95445 E. faeciu	534	19	95.0	274	6	ABU23635	Abu23635 Protein e
462	19	95.0	254	6	ADA05790	Ada05790 Human NOV	535	19	95.0	274	6	ABU46447	Abu46447 Protein e
463	19	95.0	256	6	ABW67840	Abw67840 Phototrab	536	19	95.0	274	7	ADC32869	Adc32869 Human nov

537	19	95.0	275	6	ABU241121	Abu24121 Protein e	610	19	95.0	300	7	ADC31643	Adc31643 Human nov
538	19	95.0	276	3	AAB242611	Aab242611 Human ORF	611	19	95.0	301	4	AAG82151	Aag82151 S. epider
539	19	95.0	277	3	AAW18875	Aaw18875 Arabidops	612	19	95.0	302	3	AAG15595	Aag15595 Arabidops
540	19	95.0	277	3	AAG22852	Aag22852 Arabidops	613	19	95.0	303	3	AAG20322	Aag20322 Arabidops
541	19	95.0	278	3	AAG04958	Aag04958 Arabidops	614	19	95.0	303	4	AAG89980	Aag89980 C glutami
542	19	95.0	278	3	AAG07719	Aag07719 Arabidops	615	19	95.0	304	3	AAG37633	Aag37633 Arabidops
543	19	95.0	278	3	AAG39551	Aag39551 Arabidops	616	19	95.0	304	3	AAG04957	Aag04957 Arabidops
544	19	95.0	278	3	AAG37634	Aag37634 Arabidops	617	19	95.0	304	3	AAG30063	Aag30063 Arabidops
545	19	95.0	278	5	ABP30329	Abp30329 Streptoco	618	19	95.0	304	3	AAG30713	Aag30713 Arabidops
546	19	95.0	278	6	ABP77659	Abp77659 N. gonorr	619	19	95.0	304	3	AAG39550	Aag39550 Arabidops
547	19	95.0	278	6	ABU37537	Abu37537 Protein e	620	19	95.0	305	3	AAG30713	Aag30713 Arabidops
548	19	95.0	278	6	ABU37837	Abu37837 Protein e	621	19	95.0	305	4	AAG10620	Aag10620 Arabidops
549	19	95.0	279	3	AAG54754	Aag54754 Arabidops	622	19	95.0	305	4	AAG92837	Aag92837 C glutami
550	19	95.0	279	4	ABG30336	Abg30336 Novel hum	623	19	95.0	306	3	AAG40089	Aag40089 Arabidops
551	19	95.0	279	5	ABBS5091	Abbs5091 Lactococc	624	19	95.0	306	3	AAG13663	Aag13663 Arabidops
552	19	95.0	280	2	AAW03521	Aaw03521 Bali modi	625	19	95.0	306	4	AAG03620	Aag03620 Group B S
553	19	95.0	280	2	AAV37073	Aav37073 Amino aci	626	19	95.0	306	5	ABP29888	Abp29888 Streptoco
554	19	95.0	280	4	AAG30751	Aag30751 C glutami	627	19	95.0	306	5	ABP28497	Abp28497 Streptoco
555	19	95.0	281	3	AAG26675	Aag26675 Arabidops	628	19	95.0	306	7	ADB70040	Adb70040 C. neofo
556	19	95.0	281	5	ABG77963	Abg77963 Ehrlichia	629	19	95.0	307	7	ADC37261	Adc37261 Nuclear f
557	19	95.0	281	6	ADA09791	Ada09791 E. canis	630	19	95.0	308	3	AB533390	Ab533390 Human col
558	19	95.0	282	2	AAW34205	Aaw34205 Streptomy	631	19	95.0	308	4	AB533390	Ab533390 Human col
559	19	95.0	282	2	AAW55806	Aaw55806 Streptomy	632	19	95.0	308	5	AB54256	Ab54256 Lactococc
560	19	95.0	282	3	AB571116	Ab571116 Human pro	633	19	95.0	308	5	ABP60904	Abp60904 Lactococc
561	19	95.0	282	3	AAG13664	Aag13664 Arabidops	634	19	95.0	308	5	ABP65647	Abp65647 Bifidobac
562	19	95.0	282	3	AAG40090	Aag40090 Arabidops	635	19	95.0	308	7	ADC79410	Adc79410 Human G p
563	19	95.0	282	6	ABM67054	Abm67054 Photorhab	636	19	95.0	309	3	AB531285	Ab531285 Arabidops
564	19	95.0	282	6	ABU19351	Abu19351 Protein e	637	19	95.0	309	5	AB931102	Ab931102 Herbicida
565	19	95.0	283	2	AAW89755	Aaw89755 Staphyloc	638	19	95.0	309	5	ABP61176	Abp61176 Human GPC
566	19	95.0	284	4	AAB39850	Aab39850 Human pro	639	19	95.0	310	3	AB21021	Ab21021 Human nuc
567	19	95.0	285	2	AAR95957	Aar95957 Eukaryoti	640	19	95.0	310	5	AAW51006	Aaw51006 Corynebac
568	19	95.0	285	6	ABU21606	Abu21606 Protein e	641	19	95.0	310	6	AAG79924	Aag79924 Human Sir
569	19	95.0	285	6	ABU41998	Abu41998 Protein e	642	19	95.0	310	6	ABU39481	Abu39481 Protein e
570	19	95.0	286	6	ADA05784	Ada05784 Human NOV	643	19	95.0	311	3	AB111697	Ab111697 Mouse ser
571	19	95.0	286	6	ABU41392	Abu41392 Protein e	644	19	95.0	311	3	AB111697	Ab111697 Mouse ser
572	19	95.0	287	3	AAG26674	Aag26674 Arabidops	645	19	95.0	311	4	AB511899	Ab511899 Human G-p
573	19	95.0	287	3	ABU00416	Abu00416 Human nov	646	19	95.0	311	4	AB511899	Ab511899 Human G-p
574	19	95.0	288	6	ABM69140	Abm69140 Photorhab	647	19	95.0	311	4	AB511899	Ab511899 Human G-p
575	19	95.0	288	6	ABU38998	Abu38998 Protein e	648	19	95.0	311	4	AB511899	Ab511899 Human G-p
576	19	95.0	289	4	ABU35600	Abu35600 Haemophil	649	19	95.0	311	4	AB511899	Ab511899 Human G-p
577	19	95.0	289	6	ABU30505	Abu30505 Protein e	650	19	95.0	311	4	AB511899	Ab511899 Human G-p
578	19	95.0	290	3	AAV78511	Aav78511 Human unc	651	19	95.0	311	4	AB511899	Ab511899 Human G-p
579	19	95.0	290	3	AAG23887	Aag23887 Arabidops	652	19	95.0	311	4	AB511899	Ab511899 Human G-p
580	19	95.0	290	3	ADA05786	Ada05786 Human NOV	653	19	95.0	311	4	AB511899	Ab511899 Human G-p
581	19	95.0	291	5	ABB90394	Abb90394 Human pol	654	19	95.0	311	5	ABP95725	Abp95725 Human GPC
582	19	95.0	291	7	ADC31166	Adc31166 Human nov	655	19	95.0	311	5	ABP95725	Abp95725 Human GPC
583	19	95.0	291	7	ADC87617	Adc87617 Human GPC	656	19	95.0	311	5	ABP95725	Abp95725 Human GPC
584	19	95.0	292	3	AAG26171	Aag26171 Arabidops	657	19	95.0	311	5	ABP95725	Abp95725 Human GPC
585	19	95.0	292	3	AAG60250	Aag60250 Arabidops	658	19	95.0	311	5	ABP95725	Abp95725 Human GPC
586	19	95.0	293	6	ABU48542	Abu48542 Protein e	659	19	95.0	311	5	ABP95725	Abp95725 Human GPC
587	19	95.0	294	5	ABG91459	Abg91459 Furine/py	660	19	95.0	311	5	ABP95725	Abp95725 Human GPC
588	19	95.0	294	6	ABR53328	Ab53328 Protein s	661	19	95.0	311	5	ABP95725	Abp95725 Human GPC
589	19	95.0	294	6	ABP98029	Abp98029 Protein p	662	19	95.0	311	5	ABP95725	Abp95725 Human GPC
590	19	95.0	295	3	AAG31286	Aag31286 Arabidops	663	19	95.0	311	5	ABP95725	Abp95725 Human GPC
591	19	95.0	295	5	ABP28274	Abp28274 Streptoco	664	19	95.0	311	5	ABP95725	Abp95725 Human GPC
592	19	95.0	295	5	ABG91460	Abg91460 Furine/py	665	19	95.0	311	5	ABP95725	Abp95725 Human GPC
593	19	95.0	295	5	ABG91461	Abg91461 Furine/py	666	19	95.0	311	5	ABP95725	Abp95725 Human GPC
594	19	95.0	295	5	ABG91449	Abg91449 Furine/py	667	19	95.0	311	5	ABP95725	Abp95725 Human GPC
595	19	95.0	296	5	AAW52345	Aaw52345 Aromatic	668	19	95.0	311	5	ABP95725	Abp95725 Human GPC
596	19	95.0	297	6	ABU22319	Abu22319 Protein e	669	19	95.0	311	5	ABP95725	Abp95725 Human GPC
597	19	95.0	297	6	ABU22270	Abu22270 Protein e	670	19	95.0	311	5	ABP95725	Abp95725 Human GPC
598	19	95.0	299	2	AAV06968	Aav06968 E. canis	671	19	95.0	312	4	ABP95725	Abp95725 Human GPC
599	19	95.0	299	3	AAV07975	Aav07975 A corn tr	672	19	95.0	312	4	ABP95725	Abp95725 Human GPC
600	19	95.0	299	4	AAB93403	Aab93403 Human pro	673	19	95.0	312	4	ABP95725	Abp95725 Human GPC
601	19	95.0	299	4	AAB87731	Aab87731 Human t2R	674	19	95.0	312	4	ABP95725	Abp95725 Human GPC
602	19	95.0	299	5	ABG77957	Abg77957 Ehrlichia	675	19	95.0	312	4	ABP95725	Abp95725 Human GPC
603	19	95.0	299	5	ABR38899	Ab38899 Human hr2	676	19	95.0	312	4	ABP95725	Abp95725 Human GPC
604	19	95.0	299	6	ADA09779	Ada09779 E. canis	677	19	95.0	312	4	ABP95725	Abp95725 Human GPC
605	19	95.0	299	7	ADC97734	Adc97734 Rhizobio	678	19	95.0	312	4	ABP95725	Abp95725 Human GPC
606	19	95.0	300	3	AAG45274	Aag45274 Arabidops	679	19	95.0	312	4	ABP95725	Abp95725 Human GPC
607	19	95.0	300	3	AAG30714	Aag30714 Arabidops	680	19	95.0	312	4	ABP95725	Abp95725 Human GPC
608	19	95.0	300	3	AAG23886	Aag23886 Arabidops	681	19	95.0	312	4	ABP95725	Abp95725 Human GPC
609	19	95.0	300	5	ABP27828	Abp27828 Streptoco	682	19	95.0	312	4	ABP95725	Abp95725 Human GPC

683	19	95.0	312	7	ADC85589	Human GPC	756	19	95.0	328	4	AAU35342	Enterococ
684	19	95.0	312	7	ADD13513	C. glutam	757	19	95.0	328	5	ABB91780	Herbicida
685	19	95.0	313	2	AAR37346	PEP PM. 1	758	19	95.0	328	6	ABO23285	Mouse ary
686	19	95.0	313	5	ABR49170	Listeria	759	19	95.0	328	6	ABO23284	Cow aryl-
687	19	95.0	314	3	AAV99818	Wheat par	760	19	95.0	328	6	ABU28954	Protein e
688	19	95.0	314	6	ABR01619	Human G p	761	19	95.0	328	6	ABW73204	Staphyloc
689	19	95.0	314	6	ABR011619	Human G p	762	19	95.0	329	5	AAW80623	S. pneumo
690	19	95.0	314	6	ABU17461	Protein e	763	19	95.0	329	5	ABP27977	Streptoco
691	19	95.0	315	4	ABBS2707	Escherich	764	19	95.0	329	7	ABM73892	DNA clone
692	19	95.0	315	4	ABG71585	Human olf	765	19	95.0	331	2	AAV37504	Protein i
693	19	95.0	315	4	ABG72285	Human olf	766	19	95.0	331	2	AAV37504	Protein i
694	19	95.0	315	4	ABG72890	Human olf	767	19	95.0	331	4	AAU343812	Arabidops
695	19	95.0	315	5	ABE17492	Human sec	768	19	95.0	331	4	AAU343812	Arabidops
696	19	95.0	315	5	ABE17492	Human sec	769	19	95.0	331	4	AAU343812	Arabidops
697	19	95.0	315	6	ABM70746	Phototrab	770	19	95.0	334	2	AAU343812	Arabidops
698	19	95.0	315	6	ABR01616	Human G p	771	19	95.0	334	5	ABP41314	Human ova
699	19	95.0	315	7	ADG37263	Nuclear f	772	19	95.0	334	5	ABP41314	Human ova
700	19	95.0	315	7	ADD12827	Novel hum	773	19	95.0	334	5	ABP41314	Human ova
701	19	95.0	315	7	ADG37263	Novel hum	774	19	95.0	334	6	ADA57046	Human sec
702	19	95.0	316	3	AAU55622	Propionib	775	19	95.0	334	6	ADA57046	Human sec
703	19	95.0	316	4	AAU55622	Propionib	776	19	95.0	334	6	ADA57046	Human sec
704	19	95.0	316	6	ABP98031	Protein p	777	19	95.0	335	2	AAU57736	Hyperse
705	19	95.0	316	6	ABW52141	Propionib	778	19	95.0	335	3	AAU57736	Hyperse
706	19	95.0	317	2	AAU011381	Rat osteo	779	19	95.0	335	3	AAU57736	Hyperse
707	19	95.0	317	3	AAU011381	Rat osteo	780	19	95.0	336	3	AAU57736	Hyperse
708	19	95.0	317	3	AAU011381	Rat osteo	781	19	95.0	336	3	AAU57736	Hyperse
709	19	95.0	317	6	ABM69850	Phototrab	782	19	95.0	336	6	ABU50329	Protein e
710	19	95.0	317	7	AAW21746	Rat Prote	783	19	95.0	336	6	ABU50329	Protein e
711	19	95.0	318	2	AAW48894	Homo sapi	784	19	95.0	337	3	AAU67495	Arabidops
712	19	95.0	318	2	AAW48894	Homo sapi	785	19	95.0	337	3	AAU67495	Arabidops
713	19	95.0	318	3	AAU30052	Arabidops	786	19	95.0	337	3	AAU67495	Arabidops
714	19	95.0	318	3	AAU30052	Arabidops	787	19	95.0	337	3	AAU67495	Arabidops
715	19	95.0	318	3	AAU30052	Arabidops	788	19	95.0	337	3	AAU67495	Arabidops
716	19	95.0	318	5	ABP60935	Zymomonas	789	19	95.0	338	2	ADA35864	Acinetoba
717	19	95.0	318	7	ADG25727	Human pro	790	19	95.0	338	2	ADA35864	Acinetoba
718	19	95.0	318	7	ADG25727	Human pro	791	19	95.0	339	4	ABM61273	Human TAN
719	19	95.0	319	3	AAU31049	Arabidops	792	19	95.0	339	4	ABM61273	Human TAN
720	19	95.0	319	4	ABM61257	Mature hu	793	19	95.0	339	4	ABM61274	Human TAN
721	19	95.0	319	4	ABM61257	Mature hu	794	19	95.0	339	4	ABM61274	Human TAN
722	19	95.0	319	6	ABP98028	Protein p	795	19	95.0	339	4	ABM61274	Human TAN
723	19	95.0	319	6	ABU11223	Human TAN	796	19	95.0	339	4	ABM61274	Human TAN
724	19	95.0	320	3	AAU50958	Arabidops	797	19	95.0	339	4	ABM61274	Human TAN
725	19	95.0	320	3	AAU50958	Arabidops	798	19	95.0	339	4	ABM61274	Human TAN
726	19	95.0	320	3	AAU50958	Arabidops	799	19	95.0	339	4	ABM61274	Human TAN
727	19	95.0	320	3	AAU50958	Arabidops	800	19	95.0	339	4	ABM61274	Human TAN
728	19	95.0	320	4	AAU50958	Arabidops	801	19	95.0	339	4	ABM61274	Human TAN
729	19	95.0	320	4	AAU50958	Arabidops	802	19	95.0	339	4	ABM61274	Human TAN
730	19	95.0	321	3	AAU50958	Arabidops	803	19	95.0	339	4	ABM61274	Human TAN
731	19	95.0	321	3	AAU50958	Arabidops	804	19	95.0	339	4	ABM61274	Human TAN
732	19	95.0	321	6	ADA89479	Staphyloc	805	19	95.0	339	4	ABM61274	Human TAN
733	19	95.0	322	3	AAU94666	Human unc	806	19	95.0	339	4	ABM61274	Human TAN
734	19	95.0	322	3	AAU94666	Human unc	807	19	95.0	339	4	ABM61274	Human TAN
735	19	95.0	322	3	AAU94666	Human unc	808	19	95.0	339	4	ABM61274	Human TAN
736	19	95.0	322	3	AAU94666	Human unc	809	19	95.0	339	4	ABM61274	Human TAN
737	19	95.0	322	3	AAU94666	Human unc	810	19	95.0	339	4	ABM61274	Human TAN
738	19	95.0	322	6	ABU72033	Staphyloc	811	19	95.0	339	4	ABM61274	Human TAN
739	19	95.0	323	3	AAU6285	Arabidops	812	19	95.0	339	4	ABM61274	Human TAN
740	19	95.0	323	6	ABU41982	Protein e	813	19	95.0	339	4	ABM61274	Human TAN
741	19	95.0	324	3	AAU6284	Arabidops	814	19	95.0	339	4	ABM61274	Human TAN
742	19	95.0	324	6	ABU33384	Protein e	815	19	95.0	339	4	ABM61274	Human TAN
743	19	95.0	324	6	ABU33384	Protein e	816	19	95.0	339	4	ABM61274	Human TAN
744	19	95.0	324	6	ABU33384	Protein e	817	19	95.0	339	4	ABM61274	Human TAN
745	19	95.0	325	2	AAU50034	Porcine c	818	19	95.0	339	4	ABM61274	Human TAN
746	19	95.0	325	3	AAU94665	Human unc	819	19	95.0	339	4	ABM61274	Human TAN
747	19	95.0	325	3	AAU94665	Human unc	820	19	95.0	339	4	ABM61274	Human TAN
748	19	95.0	325	3	AAU94665	Human unc	821	19	95.0	339	4	ABM61274	Human TAN
749	19	95.0	325	6	ADA50732	Human NOV	822	19	95.0	339	4	ABM61274	Human TAN
750	19	95.0	326	3	AAU39939	Hepatitis	823	19	95.0	339	4	ABM61274	Human TAN
751	19	95.0	326	3	AAU39939	Hepatitis	824	19	95.0	339	4	ABM61274	Human TAN
752	19	95.0	326	3	AAU39939	Hepatitis	825	19	95.0	339	4	ABM61274	Human TAN
753	19	95.0	326	3	AAU39939	Hepatitis	826	19	95.0	339	4	ABM61274	Human TAN
754	19	95.0	327	2	AAU50033	Porcine c	827	19	95.0	339	4	ABM61274	Human TAN
755	19	95.0	327	6	ABU11347	Protein e	828	19	95.0	339	4	ABM61274	Human TAN

829	19	95.0	350	3	AA02086	Aab02086 F420-depe	902	19	95.0	377	6	ABU25867	Abu25867 Protein e
830	19	95.0	350	5	AA015202	Aa015202 Rhodococc	903	19	95.0	378	4	AAW93361	Aam93361 Human pol
831	19	95.0	350	5	AAU97147	Aau97147 Rhodococc	904	19	95.0	378	5	AAE20087	Aae20087 Lactobaci
832	19	95.0	350	5	AAE16748	Aae16748 Rhodococc	905	19	95.0	379	6	ABU23947	Abu23947 Protein e
833	19	95.0	351	6	ABU18964	Abu18964 Protein e	906	19	95.0	379	6	ABU49216	Abu49216 Protein e
834	19	95.0	352	5	ABBA48732	Abba48732 Listeria	907	19	95.0	379	6	ABM04817	Abm04817 Rat cdc 3
835	19	95.0	352	6	ABU32749	Abu32749 Protein e	908	19	95.0	379	7	ADD45256	Add45256 Rat Prote
836	19	95.0	353	3	AAU94667	Aau94667 Human unc	909	19	95.0	380	2	AAW98800	Aaw98800 H. pylori
837	19	95.0	353	3	AA080899	Aag080899 Arabidops	910	19	95.0	380	4	AAU35898	Aau35898 Helicobac
838	19	95.0	353	3	ABG16162	Abg16162 Novel hum	911	19	95.0	380	5	ABG30883	Abg30883 Cystathio
839	19	95.0	354	3	AA043810	Aag43810 Arabidops	912	19	95.0	380	6	ABU33267	Abu33267 Protein e
840	19	95.0	354	3	AA043810	Aag43810 Human col	913	19	95.0	382	5	ABP43943	Abp43943 Unidentif
841	19	95.0	355	4	AA043810	Aag43810 Human col	914	19	95.0	382	6	ABU33959	Abu33959 Protein e
842	19	95.0	356	3	AAU73382	Aay73382 HTRM clon	915	19	95.0	383	4	AAU60853	Aau60853 Mevalonat
843	19	95.0	356	6	ADA36384	Ada36384 Acinetoba	916	19	95.0	383	6	ABU15985	Abu15985 protein e
844	19	95.0	357	3	AA029807	Aag29807 Arabidops	917	19	95.0	383	6	ABU97187	Abu97187 Enzyme po
845	19	95.0	357	3	AA029807	Aag29807 Arabidops	918	19	95.0	384	3	AAU71056	Aay71056 Human mem
846	19	95.0	357	5	ABP63001	Abp63001 Human pol	919	19	95.0	384	4	AAU40198	Aam40198 Human pol
847	19	95.0	357	5	ABBA48768	Abba48768 Listeria	920	19	95.0	384	4	AAU40199	Aam40199 Human pol
848	19	95.0	358	3	AA029806	Aag29806 Arabidops	921	19	95.0	384	5	ABU34802	Abu34802 Human pro
849	19	95.0	358	3	AA029806	Aag29806 Arabidops	922	19	95.0	384	5	ABU34802	Abu34802 Human pro
850	19	95.0	359	3	AA029806	Aag29806 Arabidops	923	19	95.0	384	5	ABU34802	Abu34802 Human pro
851	19	95.0	359	3	AA029806	Aag29806 Arabidops	924	19	95.0	384	5	ABU34802	Abu34802 Human pro
852	19	95.0	360	4	AAU40979	Aam40979 Human pol	925	19	95.0	385	3	AA023282	Abo23282 Chlmanze
853	19	95.0	360	7	AAU40979	Aam40979 Human pol	926	19	95.0	385	3	AA023282	Abo23282 Chlmanze
854	19	95.0	361	3	AA029806	Aag29806 Arabidops	927	19	95.0	385	5	AAU72542	Aau72542 Arabidops
855	19	95.0	361	3	AA029806	Aag29806 Arabidops	928	19	95.0	386	3	AAU72542	Aau72542 Arabidops
856	19	95.0	361	3	AA029806	Aag29806 Arabidops	929	19	95.0	386	3	AAU72542	Aau72542 Arabidops
857	19	95.0	367	3	AA029806	Aag29806 Arabidops	930	19	95.0	386	4	AAU72542	Aau72542 Arabidops
858	19	95.0	367	3	AA029806	Aag29806 Arabidops	931	19	95.0	388	5	ABG30682	Abg30682 Cystathio
859	19	95.0	369	4	AAU72791	Aay72791 Human pol	932	19	95.0	388	6	ABU55193	Abu55193 Amino aci
860	19	95.0	369	4	AAU72791	Aay72791 Human pol	933	19	95.0	389	4	ABU55193	Abu55193 Amino aci
861	19	95.0	369	4	AAU72791	Aay72791 Human pol	934	19	95.0	389	4	ABU55193	Abu55193 Amino aci
862	19	95.0	369	4	AAU72791	Aay72791 Human pol	935	19	95.0	389	4	ABU55193	Abu55193 Amino aci
863	19	95.0	369	4	AAU72791	Aay72791 Human pol	936	19	95.0	389	4	ABU55193	Abu55193 Amino aci
864	19	95.0	369	4	AAU72791	Aay72791 Human pol	937	19	95.0	389	4	ABU55193	Abu55193 Amino aci
865	19	95.0	369	4	AAU72791	Aay72791 Human pol	938	19	95.0	389	4	ABU55193	Abu55193 Amino aci
866	19	95.0	369	4	AAU72791	Aay72791 Human pol	939	19	95.0	389	4	ABU55193	Abu55193 Amino aci
867	19	95.0	369	4	AAU72791	Aay72791 Human pol	940	19	95.0	389	4	ABU55193	Abu55193 Amino aci
868	19	95.0	369	4	AAU72791	Aay72791 Human pol	941	19	95.0	389	4	ABU55193	Abu55193 Amino aci
869	19	95.0	369	4	AAU72791	Aay72791 Human pol	942	19	95.0	389	4	ABU55193	Abu55193 Amino aci
870	19	95.0	369	4	AAU72791	Aay72791 Human pol	943	19	95.0	389	4	ABU55193	Abu55193 Amino aci
871	19	95.0	369	4	AAU72791	Aay72791 Human pol	944	19	95.0	389	4	ABU55193	Abu55193 Amino aci
872	19	95.0	369	4	AAU72791	Aay72791 Human pol	945	19	95.0	389	4	ABU55193	Abu55193 Amino aci
873	19	95.0	369	4	AAU72791	Aay72791 Human pol	946	19	95.0	389	4	ABU55193	Abu55193 Amino aci
874	19	95.0	369	4	AAU72791	Aay72791 Human pol	947	19	95.0	389	4	ABU55193	Abu55193 Amino aci
875	19	95.0	369	4	AAU72791	Aay72791 Human pol	948	19	95.0	389	4	ABU55193	Abu55193 Amino aci
876	19	95.0	369	4	AAU72791	Aay72791 Human pol	949	19	95.0	389	4	ABU55193	Abu55193 Amino aci
877	19	95.0	369	4	AAU72791	Aay72791 Human pol	950	19	95.0	389	4	ABU55193	Abu55193 Amino aci
878	19	95.0	369	4	AAU72791	Aay72791 Human pol	951	19	95.0	389	4	ABU55193	Abu55193 Amino aci
879	19	95.0	369	4	AAU72791	Aay72791 Human pol	952	19	95.0	389	4	ABU55193	Abu55193 Amino aci
880	19	95.0	369	4	AAU72791	Aay72791 Human pol	953	19	95.0	389	4	ABU55193	Abu55193 Amino aci
881	19	95.0	369	4	AAU72791	Aay72791 Human pol	954	19	95.0	389	4	ABU55193	Abu55193 Amino aci
882	19	95.0	369	4	AAU72791	Aay72791 Human pol	955	19	95.0	389	4	ABU55193	Abu55193 Amino aci
883	19	95.0	369	4	AAU72791	Aay72791 Human pol	956	19	95.0	389	4	ABU55193	Abu55193 Amino aci
884	19	95.0	369	4	AAU72791	Aay72791 Human pol	957	19	95.0	389	4	ABU55193	Abu55193 Amino aci
885	19	95.0	369	4	AAU72791	Aay72791 Human pol	958	19	95.0	389	4	ABU55193	Abu55193 Amino aci
886	19	95.0	369	4	AAU72791	Aay72791 Human pol	959	19	95.0	389	4	ABU55193	Abu55193 Amino aci
887	19	95.0	369	4	AAU72791	Aay72791 Human pol	960	19	95.0	389	4	ABU55193	Abu55193 Amino aci
888	19	95.0	369	4	AAU72791	Aay72791 Human pol	961	19	95.0	389	4	ABU55193	Abu55193 Amino aci
889	19	95.0	369	4	AAU72791	Aay72791 Human pol	962	19	95.0	389	4	ABU55193	Abu55193 Amino aci
890	19	95.0	369	4	AAU72791	Aay72791 Human pol	963	19	95.0	389	4	ABU55193	Abu55193 Amino aci
891	19	95.0	369	4	AAU72791	Aay72791 Human pol	964	19	95.0	389	4	ABU55193	Abu55193 Amino aci
892	19	95.0	369	4	AAU72791	Aay72791 Human pol	965	19	95.0	389	4	ABU55193	Abu55193 Amino aci
893	19	95.0	369	4	AAU72791	Aay72791 Human pol	966	19	95.0	389	4	ABU55193	Abu55193 Amino aci
894	19	95.0	369	4	AAU72791	Aay72791 Human pol	967	19	95.0	389	4	ABU55193	Abu55193 Amino aci
895	19	95.0	369	4	AAU72791	Aay72791 Human pol	968	19	95.0	389	4	ABU55193	Abu55193 Amino aci
896	19	95.0	369	4	AAU72791	Aay72791 Human pol	969	19	95.0	389	4	ABU55193	Abu55193 Amino aci
897	19	95.0	369	4	AAU72791	Aay72791 Human pol	970	19	95.0	389	4	ABU55193	Abu55193 Amino aci
898	19	95.0	369	4	AAU72791	Aay72791 Human pol	971	19	95.0	389	4	ABU55193	Abu55193 Amino aci
899	19	95.0	369	4	AAU72791	Aay72791 Human pol	972	19	95.0	389	4	ABU55193	Abu55193 Amino aci
900	19	95.0	369	4	AAU72791	Aay72791 Human pol	973	19	95.0	389	4	ABU55193	Abu55193 Amino aci
901	19	95.0	369	4	AAU72791	Aay72791 Human pol	974	19	95.0	389	4	ABU55193	Abu55193 Amino aci

975 19 95.0 403 3 ARG50762
 976 19 95.0 403 3 ARG13524
 977 19 95.0 403 4 ABE58218
 978 19 95.0 404 3 AAG53518
 979 19 95.0 404 3 AAG39960
 980 19 95.0 404 6 ABU40766
 981 19 95.0 405 2 AAY14954
 982 19 95.0 405 4 AAB83254
 983 19 95.0 405 6 ABM69291
 984 19 95.0 406 2 AAR21549
 985 19 95.0 406 6 ABU23329
 986 19 95.0 407 4 AAM39361
 987 19 95.0 407 5 ABP27964
 988 19 95.0 407 5 ABP61471
 989 19 95.0 407 6 ABU46908
 990 19 95.0 408 4 AAG91382
 991 19 95.0 409 5 AAE30494
 992 19 95.0 410 2 AAR54663
 993 19 95.0 410 2 AAR89212
 994 19 95.0 410 5 AAE30503
 995 19 95.0 411 4 AAU56508
 996 19 95.0 411 6 ABM53027
 997 19 95.0 411 6 ABU50525
 998 19 95.0 412 3 AAB58972
 999 19 95.0 412 3 AAB57091
 1000 19 95.0 412 6 ABU14941

ALIGNMENT'S

RESULT 1
 AAM47151
 ID AAM47151 standard; peptide; 6 AA.
 AC
 XX
 DT 12-FEB-2002 (first entry)

S chrysomallus actinomycin biosynthesis protein acmc fragment #9.

Modular enzyme system; cyclic gene synthesis; repetitive coding sequence;
 antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
 polyketide synthase; actinomycin biosynthesis.

Streptomyces chrysomallus.
 Synthetic.

WO200181564-A2.

01-NOV-2001.

25-APR-2001; 2001WO-DE001578.

26-APR-2000; 2000DE-01021267.

(ACTI-) ACTINODRUG PHARM GMBH.

Schauwecker F;

WPI; 2002-049276/06.

N-PSDB; ABA03345.

Preparing DNA encoding modular protein for e.g. producing new enzymes for
 synthesis of polyketide antibiotics, comprises cyclic integration of
 fragments into a vector.

Example 3; Page 54; 83pp; German.

The present invention relates to the preparation of DNA, in a circular
 vector, that encodes one or more segments of a modular polypeptide. DNA
 or DNA libraries produced this way are used to produce modular
 polypeptides, particularly enzymes, which can be used to act on

CC substrates to produce compounds for therapeutic testing. Enzymes of
 particular interest are those involved in non-ribosomal peptide synthesis
 or polyketide synthesis, and compounds for testing are particularly
 CC macrolide antibiotics, including penicillins, vancomycins or
 erythromycins, but may also be modular receptors. The present sequence is
 CC a fragment of a protein encoded by a Streptomyces chrysomallus
 CC actinomycin biosynthesis gene which was used in a plasmid in the
 CC exemplification of the invention

XX Sequence 6 AA;

SQ Query Match 95.0%; Score 19; DB 5; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0;

OY 2 VAEF 5

Db 3 VAEF 6

RESULT 2

ID AAB07871 standard; peptide; 7 AA.

XX AAB07871;

DT 14-NOV-2000 (first entry)

XX A beta-secretase inhibitor peptide.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 XX inhibitor.

XX Synthetic.

EH Key Location/Qualifiers

FT Modified-site 3 /note="hydroxyethylene"

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US003819.

XX 10-FEB-1999; 99US-0119571P.

PR 15-JUN-1999; 99US-0139172P.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tateano G, Tung J, Wang S, Mcconlogue L;

XX WPI; 2000-533011/48.

XX Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.

XX Disclosure; Page 12; 121pp; English.

XX The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents an inhibitor of beta-secretase enzyme

XX

Q Sequence 7 AA;

Query Match 95.0%; Score 19; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 ||||
 b 4 VAEF 7

RESULT 3

AB07872

D AAB07872 standard; peptide; 8 AA.

X C

AAB07872;

X X

14-NOV-2000 (first entry)

X T

A beta-secretase inhibitor peptide.

X E

Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 inhibitor.

X W

W

X W

W

X X

X

X S

S

X H

H

X Key

Location/Qualifiers

X T

T

X Modified-site

/note= "hydroxyethylene"

X X

X

X WO200047618-A2.

X N

N

X D

D

X 17-AUG-2000.

X F

F

X 10-FEB-2000; 2000WO-US003819.

X R

R

X 10-FEB-1999; 99US-0119571P.

X R

R

X 15-JUN-1999; 99US-0139172P.

X X

X

X (ELAN-) ELAN PHARM INC.

X A

A

X Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;

X I

I

X Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;

X X

X

X WPI; 2000-533011/48.

X X

X

X Purified beta-secretase protein used in assays to discover inhibitors

X T

T

X which can be used for the treatment of amyloidogenic diseases e.g.

X T

T

X Alzheimer's disease.

X T

T

X Disclosure; Page 12; 12lpp; English.

X X

X

X The specification describes a beta-secretase enzyme. The enzyme cleaves

X X

X

X beta-amyloid precursor protein to produce beta-amyloid peptide. This

X X

X

X enzyme is therefore implicated in the production of amyloid plaque

X X

X

X components which accumulate in the brains of individuals afflicted with

X X

X

X Alzheimer's disease. Inhibitors of beta-secretase are administered to a

X X

X

X mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-

X X

X

X like pathology to test if they maintain or improve cognitive ability or

X X

X

X reduce the plaque burden. The compounds are used for the treatment of

X X

X

X amyloidogenic diseases e.g. Alzheimer's disease. The present sequence

X X

X

X represents an inhibitor of beta-secretase enzyme

X X

X

Q Sequence 8 AA;

Query Match 95.0%; Score 19; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 ||||
 b 5 VAEF 8

RESULT 5

AAU28720

D AAU28720 standard; peptide; 8 AA.

X X

X

X AC

X

X AAU28720;

X X

X

X 03-JAN-2002 (first entry)

RESULT 4

ABB56241

D ABB56241 standard; peptide; 8 AA.

X X

AC

X AC

ABB56241;

X X

X

X 15-FEB-2002 (first entry)

X X

X

X Vascular dementia-associated protein isoform (VPI) 441.

X X

X

X Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;

X K

W

X diagnosis; prognosis; gene therapy.

X X

X

X OS

Homo sapiens.

X X

X

X WO200169261-A2.

X PN

X 20-SEP-2001.

X X

X

X 14-MAR-2001; 2001WO-GB001106.

X PF

X

X 15-MAR-2000; 2000GB-00006285.

X PR

X

X 24-NOV-2000; 2000GB-00028734.

X PR

X

X 28-NOV-2000; 2000US-00724391.

X X

X

X (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

X PA

X

X Herath HWAC, Parekh RB, Rohlf C;

X PI

X

X WPI; 2001-557937/62.

X DR

X

X Screening, diagnosis or prognosis of vascular dementia (VD), useful for

X X

X

X determining stage of VD and monitoring the effect of VD therapy.

X PT

X

X comprises analyzing body fluid by 2-dimensional electrophoresis for

X PT

X

X features correlated with VD.

X X

X

X Claim 6; Page 39; 15lpp; English.

X X

X

X The invention relates to screening, diagnosis or prognosis of Vascular

X CC

X

X Dementia (VD) in a subject comprising analysing body fluid from the

X CC

X

X subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of

X CC

X

X features containing at least one chosen feature whose relative abundance

X CC

X

X correlates with the presence, absence, stage or severity of VD or

X CC

X

X predicts the onset or course of VD, especially detecting in a sample of

X CC

X

X cerebrospinal fluid (CSF) from the subject one of 223 VD-associated

X CC

X

X protein isoforms (VPis) (ABB55801-ABB56295) as fully defined in the

X CC

X

X screening, diagnosis or prognosis of VD, for determining the stage or

X CC

X

X severity of VD, for identifying a subject at risk of VD or for monitoring

X CC

X

X the effect of therapy administered to a subject having VD. Nucleic acids

X CC

X

X encoding a VPI or inhibiting the function of a VPI are useful for the

X CC

X

X treatment of VD and for gene therapy

X X

X

X Sequence 8 AA;

X SQ

X

Query Match 95.0%; Score 19; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY *

2 VAEF 5

||||

Db 2 VAEF 5

RESULT 5

AAU28720

D AAU28720 standard; peptide; 8 AA.

X X

X

X AC

X

X AAU28720;

X X

X

X 03-JAN-2002 (first entry)

XX DE DPI tryptic digest peptide #317.
 XX KW Human; depression associated protein isoform; tryptic digest peptide;
 XX DP; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW maniac-depressive illness; schizoaffective disorder.
 XX OS Homo sapiens.
 XX FN WO200162787-A1.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000786.
 XX PR 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX WIPI; 2001-570626/64.
 XX PT Novel nucleic acid encoding a protein associated with bipolar affective
 disorder, which is used for diagnosis, prophylaxis and therapy of
 PT neuropsychiatric disorders, such as bipolar affective disorder.
 XX PS Disclosure; Page 37; 153pp; English.
 XX CC The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 CC increased in BAD subjects. Also described are peptide sequences
 CC identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
 CC encoded by. The sequences of the invention are useful for clinical
 CC screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), maniac-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents one of the DPI tryptic digest peptides of the present
 CC invention
 XX SQ Sequence 8 AA;
 XX Query Match 95.0%; Score 19; DB 4; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 DB |||||
 2 VAEF 5
 RESULT 6
 AAU25114
 ID AAU25114 standard; peptide; 8 AA.
 XX AC AAU25114;
 XX DT 18-DEC-2001 (first entry)
 XX DE Schizophrenia-Associated Protein Isoform (SPI) peptide #343.
 XX KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
 XX OS Homo sapiens.

PN WO200162785-A2.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000792.
 XX PR 24-FEB-2000; 2000GB-00004415.
 PR 28-DEC-2000; 2000US-00750395.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX WIPI; 2001-570624/64.
 XX PT New schizophrenia associated protein isoforms and encoding nucleic acid
 PT molecules, useful for treatment, diagnosis and prognosis of schizophrenia
 PT and screening for potential drugs for treatment and new drug targets.
 XX PS Disclosure; Page 36; 148pp; English.
 XX CC The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs
 XX SQ Sequence 8 AA;
 XX Query Match 95.0%; Score 19; DB 4; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 DB |||||
 2 VAEF 5
 RESULT 7
 AAU26368
 ID AAU26368 standard; peptide; 8 AA.
 XX AC AAU26368;
 XX DT 18-DEC-2001 (first entry)
 XX DE Depression-Associated Protein isoform DPI-124.
 XX KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DP; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; antianemic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.
 XX OS Homo sapiens.
 XX FN WO200163294-A2.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000791.
 XX PR 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMAC, Parekh RB, Rohlf C;
 XX WIPI; 2001-570624/64.

R WPI; 2001-582081/65.
 X Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 T unipolar depression, or for screening for modulators, comprises a BAD-
 T associated protein isoform.
 X
 X Claim 8; Page 37; 163pp; English.
 X
 X The invention relates to a preparation comprising an isolated Bipolar
 X Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 X used to screen, diagnose or prognosis of BAD or unipolar depression,
 X determine the stage or severity of BAD or unipolar depression, identify a
 X subject at risk of developing BAD or unipolar depression, or monitor the
 X effect of therapy in a subject. They are also used to screen for or
 X identify agents that interact with a DPI. These agents, antibodies
 X against the DPIs, and nucleic acids encoding the DPIs are used to treat
 X or prevent BAD or unipolar depression. Diseases that can be treated are
 X attention deficient disorder, a schizoaffective disorder, a bipolar or a
 X unipolar affective disorder. The DPIs are used in proteomics. The
 X proteomic approach of using DPIs for screening, diagnosis or prognosis of
 X BAD or unipolar depression overcomes the problems of using gene
 X expression analysis, such as not being able to obtain central nervous
 X system (CNS) tissue from a living patient under normal circumstances. The
 X present sequence is a DIP increased in the CSF (cerebro-spinal fluid) of
 X subjects having BAD

X Sequence 8 AA;
 Query Match 95.0%; Score 19; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

X 2 VAEF 5
 X ||||
 X 2 VAEF 5

X RESULT 8
 X AAU15458
 X AAU15458 standard; peptide; 8 AA.

X 24-OCT-2001 (first entry)
 X Schizophrenia-associated isoform peptide #343.
 X Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 X neurological disorder; neuropathy.
 X Homo sapiens.
 X WO200163293-A2.
 X 30-AUG-2001.

X 23-FEB-2001; 2001WO-GB000783.
 X 24-FEB-2000; 2000GB-00004415.
 X 28-DEC-2000; 2000US-00750395.

X (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 X Herath HMAC, Parekh RB, Rohlf C;
 X WPI; 2001-502868/55.

X Diagnosing and monitoring Schizophrenia by detecting the presence of
 X Schizophrenia Associated Features and Schizophrenia Associated Protein
 X Isoforms in samples of cerebrospinal fluid.

X Claim 6; Page 36; 160pp; English.

CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunoblotting or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SFs, SPIs and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neuroalgalic defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and characterisation of
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-
 CC AAU15762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention

X Sequence 8 AA;

Query Match 95.0%; Score 19; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 X ||||
 Db 2 VAEF 5

X RESULT 9
 X AAR78909
 X AAR78909 standard; peptide; 9 AA.

X 25-MAR-2003 (revised)
 X 27-MAR-1996 (first entry)
 X MAGE 3 105-113 cytotoxic T lymphocyte epitope.
 X MAGE 3 105-113; cytotoxic T; CTL; epitope; helper T; HTL; cell;
 X lymphocyte; antigens; treatment; disease prevention; tumours; cancer;
 X melanomas.
 X Homo sapiens.
 X WO9522317-A1.
 X 24-AUG-1995.

X 16-FEB-1995; 95WO-US002121.
 X 16-FEB-1994; 94US-00197484.

X (CYTE-) CYTEL CORP.
 X Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;
 X WPI; 1995-302545/39.

X Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 X bacterial, parasitic or tumour antigens - useful in the treatment and
 X prevention of diseases associated with the antigen e.g. hepatitis B.
 X Example 13; Page 71; 109pp; English.

X A compsn. which induces a cytotoxic T lymphocyte (CTL) response to a

CC human MAGE antigen (Ag) in a mammal comprises, a MAGE CTL Ag response
 CC inducing peptide (i.e. AAR78904 to AAR78917) and a lipid conjugated
 CC helper T cell inducing peptide. The compsn. is useful in the treatment
 CC and prevention of MAGE tumour Ag associated diseases, e.g. melanoma
 CC cancers. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 9 AA;

Query Match 95.0%; Score 19; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 2 VAEF 5
 |||||

RESULT 10
 ABB77871
 ID ABB77871 standard; peptide; 9 AA.
 AC ABB77871;
 XX
 XX
 DT 27-SEP-2002 (first entry)
 DE A beta-amyloid precursor protein (APP) inhibitor peptide.
 XX Beta-amyloid precursor protein; APP; APP inhibitor peptide; BACE;
 KW beta site APP cleaving enzyme; protein coordinate data; APP751;
 KW Swedish family mutation; Alzheimer's disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 5 /label= Sta
 FT /note= "statins"
 XX
 XX WO200225276-A1.
 XX
 PD 28-MAR-2002.
 XX
 XX 19-SEP-2001; 2001WO-US029387.
 XX
 XX 22-SEP-2000; 2000US-0234576P.
 XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Choppa R, Svenson K, Annis B, Akopian TN, Bard J, Stahl ML;
 PI Somers WS;
 XX
 DR WPI; 2002-519081/55.
 XX
 PT Crystallized complex of beta-site amyloid precursor protein (APP)
 PT cleaving enzyme (BACE) and APP inhibitor peptide useful for identifying
 PT agents that interact with active site of BACE or active site of APP
 PT binding protein or peptide.
 XX
 PS Claim 1; Page 22; 88pp; English.
 XX
 CC The present sequence represents a beta-amyloid precursor protein (APP)
 CC inhibitor peptide. This peptide inhibits binding between APP and BACE
 CC (beta site APP cleaving enzyme). The specification describes a
 CC crystallized complex of BACE and the present APP inhibitor. Protein
 CC coordinate data for BACE is given in the specification. The APP inhibitor
 CC peptide is based on the P10 to P4' APP751 Swedish family mutation. The
 CC crystallized complex is used for identifying an agent that interacts with
 CC an active site of BACE or an active site of an APP binding protein or
 CC peptide. The agents are useful in the treatment and/or prevention of
 CC Alzheimer's disease
 XX
 SQ Sequence 9 AA;

Query Match 95.0%; Score 19; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 6 VAEF 9
 |||||

RESULT 11
 ABB06593
 ID ABB06593 standard; peptide; 10 AA.
 XX
 AC ABB06593;
 XX
 XX 31-MAY-2002 (first entry)
 XX Beta-secretase related peptide SEQ ID NO:197.
 DE Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 XX aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KW Alzheimer's disease.
 KW
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200206306-A2.
 PN
 PD 24-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US023035.
 XX
 XX 19-JUL-2000; 2000US-0219795P.
 PR
 PR 12-MAR-2001; 2001US-0275251P.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrichson RL;
 PI
 XX WPI; 2002-216995/27.
 DR
 XX
 XX Novel substrates for human aspartyl protease useful for identifying
 PT modulators of beta secretase activity of aspartyl protease for treating
 PT Alzheimer's disease.
 PT
 XX
 PS Disclosure; Page 188; 188pp; English.
 XX
 CC The present invention describes an isolated peptide (I) comprising a
 CC sequence of at least four amino acids, where the peptide is a substrate
 CC for conducting aspartyl protease assays. (I) has neuroprotective and
 CC nootropic activities, and can be used as an inhibitor of beta-secretase
 CC activity. A beta-secretase modulator from the present invention can be
 CC used for inhibiting beta-secretase activity in vivo, and in the
 CC manufacture of a medicament for the treatment of Alzheimer's disease.
 CC Pharmaceutical compositions from the present invention can be used for
 CC treating a disease or condition characterised by an abnormal beta-
 CC secretase activity. (I) is useful for identifying agents that modulate
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
 CC a core structure to construct derivatives. ABL49914 to ABL49925 and
 CC ABB06409 to ABB06593 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 10 AA;

Query Match 95.0%; Score 19; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8
 |||||

RESULT 12
 BB06592
 D ABB06592 standard; peptide; 12 AA.
 X C C ABB06592;
 X T 31-MAY-2002 (first entry)
 X X Beta-secretase related peptide SEQ ID NO:196.
 E X
 X Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 W aspartyl protease; neuroprotective; nontropic; beta-secretase inhibitor;
 W Alzheimer's disease.
 X X
 X Homo sapiens.
 X Synthetic.
 X W0200206306-A2.
 X N 24-JAN-2002.
 X D 19-JUL-2001; 2001WO-US023035.
 X F 19-JUL-2000; 2000US-0219795P.
 X R 12-MAR-2001; 2001US-0275251P.
 X X (PHAA) PHARMACIA & UPJOHN CO.
 X A Yan R. Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 T Heinrichson RH;
 X WPI; 2002-216995/27.
 X Novel substrates for human aspartyl protease useful for identifying
 T modulators of beta secretase activity of aspartyl protease for treating
 T Alzheimer's disease.
 X X Disclosure; Page 188; 189pp; English.
 X The present invention describes an isolated peptide (I) comprising a
 C sequence of at least four amino acids, where the peptide is a substrate
 C for conducting aspartyl protease assays. (I) has neuroprotective and
 C nontropic activities, and can be used as an inhibitor of beta-secretase
 C activity. A beta-secretase modulator from the present invention can be
 C used for inhibiting beta-secretase activity in vivo, and in the
 C manufacture of a medicament for the treatment of Alzheimer's disease.
 C Pharmaceutical compositions from the present invention can be used for
 C treating a disease or condition characterised by an abnormal beta-
 C secretase activity. (I) is useful for identifying agents that modulate
 C the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
 C a core structure to construct derivatives. ABL49914 to ABL49925 and
 C ABB06409 to ABB06593 represent sequences used in the exemplification of
 C the present invention
 X Q Sequence 12 AA;
 Query Match 95.0%; Score 19; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 b 5 VAEF 8
 ||||
 ||||
 RESULT 13
 BG78404
 D ABG78404 standard; peptide; 12 AA.
 X C
 X ABG78404;
 X X

DT 15-NOV-2002 (first entry)
 XX Memapsin 2 substrate specificity determination peptide #10.
 DE Human; memapsin 2; aspartic protease; beta secretase;
 XX degenerative disease; Alzheimer's disease; amyloid precursor protein;
 XW APP; neuroprotective; nontropic; inhibitor;
 XW substrate side-chain preference.
 XX Homo sapiens.
 OS Synthetic.
 XX W0200253594-A2.
 XX 11-JUL-2002.
 XX 28-DEC-2001; 2001WO-US050826.
 XX 28-DEC-2000; 2000US-0258705P.
 PR 14-MAR-2001; 2001US-0275756P.
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA (UNII) UNIV ILLINOIS FOUND.
 XX Tang JJN, Koelsch G, Ghosh AK;
 PI WPI; 2002-619088/66.
 DR New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
 PT disease.
 PT Example 5; Page 51; 74pp; English.
 PS The invention relates to an inhibitor of catalytically active memapsin 2
 XX (an aspartic protease which can cleave at beta secretase sites), which
 CC binds to the active site of memapsin 2 defined by the presence of two
 CC catalytic aspartic residues and substrate binding cleft. Also included is
 CC a method of determination of the substrate side-chain preference in
 CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
 CC substrates with memapsin 2, and determining the sub-site preference of
 CC memapsin 2 by determining relative initial hydrolysis rates of the
 CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
 CC library of memapsin 2 inhibitors containing a base sequence taken from
 CC QK99-2 (Glu-Val-An-Leu-Ala-Ala-Glu-Phe), probing the library of
 CC inhibitors with memapsin 2 which binds to several inhibitors to generate
 CC several bound memapsin 2, and detecting the bound memapsin 2 with an
 CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
 CC secondary antibody. The inhibitors may be used in the manufacture of a
 CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
 CC be involved in the cleavage of amyloid precursor protein (APP), and for
 CC determining the substrate side-chain preference in memapsin 2 sub-sites.
 CC The present sequence represents a sub-site variant peptide used to
 CC determine the substrate specificity of human memapsin 2
 XX Sequence 12 AA;
 SQ Query Match 95.0%; Score 19; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VAEF 5
 Db 5 VAEF 8
 ||||
 ||||
 RESULT 14
 ADD35467
 ID ADD35467 standard; peptide; 12 AA.
 XX
 AC ADD35467;
 XX
 DT 15-JAN-2004 (first entry)
 XX

DE Escherichia coli DnaK peptide #3.
 XX crystallised recombinant protein; metabolism; Staphylococcus aureus;
 KW Streptococcus pneumoniae; Helicobacter pylori; Escherichia coli;
 KW Pseudomonas aeruginosa; vaccine.
 XX Escherichia coli.
 OS WO2003044185-A2.
 PN 30-MAY-2003.
 XX 21-NOV-2002; 2002WO-CA001768.
 XX 21-NOV-2001; 2001US-0332160P.
 PR 27-NOV-2001; 2001US-0333661P.
 PR 27-NOV-2001; 2001US-0333665P.
 PR 18-DEC-2001; 2001US-0341770P.
 PR 19-DEC-2001; 2001US-0341954P.
 PR 19-DEC-2001; 2001US-0342003P.
 PR 20-DEC-2001; 2001US-0342542P.
 PR 21-DEC-2001; 2001US-0344252P.
 PR 28-DEC-2001; 2001US-0343570P.
 PR 28-DEC-2001; 2001US-0343606P.
 PR 28-DEC-2001; 2001US-0343679P.
 XX (AFFI-) AFFINIUM PHARM INC.
 PA Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
 XX Canadian V, Domagala M, Houston S, Mansoury K, Necakov S, Nethery K;
 PI Ng I, Pinder B, Sheldrick B, Vallee F, Wrezel O;
 XX WPI; 2003-513596/48.
 DR New crystallized recombinant polypeptides from Staphylococcus aureus,
 XX Streptococcus pneumoniae, Helicobacter pylori or Pseudomonas aeruginosa
 PT involved in general metabolism, useful as drug targets for pathogenic
 PT bacteria.
 XX Disclosure; SEQ ID NO 66; 277pp; English.
 PS The invention comprises a crystallised recombinant protein that is
 XX involved in general metabolism, the recombinant protein may be from
 CC Staphylococcus aureus, Streptococcus pneumoniae, Helicobacter pylori,
 CC Escherichia coli or Pseudomonas aeruginosa. The crystallised recombinant
 CC protein of the invention is useful in the prevention (vaccine) or
 CC treatment of a disease or disorder caused by S. pneumoniae, H. pylori, E.
 CC coli or P. aeruginosa. The present amino acid sequence was used in the
 CC exemplification of the invention.
 XX Sequence 12 AA;
 SQ
 Query Match 95.0%; Score 19; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db 9 VAEF 12
 RESULT 15
 AAB07889
 ID AAB07889 standard; peptide; 13 AA.
 XX AAB07889;
 AC 14-NOV-2000 (first entry)
 XX A beta-secretase inhibitor peptide.
 DE Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 KW

KW inhibitor.
 XX Synthetic.
 XX WO200047618-A2.
 PN 17-AUG-2000.
 XX 10-FEB-2000; 2000WO-US003819.
 XX 10-FEB-1999; 99US-0119571P.
 PR 15-JUN-1999; 99US-0139172P.
 XX (ELAN-) ELAN PHARM INC.
 PA Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
 XX WPI; 2000-533011/48.
 DR Purified beta-secretase protein used in assays to discover inhibitors
 XX which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 PT Claim 33; Page 24; 121pp; English.
 PS The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents an inhibitor of beta-secretase enzyme
 XX Sequence 13 AA;
 SQ
 Query Match 95.0%; Score 19; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db 10 VAEF 13
 RESULT 16
 AAM99276
 ID AAM99276 standard; peptide; 13 AA.
 XX AAM99276;
 AC 07-DEC-2001 (first entry)
 XX Vaccine related MHC ligand peptide SEQ ID NO:379.
 DE Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 KW human immunodeficiency virus.
 XX Mycobacterium leprae.
 OS WO200170772-A2.
 XX 27-SEP-2001.
 PD 22-MAR-2001; 2001WO-FR000872.
 XX

X 23-MAR-2000; 2000FR-00003711.
 X (FABR) FABRE MEDICAMENT SA PIERRE.
 X Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
 X WPI; 2001-611470/70.
 X Stabilized pharmaceutical containing N-terminal glutamic acid or
 T glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 T with strong acid.
 X Claim 9; Page 96; 149pp; French.
 X The present invention describes a pharmaceutical compound (I) that
 C contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 C the form of an addition salt with a strong, physiologically acceptable
 C acid (II). Also described are: (a) a pharmaceutical composition
 C containing at least one (I); (b) a vaccine containing at least one (I)
 C where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 C method for in vitro diagnosis of diseases associated with the presence of
 C (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 C for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 C neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
 C cytostatic activities. (I) are useful, in human or veterinary medicine,
 C in pharmaceutical compositions (for treating immune disorders, e.g.
 C immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 C rejection, infection, hormonal disorders and central nervous system
 C diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 C treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 C infections; or (ii) of cancers. A particular application is in anti-
 C melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 C associated with interactions between MHC and (I), e.g. melanoma and human
 C immunodeficiency virus infection. AM98898 to AM99592 represent peptides
 C which can be used in pharmaceutical compounds from the present invention
 X Q Sequence 13 AA;
 Query Match 95.0%; Score 19; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 b 4 VAEF 7
 RESULT 17
 AB07888
 D AAB07888 standard; peptide; 14 AA.
 C AAB07888;
 T 14-NOV-2000 (first entry)
 X A peptide fragment derived from beta-amyloid precursor protein.
 X Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
 W amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
 W inhibitor.
 X Homo sapiens.
 S WO200047618-A2.
 N 17-AUG-2000.
 X 10-FEB-2000; 2000WO-US003819.
 F 10-FEB-1999; 99US-0119571P.
 R 15-JUN-1999; 99US-0139172P.
 X

PA (ELAN-) ELAN PHARM INC.
 XX Anderson JP, Baei G, Doane MT, Frigon N, John V, Power M;
 PI Sinha S, Tatsuno G, Tung J, Wang S, McConlogue L;
 XX WPI; 2000-533011/48.
 DR Purified beta-secretase protein used in assays to discover inhibitors
 PT which can be used for the treatment of amyloidogenic diseases e.g.
 PT Alzheimer's disease.
 XX Disclosure; Page 12; 121pp; English.
 CC The specification describes a beta-secretase enzyme. The enzyme cleaves
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
 CC enzyme is therefore implicated in the production of amyloid plaque
 CC components which accumulate in the brains of individuals afflicted with
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
 CC like pathology to test if they maintain or improve cognitive ability or
 CC reduce the plaque burden. The compounds are used for the treatment of
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
 CC represents a peptide derived from beta-amyloid precursor protein
 XX Sequence 14 AA;
 SQ Query Match 95.0%; Score 19; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db 11 VAEF 14
 RESULT 18
 AAM97460
 ID AAM97460 standard; peptide; 14 AA.
 XX AC AAM97460;
 XX 24-JAN-2002 (first entry)
 DT Human peptide #735 encoded by a SNP oligonucleotide.
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX Homo sapiens.
 OS WO200147944-A2.
 PN 05-JUL-2001.
 PD 28-DEC-2000; 2000WO-US035498.
 PF 28-DEC-1999; 99US-0173419P.
 PR 27-DEC-2000; 2000US-00173419.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT

PT autoimmune diseases and infections.
 XX Disclosure; Page 3829; 4143pp; English.
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 XX SQ Sequence 14 AA;

Query Match 95.0%; Score 19; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 ||||
 DB 5 VAEF 8

RESULT 19
 AAE32223
 ID AAE32223 standard; peptide; 15 AA.
 AC AAE32223;
 XX
 XX DT 24-MAR-2003 (first entry)
 XX Arabidopsis thaliana S11 peptide #6.
 DE
 XX Genomic database; mass spectrometer; proteomic business; pharmaceutical;
 XX nuclear transport; signalling pathway; cellular organelle.
 XX Arabidopsis thaliana.
 OS
 XX Arabidopsis thaliana.
 XX WO200280649-A2.
 PN
 XX 17-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US011417.
 PF
 XX 09-APR-2001; 2001US-0282551P.
 PR 20-APR-2001; 2001US-0285362P.
 XX
 XX (MDS-) MDS PROTEOMICS INC.
 XX Mann M, Mortensen P;
 PI
 XX WPI; 2003-058452/05.
 DR

Identifying coding sequence in genomic databases for conducting
 PT proteomics business, by using polypeptide sequence information obtained
 PT from peptide sequencing projects, especially those using mass
 PT spectrometers.

XX Example 1; Page 41; 100pp; English.

XX The invention relates to a method for identifying coding sequence in
 CC genomic databases, by using polypeptide sequence information obtained
 CC from peptide sequencing projects, especially those using mass
 CC spectrometers. It is useful for conducting a proteomics business. It is

CC also used for establishing a distribution system for distributing the
 CC pharmaceutical preparation for sale, and may optionally include
 CC establishing a sales group for marketing the pharmaceutical preparation.
 CC It is also used for predicting the gene structure, such as intron/exon
 CC boundaries; for searching genomic databases for sequences derived from
 CC multi-protein complexes e.g. assemblies with a particular function such
 CC as splicing, transport or nuclear import or export; for elucidating
 CC transient rather than structural complexes (that are involved in
 CC signalling pathways) and for identifying proteins in cellular organelles.
 CC The present sequence is Arabidopsis thaliana peptide used to illustrate
 CC the method of the invention
 XX
 XX SQ Sequence 15 AA;

Query Match 95.0%; Score 19; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 ||||
 DB 10 VAEF 13

RESULT 20
 AAW42944
 ID AAW42944 standard; peptide; 20 AA.
 XX
 XX AC AAW42944;
 XX
 XX DT 28-APR-1998 (first entry)
 XX Immunogenic Hepatitis A virus peptide YK-1369.

XX Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
 KW antibody.

XX Synthetic.
 OS Hepatitis A virus.
 XX WO9740147-A1.
 PN
 XX 30-OCT-1997.
 PD
 XX 18-APR-1997; 97WO-US006891.
 PF
 XX 19-APR-1996; 96US-0015644P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Fields HA, Khudyakov YE;
 PI
 XX WPI; 1997-535831/49.
 DR

Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune
 PT response to HAV in a mammal or to detect the presence of antibodies
 PT against HAV in a mammal.

XX Claim 33; Page 115; 140pp; English.

XX Peptides AAW42943-46 are immunogenic peptides corresponding to
 CC immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are
 CC substantially similar to a portion of the amino acid sequence of the P3A
 CC protein of HAV corresponding to amino acids 1423-1496. The present
 CC peptide is derived from amino acids 1430-1449 and has a reactivity of
 CC 58.5% with acute sera. Compositions containing the peptides can be used
 CC to induce an immune response to HAV in a mammal. The peptides can also be
 CC used to detect the presence of antibodies against HAV in mammalian serum.
 CC The peptides can also be used to make an antibody against HAV by
 CC administering the peptide to a mammal

XX Sequence 20 AA;

Query Match 95.0%; Score 19; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 4 VAEF 7

RESULT 21
AAW42943
D AAW42943 standard; peptide; 20 AA.
X
C AAW42943;
X
T 28-APR-1998 (first entry)
X
E Immunogenic Hepatitis A virus peptide YK-1368.
X
W Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
X antibody.
X Synthetic.
X Hepatitis A virus.
X W09740147-A1.
X
D 30-OCT-1997.
X
F 18-APR-1997; 97WO-US006891.
X
R 19-APR-1996; 96US-0015644P.
X
A (USSH) US DEPT HEALTH & HUMAN SERVICES.
X
I Fields HA, Khudyakov YE;
X WPI; 1997-535831/49.
X
T Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune
T response to HAV in a mammal or to detect the presence of antibodies
T against HAV in a mammal.
X
S Claim 33; Page 115; 140pp; English.
X
C Peptides AAW42943-46 are immunogenic peptides corresponding to
C immunogenic epitopes of the Hepatitis A virus (HAV). The peptides are
C substantially similar to a portion of the amino acid sequence of the P3A
C protein of HAV corresponding to amino acids 1423-1496. The present
C peptide is derived from amino acids 1421-1440 and has a reactivity of
C 63.4% with acute sera. Compositions containing the peptides can be used
C to induce an immune response to HAV in a mammal. The peptides can also be
C used to detect the presence of antibodies against HAV in mammalian serum.
C The peptides can also be used to make an antibody against HAV by
C administering the peptide to a mammal
X
Q Sequence 20 AA;

Query Match 95.0%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 13 VAEF 16

RESULT 22
AB69462
D AAB69462 standard; peptide; 21 AA.
X
C AAB69462;
X
T 20-APR-2001 (first entry)

XX Synthetic HAV P3A peptide, SEQ ID NO: 62.
DE Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine;
KW antigen; major structural capsid polypeptide; HAV antibody detection.
XX
OS Hepatitis A virus.
OS Synthetic.
XX W0200105824-A2.
EN
XX
PD 25-JAN-2001.
XX
PF 14-JUL-2000; 2000WO-US019267.
XX
PR 15-JUL-1999; 99US-0144412P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
FI Fields HA, Khudyakov YE;
XX
DR WPI; 2001-112681/12.
XX
PT Synthetic peptides used as antigen sources for enzyme immunoassays
PT detecting anti-hepatitis A virus and as vaccines.
XX
PS Claim 22; Page 108; 130pp; English.
XX
CC The present sequence is one of a number of synthetic peptides which are
CC immunoreactive with hepatitis A virus (HAV) antibodies. The peptides
CC comprise antigenic epitopes of the major structural capsid polypeptides
CC or non-structural polypeptides of HAV with one or more glutamine
CC molecules at the carboxy end of the peptide. The peptides are used to
CC detect the presence of antibodies against HAV in mammalian serum, to
CC detect the presence of HAV in a human or animal through the binding of
CC the peptide to an antibody, to detect acute phase infection by detecting
CC IGM antibodies in mammalian serum and detecting convalescence in a
CC mammal. The peptides are used to detect or quantify HAV antibodies in
CC samples in clinical or research-based assays using immunoblotting,
CC fluorescence in situ hybridisation analysis, gel-mobility shift assays,
CC tracking of radioactive or bioluminescent markers, chromatography or
CC electrophoresis. The peptides are used to induce an immune response to
CC HAV when administered to a human or animal. Glutamine at the carboxy end
CC of the peptides enhances the IGM antibody reactivity
XX
SQ Sequence 21 AA;

Query Match 95.0%; Score 19; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
b 13 VAEF 16

RESULT 23
AAB69463
ID AAB69463 standard; peptide; 21 AA.
XX
AC AAB69463;
XX
DT 20-APR-2001 (first entry)
XX
DE
XX
XX Synthetic HAV P3A peptide, SEQ ID NO: 63.
XX Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine;
KW antigen; major structural capsid polypeptide; HAV antibody detection.
XX
OS Hepatitis A virus.
OS Synthetic.
XX
PN W0200105824-A2.

XX PD 25-JAN-2001.
 XX PF 14-JUL-2000; 2000WO-US019267.
 XX PR 15-JUL-1999; 99US-0144412P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;
 XX DR WPI; 2001-112681/12.
 XX PT Synthetic peptides used as antigen sources for enzyme immunoassays
 XX PT detecting anti-hepatitis A virus and as vaccines.
 XX PS Claim 22; Page 109; 130pp; English.
 XX CC The present sequence is one of a number of synthetic peptides which are
 CC immunoreactive with hepatitis A virus (HAV) antibodies. The peptides
 CC comprise antigenic epitopes of the major structural capsid polypeptides
 CC or non-structural polypeptides of HAV with one or more glutamine
 CC molecules at the carboxy end of the peptide. The peptides are used to
 CC detect the presence of antibodies against HAV in mammalian serum, to
 CC detect the presence of HAV in a human or animal through the binding of
 CC the peptide to an antibody, to detect acute phase infection by detecting
 CC IGM antibodies in mammalian serum and detecting convalescence in a
 CC mammal. The peptides are used to detect or quantify HAV antibodies in
 CC samples in clinical or research-based assays using immunoblotting,
 CC fluorescence in situ hybridisation analysis, gel-mobility shift assays,
 CC tracking of radioactive or bioluminescent markers, chromatography or
 CC electrophoresis. The peptides are used to induce an immune response to
 CC HAV when administered to a human or animal. Glutamine at the carboxy end
 CC of the peptides enhances the IGM antibody reactivity
 XX SQ Sequence 21 AA;
 Query Match 95.0%; Score 19; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.7e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db 4 VAEF 7
 RESULT 24
 ID AAW42946
 AC AAW42946 standard; peptide; 25 AA.
 XX DT 28-APR-1998 (first entry)
 XX DE Immunogenic Hepatitis A virus peptide YK-1832.
 XX KW Immunogenic peptide; immunogenic epitope; P3A protein; immune response;
 XX KW antibody.
 XX OS Synthetic.
 XX OS Hepatitis A virus.
 XX PN WO9740147-A1.
 XX PD 30-OCT-1997.
 XX PF 18-APR-1997; 97WO-US006891.
 XX PR 19-APR-1996; 96US-0015644P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;

XX WPI; 1997-535831/49.
 XX CC Immunogenic Hepatitis A Virus (HAV) peptide(s) - used to induce an immune
 XX PT response to HAV in a mammal or to detect the presence of antibodies
 XX PT against HAV in a mammal.
 XX PS Claim 33; Page 115; 140pp; English.
 XX CC The present immunogenic peptide corresponds to an immunogenic epitope of
 CC the Hepatitis A virus (HAV). The peptide is substantially similar to a
 CC portion of the amino acid sequence of the P3A protein of HAV
 CC corresponding to amino acids 1423-1496. Compositions containing the
 CC peptide can be used to induce an immune response to HAV in a mammal. The
 CC peptide can also be used to detect the presence of antibodies against HAV
 CC in mammalian serum. The peptide can also be used to make an antibody
 CC against HAV by administering the peptide to a mammal
 XX SQ Sequence 25 AA;
 Query Match 95.0%; Score 19; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db 3 VAEF 6
 RESULT 25
 ID AAB69465
 AC AAB69465 standard; peptide; 25 AA.
 XX DT 20-APR-2001 (first entry)
 XX DE Synthetic HAV P3A peptide, SEQ ID NO: 65.
 XX KW Hepatitis A virus; HAV; immunogen; immunostimulant; virucide; vaccine;
 XX KW antigen; major structural capsid polypeptide; HAV antibody detection.
 XX OS Hepatitis A virus.
 XX OS Synthetic.
 XX PN WO200105824-A2.
 XX PD 25-JAN-2001.
 XX PF 14-JUL-2000; 2000WO-US019267.
 XX PR 15-JUL-1999; 99US-0144412P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;
 XX DR WPI; 2001-112681/12.
 XX PT Synthetic peptides used as antigen sources for enzyme immunoassays
 XX PT detecting anti-hepatitis A virus and as vaccines.
 XX PS Claim 22; Page 110; 130pp; English.
 XX CC The present sequence is one of a number of synthetic peptides which are
 CC immunoreactive with hepatitis A virus (HAV) antibodies. The peptides
 CC comprise antigenic epitopes of the major structural capsid polypeptides
 CC or non-structural polypeptides of HAV with one or more glutamine
 CC molecules at the carboxy end of the peptide. The peptides are used to
 CC detect the presence of antibodies against HAV in mammalian serum, to
 CC detect the presence of HAV in a human or animal through the binding of
 CC the peptide to an antibody, to detect acute phase infection by detecting
 CC IGM antibodies in mammalian serum and detecting convalescence in a
 CC mammal.

XC mammal. The peptides are used to detect or quantify HAV antibodies in
 XC samples in clinical or research-based assays using immunoblotting,
 XC fluorescence in situ hybridisation analysis, gel-mobility shift assays,
 XC tracking of radioactive or bioluminescent markers, chromatography or
 XC electrophoresis. The peptides are used to induce an immune response to
 XC HAV when administered to a human or animal. Glutamine at the carboxy end
 XC of the peptides enhances the IGM antibody reactivity
 XQ Sequence 25 AA;

Query Match 95.0%; Score 19; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

QY 2 VAEF 5
 Qb 3 VAEF 6

RESULT 26

AAW17832
 ID AAW17832 standard; peptide; 28 AA.

AC AAW17832;

AT 29-JUL-1997 (first entry)

DE Human mevalonate pyrophosphate decarboxylase peptide NP71.

KW Mevalonate pyrophosphate decarboxylase; MPD; cholesterol.

DS Homo sapiens.

PN WO9714787-A1.

PD 24-APR-1997.

PF 10-OCT-1996; 96WO-EP004394.

PR 18-OCT-1995; 95US-0005652P.

PA (NOVS) NOVARTIS AG.

PI Toth MJ, Huwylar LR;

PR 1997-245104/22.

Human mevalonate pyrophosphate decarboxylase coding sequence - used for
 screening for MPD inhibitors, which regulate and control cholesterol
 synthesis.

Example 3; Page 10; 37pp; English.

Peptide NP71 (AAW17832) was obtd. by trypsin digestion of human liver
 mevalonate pyrophosphate decarboxylase (MPD) (AAW17831), an enzyme of the
 cholesterol biosynthetic pathway. The sequence of the peptide was used to
 design PCR primers utilised in the amplification of cDNA from a rat liver
 cDNA library. A rat MPD partial clone was obtd. and used as a probe to
 screen a human liver cDNA library. A 1800 bp sequence (AAW66464) coding
 for human MPD was identified

Sequence 28 AA;

Query Match 95.0%; Score 19; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Qb 20 VAEF 23

RESULT 27

WO200157273-A2.

AAW33910
 ID AAW33910 standard; protein; 28 AA.
 AC AAW33910;
 AT 17-OCT-2001 (first entry)

DE Peptide #7947 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS genetic disorder.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

PR WPI; 2001-488897/53.

Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human placenta.

Claim 27; SEQ ID NO 34179; 654pp; English.

The present invention relates to single exon nucleic acid probes (SENP;
 see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 such probe. The probes are useful for producing a microarray for
 predicting, measuring and displaying gene expression in samples derived
 from human placenta. The probes are useful for antenatal diagnosis of
 human genetic disorders

Sequence 28 AA;

Query Match 95.0%; Score 19; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Qb 4 VAEF 7

RESULT 28

ABG55464

ID ABG55464 standard; peptide; 28 AA.

AC ABG55464;

DT 25-FEB-2003 (first entry)

DE Human liver peptide, SEQ ID No 34112.

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

PN WO200157273-A2.

PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241223P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244517P.
PR 08-NOV-2000; 2000US-0244517P.
PR 08-NOV-2000; 2000US-024474P.
PR 08-NOV-2000; 2000US-024475P.
PR 08-NOV-2000; 2000US-024476P.
PR 08-NOV-2000; 2000US-024477P.
PR 08-NOV-2000; 2000US-024478P.
PR 08-NOV-2000; 2000US-024523P.
PR 08-NOV-2000; 2000US-024524P.
PR 08-NOV-2000; 2000US-024525P.
PR 08-NOV-2000; 2000US-024525P.
PR 08-NOV-2000; 2000US-024525P.
PR 08-NOV-2000; 2000US-024527P.
PR 08-NOV-2000; 2000US-024528P.
PR 08-NOV-2000; 2000US-024532P.
PR 08-NOV-2000; 2000US-0246509P.
PR 08-NOV-2000; 2000US-0246510P.
PR 08-NOV-2000; 2000US-0246511P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.

DR N-PSDB; AAK55435.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 10247; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 32 AA;
Query Match 95.0%; Score 19; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 13 VAEF 16
|||
RESULT 32
AAO09024
ID AAO09024 standard; protein; 33 AA.
XX AAO09024;
XX 06-NOV-2001 (first entry)
XX Human polypeptide SEQ ID NO 22916.
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
XX WO200164835-A2.
XX 07-SEP-2001.
XX 26-FEB-2001; 2001WO-US004927.
XX 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX N-PSDB; AAK88955.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX Claim 20; SEQ ID NO 22916; 1399pp + Sequence Listing; English.

Sequence 35 AA;

Query Match 95.0%; Score 19; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 14 VAEF 17

RESULT 35
 AAWS1751
 ID AAWS1751 standard; protein; 35 AA.

XX AC AAWS1751;
 XX DT 13-JUN-2000 (first entry)
 XX DE H. influenzae antigenic Tbp2 peptide TBP2-21.
 XX KW Transferrin receptor; Tbp1; Tbp2; immunogenic; antibacterial; vaccine;
 XX KW diagnosis.
 XX OS Haemophilus influenzae.
 XX PN US6015688-A.
 XX PD 19-JAN-2000.
 XX PF 07-JUN-1995; 95US-00483577.
 XX PR 08-NOV-1993; 93US-00148968.
 XX PR 23-DEC-1993; 93US-00175116.
 XX PR 08-NOV-1994; 94US-00337483.
 XX PA (CONN-) CONNAUGHT LAB LTD.
 XX PI Loomore S, Harkness R, Schryvers A, Gray-Owen S, Yang Y;
 XX PI Mordin A, Klein M, Chong P;
 XX PI WPI; 1997-052329/05.

XX CC Haemophilus truncated transferrin receptor protein analogue, Tbp2 - used
 XX CC to induce protection against disease caused by transferrin producing
 XX CC pathogens, or as antigen to detect Haemophilus Tfr antibodies.
 XX CC Example 16; Col 39-40; 281pp; English.
 XX CC This invention describes a novel isolated and purified nucleic acid (I)
 XX CC encoding an immunogenic, C-terminally truncated analog of one of the
 XX CC transferrin receptor proteins Tbp1 or Tbp2 of Haemophilus influenzae
 XX CC which has antibacterial activity. (I) are used for recombinant production
 XX CC of truncated Tbp; as probes and primers for detecting, and diagnosing
 XX CC infection by, Haemophilus, also for isolating similar sequences from
 XX CC other bacteria; as immunogens for vaccinating against infections caused
 XX CC by bacteria that produce transferrin receptors, e.g. Haemophilus,
 XX CC Neisseria or Branhamella. The truncated proteins are useful as immunogens
 XX CC (as above); for diagnosing infection (as antigens in immunoassays) and
 XX CC for raising antibodies, used for diagnosis of infections or for passive
 XX CC immunization. AAWS1695-Y51767 represent H. influenzae transferrin
 XX CC receptor proteins Tbp1 and Tbp2 antigenic peptide fragments
 XX SQ Sequence 35 AA;

Query Match 95.0%; Score 19; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 14 VAEF 17

RESULT 37
 AAWS4105
 ID AAWS4105 standard; peptide; 35 AA.

XX AC AAWS4105;
 XX DT 20-JUL-1998 (first entry)
 XX DE Tbp2 antigenic peptide TBP2-21.

RESULT 36
 AAWS5788
 ID AAWS5788 standard; peptide; 35 AA.

XX AC AAWS5788;
 XX DT 14-JUL-1998 (first entry)
 XX DE Human aquaporin-1 NH2-terminal amino acid sequence CHIP28.
 XX KW Human; aquaporin-1; AQP-1; water channel protein; regulation;
 XX KW osmotic change; erythrocyte; dryness; blindness; hydration; asthma;
 XX KW secretion.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 30
 XX FT /label= Unknown
 XX FT /note= "not specified but is given as Ser in the full
 XX FT length protein given in AAWS5786"
 XX PN US5741671-A.
 XX PD 21-APR-1998.
 XX PF 06-JUN-1995; 95US-00468763.
 XX PR 17-AUG-1992; 92US-00930168.
 XX PR 24-FEB-1995; 95US-00393996.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Agre PC;
 XX PI WPI; 1998-260501/23.

XX CC Polynucleotide(s) encoding water channel protein Aquaporin-1 - are useful
 XX CC for recombinant production of protein for activity studies.
 XX CC Example 2; Col 20; 48pp; English.
 XX CC The present sequence represents the NH2-terminal amino acid sequence of
 XX CC aquaporin-1 (AQP-1), isolated from human erythrocytes. AQP-1 is a water
 XX CC channel protein. Water channel proteins regulate the passage of water in
 XX CC and out of cells, in response to osmotic changes. The DNA encoding AQP-1
 XX CC is useful for the recombinant production of AQP-1, found in mammalian
 XX CC erythrocytes, and is useful in the study to identify reagents which
 XX CC enhance or inhibit water channel function. This can lead to therapeutics
 XX CC which enhance secretion e.g. in the case of dryness of eyes which can
 XX CC lead to blindness or to hydrate large respiratory airways, as their
 XX CC dryness can precipitate asthma

XX SQ Sequence 35 AA;
 Query Match 95.0%; Score 19; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 14 VAEF 17

CC fragment) from strains of Haemophilus influenzae. This sequence
 CC corresponds to an epitope from the H. influenzae transferrin receptor
 CC protein Tbp2. The antibodies may be used for preventing and treating
 CC infections and disorders caused by H. influenzae, including bacterial
 CC meningitis, otitis media, epiglottitis, pneumonia and tracheobronchitis.
 CC The antibodies may also be used to detect the presence of H. influenzae
 CC proteins in samples according to standard methodologies (e.g. enzyme
 CC linked immunosorbent assay (ELISA)) and hence diagnose infections
 XX
 SQ Sequence 35 AA;

Query Match 95.0%; Score 19; DB 3; Length 35;
 Best Local Similarity 100.0%; Pred. NO. 4.7e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Db 14 VAEF 17
 |||||

RESULT 40
 AAW27782
 ID AAW27782 standard; protein; 36 AA.
 XX AC AAW27782;
 XX DT 21-JUL-1998 (first entry)
 XX DE UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
 XX KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
 XX KW Staphylococcus aureus; regulatory element; bacterial gene expression;
 XX KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
 XX KW toxic shock syndrome.
 XX OS Staphylococcus aureus.
 XX FH Key Location/Qualifiers
 FT Misc-difference 34 /note= "not specified"
 XX W09730070-A1.
 XX PD 21-AUG-1997.
 XX PF 19-FEB-1997; 97W0-US002318.
 XX PR 20-FEB-1996; 96US-0011888P.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PI Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO;
 PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;
 XX WPI; 1997-424969/39.
 DR N-PSDB; AAT83751.
 XX Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to
 XX isolate antimicrobial compounds, and in vaccines against S. aureus
 XX infection.
 XX Claim 6; Page 272; 989pp; English.
 XX The present sequence represents a Staphylococcus aureus protein, that,
 CC based on homology with a Bacillus subtilis protein, is believed to be a
 CC probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate
 CC transferase, UDP-N-acetylglucosamine enoylpyruvyl transferase). The DNA
 CC sequence was isolated from a library of clones of S. aureus WCUH 29 in
 CC Escherichia coli. The DNA sequence can be used in the construction of
 CC ribozymes and antisense sequences to control the expression of
 CC Staphylococcal genes. The DNA sequence is also useful as a source of
 CC regulatory elements for the control of bacterial gene expression. The
 CC present protein may be used to produce vaccines to enable a host to

CC produce specific antibodies with antibacterial action. These vaccines and
 CC antibodies would protect a host against invasion by S. aureus, and
 CC conditions relating to Staphylococcal infection, e.g. Staphylococcal food
 CC poisoning, scaled skin syndrome, and toxic shock syndrome
 XX
 SQ Sequence 36 AA;

Query Match 95.0%; Score 19; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. NO. 4.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Db 3 VAEF 6
 |||||

RESULT 41
 AAM99833
 ID AAM99833 standard; protein; 37 AA.
 XX AC AAM99833;
 XX DT 07-JAN-2002 (first entry)
 XX DE Human excretory related polypeptide SEQ ID NO 570.
 XX KW Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
 XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
 XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 XX KW antiparasitic; cardiast; immune disorder; cardiovascular disorder;
 XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine;
 XX KW excretory system.
 XX OS Homo sapiens.
 XX PN W0200155313-A2.
 XX PD 02-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US001323.
 XX PR 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-0184664P.
 XX PR 02-MAR-2000; 2000US-0186350P.
 XX PR 16-MAR-2000; 2000US-0189874P.
 XX PR 17-MAR-2000; 2000US-0190076P.
 XX PR 18-APR-2000; 2000US-0198123P.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PR 28-JUN-2000; 2000US-0214886P.
 XX PR 30-JUN-2000; 2000US-0215135P.
 XX PR 07-JUL-2000; 2000US-0216647P.
 XX PR 07-JUL-2000; 2000US-0216880P.
 XX PR 11-JUL-2000; 2000US-0217487P.
 XX PR 11-JUL-2000; 2000US-0217496P.
 XX PR 14-JUL-2000; 2000US-0218290P.
 XX PR 26-JUL-2000; 2000US-0220963P.
 XX PR 26-JUL-2000; 2000US-0220964P.
 XX PR 14-AUG-2000; 2000US-0224518P.
 XX PR 14-AUG-2000; 2000US-0224519P.
 XX PR 14-AUG-2000; 2000US-0225213P.
 XX PR 14-AUG-2000; 2000US-0225214P.
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 XX PR 14-AUG-2000; 2000US-0225758P.
 XX PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.
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PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
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PR 05-SEP-2000; 2000US-0229513P.
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PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232337P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
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PR 14-SEP-2000; 2000US-0232401P.
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PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241896P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246533P.
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PR 08-NOV-2000; 2000US-0246536P.
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PR 08-NOV-2000; 2000US-0246603P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251388P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465569/50.
XX N-PSDB; AA198806.
PT Isolated nucleic acid molecule encoding excretory system antigen is used
in preventing, treating or ameliorating a medical condition.
PS Claim 11; SEQ ID NO 570; 574pp + Sequence Listing; English.
XX The invention relates to novel excretory system related human
polynucleotides (AA198567-AA199503) and the encoded proteins (AAW99594-
AAW99913) useful for preventing, treating or ameliorating medical
conditions e.g. by protein or gene therapy, especially disorders related
to the excretory system. The genes are isolated from a range of human
tissues disclosed in the specification. The nucleic acids, proteins,
antibodies and (ant)agonists are useful in the diagnosis, treatment and
prevention of: (a) cancer, e.g. breast and ovarian cancer and other
cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal
tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's
disease, allergies, autoimmune haemolytic anaemia, autoimmune
thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis,
rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders
such as myocardial ischaemia; (d) wound healing; (e) neurological
diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases
such as viral, bacterial, fungal and parasitic infections. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 37 AA;
SQ

Query Match 95.0%; Score 19; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

Db ||||
14 VAEP 17

RESULT 42
RAM42648
ID AA442648 standard; protein; 37 AA.
XX AC AA442648;
XX DT 22-OCT-2001 (first entry)
XX DE Human kidney related polypeptide SEQ ID NO 517.
XX KW Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; cancer; immune disorder; cardiovascular disorder;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection.
XX OS Homo sapiens.
XX PN WO200155323-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US6001343.
XX PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205151P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224518P.
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PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
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PR 05-SEP-2000; 2000US-0229509P.
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PR 06-SEP-2000; 2000US-0230438P.
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PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
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PR 21-SEP-2000; 2000US-0234274P.
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PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-023627P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239835P.
PR 13-OCT-2000; 2000US-0239837P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.

XX 30-JAN-2001; 2001WO-US0000662.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-496933/54.

XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 14330; 327pp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 43 AA;

Query Match 95.0%; Score 19; DB 4; Length 43;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
 DB 40 VAEF 43

RESULT 45
 ABB21904
 ID ABB21904 standard; protein; 43 AA.

XX ABB21904;

XX 23-JAN-2002 (first entry)

XX Protein #3903 encoded by probe for measuring heart cell gene expression.
 DE Human; gene expression; heart; microarray; vascular system;
 DE cardiovascular disease; hypertension; cardiac arrhythmia;
 DE congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US0000666.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488999/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.

XX Claim 15; SEQ ID NO 23674; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 43 AA;

Query Match 95.0%; Score 19; DB 4; Length 43;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
 DB 40 VAEF 43

RESULT 46
 ABB51414
 ID ABB51414 standard; peptide; 43 AA.

XX ABB51414;

XX 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID No 30062.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000664.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

CC (MOLE-) MOLECULAR DYNAMICS INC.
CC Penn SG, Hanzel DK, Chen W, Rank DR;
CC WPI; 2001-488898/53.
CC Human genome-derived single exon nucleic acid probes useful for analyzing
CC gene expression in human adult liver.
CC Claim 27; SEQ ID NO 30062; 658pp; English.
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC Sequence 43 AA;
CC
CC Query Match 95.0%; Score 19; DB 4; Length 43;
CC Best Local Similarity 100.0%; Pred. No. 5.9e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 2 VAEF 5
CC Db 40 VAEF 43
CC
CC RESULT 47
CC LAM05214
CC ID AAM05214 standard; protein; 43 AA.
CC LAM05214;
CC 09-OCT-2001 (first entry)
CC Peptide #3896 encoded by probe for measuring breast gene expression.
CC Probe; human; breast disease; breast cancer; development disorder;
CC inflammatory disease; proliferative breast disease; non-carcinoma tumour.
CC Homo sapiens.
CC WO200157270-A2.
CC 09-AUG-2001.
CC 29-JAN-2001; 2001WO-US000661.
CC 04-FEB-2000; 2000US-0180312P.
CC 26-MAY-2000; 2000US-0207456P.
CC 30-JUN-2000; 2000US-00608408.
CC 03-AUG-2000; 2000US-00632366.
CC 21-SEP-2000; 2000US-0234687P.
CC 27-SEP-2000; 2000US-0236359P.
CC 04-OCT-2000; 2000GB-00024263.
CC (MOLE-) MOLECULAR DYNAMICS INC.
CC Penn SG, Hanzel DK, Chen W, Rank DR;
CC WPI; 2001-476286/51.

PT Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
PT Claim 27; SEQ ID NO 13954; 322pp; English.
PT
CC The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
CC probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridizes at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC Sequence 43 AA;
CC
CC Query Match 95.0%; Score 19; DB 4; Length 43;
CC Best Local Similarity 100.0%; Pred. No. 5.9e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 2 VAEF 5
CC Db 40 VAEF 43
CC
CC RESULT 48
CC AAB27178
CC ID AAB27178 standard; protein; 47 AA.
CC AAB27178;
CC 27-FEB-2001 (first entry)
CC RSV partial protein sequence SEQ ID NO: 26.
CC Negative stranded RNA virus; vaccine; attenuated virus; RSV; PIV;
CC measles; respiratory syncytial virus; parainfluenza virus.
CC Respiratory syncytial virus.
CC WO200061737-A2.
CC 19-OCT-2000.
CC 12-APR-2000; 2000WO-US009695.
CC 13-APR-1999; 99US-0129006P.
CC (USSH) US DEPT HEALTH & HUMAN SERVICES.
CC Murphy BR, Collins PL, Durbin AP, Skiadopoulos MH;
CC WPI; 2000-687044/67.
CC Producing attenuated negative stranded RNA virus vaccines from cloned
CC sequences, useful for immunizing against e.g. respiratory syncytial
CC virus, human parainfluenza virus, Sendai virus Newcastle disease virus,
CC mumps virus and measles virus.
CC Example 1; Page 62; 137pp; English.
CC The present invention is concerned with producing vaccines against
CC negative stranded RNA viruses. These viruses include measles, respiratory
CC syncytial virus (RSV) and parainfluenza virus (PIV) in particular. The
CC method of the invention comprises the production of a mutated form of the
CC virus which attenuates the strain and enables it to be used as a vaccine.
CC The present sequence comprises a partial viral protein sequence


```
SQ Sequence 47 AA;
Query Match 95.0%; Score 19; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. NO. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 34 VAEF 37
|||||
RESULT 49
AAM18541
ID AAM18541 standard; protein; 48 AA.
XX
AC AAM18541;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #4975 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488901/53.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human cervical epithelial cells.
XX
Claim 27; SEQ ID NO 23367; 487pp; English.
XX
The present invention relates to human single exon nucleic acid probes
(SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded
by one such probe. The SENPs are derived from human HeLa cells. The SENPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 48 AA;
Query Match 95.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. NO. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 3 VAEF 6
|||||
RESULT 51
AAM30996
ID AAM30996 standard; protein; 48 AA.
XX
AC AAM30996;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5033 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
```

```
RESULT 50
ABB37578
ID ABB37578 standard; peptide; 48 AA.
XX
AC ABB37578;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #5084 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-483447/52.
XX
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human fetal liver.
XX
Claim 27; SEQ ID NO 30213; 639pp + Sequence Listing; English.
XX
The invention relates to a single exon nucleic acid probe for measuring
human gene expression in a sample derived from human foetal liver. The
single exon nucleic acid probes may be used for predicting, measuring and
displaying gene expression in samples derived from human fetal liver. The
present sequence is a peptide encoded by a single exon nucleic acid probe
of the invention. Note: The sequence data for this patent did not form
part of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 48 AA;
Query Match 95.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. NO. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 3 VAEF 6
|||||
RESULT 51
AAM30996
ID AAM30996 standard; protein; 48 AA.
XX
AC AAM30996;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5033 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
```

X WO200157272-A2.
 N
 X
 D 09-AUG-2001.
 X
 F 30-JAN-2001; 2001WO-US000663.
 X
 R 04-FEB-2000; 2000US-0180312P.
 R 26-MAY-2000; 2000US-0207456P.
 R 30-JUN-2000; 2000US-00608408.
 R 03-AUG-2000; 2000US-00632366.
 R 21-SEP-2000; 2000US-0234687P.
 R 27-SEP-2000; 2000US-0236359P.
 R 04-OCT-2000; 2000GB-00024263.
 X (MOLE-) MOLECULAR DYNAMICS INC.
 A
 X Penn SG, Hanzel DK, Chen W, Rank DR;
 I WPI; 2001-488897/53.
 X
 R Human genome-derived single exon nucleic acid probes useful for analyzing
 T gene expression in human placenta.
 T
 X Claim 27; SEQ ID NO 31265; 654pp; English.
 S
 X The present invention relates to single exon nucleic acid probes (SENP;
 C see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 C such probe. The probes are useful for producing a microarray for
 C predicting, measuring and displaying gene expression in samples derived
 C from human placenta. The probes are useful for antenatal diagnosis of
 C human genetic disorders
 X
 X Sequence 48 AA;
 Q
 Query Match 95.0%; Score 19; DB 4; Length 48;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 b ||||
 3 VAEF 6
 RESULT 52
 BB22868
 D ABB22868 standard; protein; 48 AA.
 X
 C ABB22868;
 X
 T 23-JAN-2002 (first entry)
 X
 E Protein #4867 encoded by probe for measuring heart cell gene expression.
 X
 X Human; gene expression; heart; microarray; vascular system;
 W cardiovascular disease; hypertension; cardiac arrhythmia;
 W congenital heart disease.
 X
 X Homo sapiens.
 S
 X WO200157274-A2.
 N
 X
 D 09-AUG-2001.
 X
 F 30-JAN-2001; 2001WO-US000666.
 R
 X 04-FEB-2000; 2000US-0180312P.
 R 26-MAY-2000; 2000US-0207456P.
 R 30-JUN-2000; 2000US-00608408.
 R 03-AUG-2000; 2000US-00632366.
 R 21-SEP-2000; 2000US-0234687P.
 R 27-SEP-2000; 2000US-0236359P.
 R 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 PT
 XX Claim 15; SEQ ID NO 24638; 530pp; English.
 PS
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 48 AA;
 Query Match 95.0%; Score 19; DB 4; Length 48;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 Db ||||
 3 VAEF 6
 RESULT 53
 AAM70687
 ID AAM70687 standard; protein; 48 AA.
 XX
 AC AAM70687;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30993.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488900/53.
 XX
 DR Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 30993; 658pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
XX Sequence 48 AA;
SQ

Query Match 95.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 3 VAEF 6

RESULT 54
ABG52389
ID ABG52389 standard; peptide; 48 AA.
XX AC ABG52389;
XX
DT 25-FEB-2003 (first entry)
DE Human liver peptide, SEQ ID NO 31037.
XX
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
XX 09-AUG-2001.
PD
PF 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488998/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 31037; 658pp; English.
PS
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification

CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 48 AA;
SQ

Query Match 95.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 3 VAEF 6

RESULT 55
AAM06107
ID AAM06107 standard; protein; 48 AA.
XX AC AAM06107;
XX
DT 09-OCT-2001 (first entry)
DE Peptide #4789 encoded by probe for measuring breast gene expression.
XX
XX Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN WO200157270-A2.
XX
XX 09-AUG-2001.
PD
PF 29-JAN-2001; 2001WO-US000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX
XX Claim 27; SEQ ID NO 14947; 322pp; English.
PS
XX The present invention relates to novel single exon nucleic acid probes
CC (see AAI00010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 48 AA;
SQ

Query Match 95.0%; Score 19; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Y      2 VAEF 5
b      3 VAEF 6

RESULT 56
AO10565
D      AAO10565 standard; protein; 53 AA.
X      C      AAO10565;
X      X
X      T      06-NOV-2001 (first entry)
X      E      Human polypeptide SEQ ID NO 24457.
X      W      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
W      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
W      tissue growth factor; immunomodulatory; cancer; leukaemia;
W      nervous system disorders; arthritis; inflammation.
X      X
X      S      Homo sapiens.
X      N      WO200164835-A2.
X      D      07-SEP-2001.
X      F      26-FEB-2001; 2001WO-US004927.
X      R      28-FEB-2000; 2000US-00515126.
X      R      18-MAY-2000; 2000US-00577409.
X      A      (HYSE-) HYSEQ INC.
X      T      Tang YT, Liu C, Drmanac RT;
X      R      WPI; 2001-514838/56.
X      R      N-PSDB; AAI90496.
X      T      Isolated nucleic acids and polypeptides, useful for preventing diagnosing
X      and treating e.g. leukemia, inflammation and immune disorders.
X      S      Claim 20; SEQ ID NO 24457; 1399pp + Sequence Listing; English.
X      C      The invention relates to human polynucleotides (AA179941-AA193841) and
X      the encoded proteins (AA000010-AA013910) that exhibit activity relating to
X      cytokine, cell proliferation or cell differentiation or which may induce
X      production of other cytokines in other cell populations. The
X      polynucleotides and polypeptides are useful in gene therapy, vaccines or
X      peptide therapy. The polypeptides have various cytokine-like activities,
X      e.g. stem cell growth factor activity, haematopoiesis regulating
X      activity, tissue growth factor activity, immunomodulatory activity and
X      activin/inhibin activity and may be useful in the diagnosis and/or
X      treatment of cancer, leukaemia, nervous system disorders, arthritis and
X      inflammation. Note: The sequence data for this patent did not form part
X      of the printed specification, but was obtained in electronic format
X      directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
X      S      Sequence 53 AA;
X      Query Match      95.0%; Score 19; DB 4; Length 53;
X      Best Local Similarity 100.0%; Pred. No. 7.3e+02;
X      Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
X      Y      2 VAEF 5
X      33 VAEF 36

RESULT 57
AO05247
D      AAO05247 standard; protein; 53 AA.
X      X
X      T      06-NOV-2001 (first entry)
X      E      Human polypeptide SEQ ID NO 19139.
X      W      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
W      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
W      tissue growth factor; immunomodulatory; cancer; leukaemia;
W      nervous system disorders; arthritis; inflammation.
X      X
X      S      Homo sapiens.
X      N      WO200164835-A2.
X      D      07-SEP-2001.
X      F      26-FEB-2001; 2001WO-US004927.
X      R      28-FEB-2000; 2000US-00515126.
X      R      18-MAY-2000; 2000US-00577409.
X      A      (HYSE-) HYSEQ INC.
X      T      Tang YT, Liu C, Drmanac RT;
X      R      WPI; 2001-514838/56.
X      R      N-PSDB; AAI85178.
X      T      Isolated nucleic acids and polypeptides, useful for preventing diagnosing
X      and treating e.g. leukemia, inflammation and immune disorders.
X      S      Claim 20; SEQ ID NO 19139; 1399pp + Sequence Listing; English.
X      C      The invention relates to human polynucleotides (AA179941-AA193841) and
X      the encoded proteins (AA000010-AA013910) that exhibit activity relating to
X      cytokine, cell proliferation or cell differentiation or which may induce
X      production of other cytokines in other cell populations. The
X      polynucleotides and polypeptides are useful in gene therapy, vaccines or
X      peptide therapy. The polypeptides have various cytokine-like activities,
X      e.g. stem cell growth factor activity, haematopoiesis regulating
X      activity, tissue growth factor activity, immunomodulatory activity and
X      activin/inhibin activity and may be useful in the diagnosis and/or
X      treatment of cancer, leukaemia, nervous system disorders, arthritis and
X      inflammation. Note: The sequence data for this patent did not form part
X      of the printed specification, but was obtained in electronic format
X      directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
X      S      Sequence 53 AA;
X      Query Match      95.0%; Score 19; DB 4; Length 53;
X      Best Local Similarity 100.0%; Pred. No. 7.3e+02;
X      Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
X      Y      2 VAEF 5
X      33 VAEF 36

RESULT 58
AA087390
D      AA087390 standard; protein; 56 AA.
X      X
X      T      07-NOV-2001 (first entry)
X      E      Human immune/haematopoietic antigen SEQ ID NO:14983.
X      W      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
W      cytostatic; gene therapy; vaccine; metastasis.
X      X
X      S      Homo sapiens.

```


I Rosen CA, Barash SC, Ruben SM;
 X WPI; 2001-483426/52.
 R N-PSDB; AAK60171.
 X Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 T useful for preventing, diagnosing and/or treating cancers and metastasis.
 T Claim 11; SEQ ID NO 14993; 3071pp + Sequence Listing; English.
 S
 X AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 C amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 C activity, and can be used in gene therapy and vaccine production. (I)
 C proteins and polynucleotides may be used in the prevention, diagnosis and
 C treatment of diseases associated with inappropriate (I) expression. For
 C example, they may be used to treat disorders associated with decreased
 C expression by rectifying mutations or deletions in a patient's genome
 C that affect the activity of (I) by expressing inactive proteins or to
 C supplement the patient's own production of (I). Additionally, (I)
 C polynucleotides may be used to produce the secreted (I), by inserting the
 C nucleic acids into a host cell and culturing the cell to express the
 C protein. (I) proteins and polynucleotides may be used to prevent,
 C diagnose and treat immune/hematopoietic-related diseases, especially
 C cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 C to AAK87694 represent human immune/hematopoietic antigen genomic
 C sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 C represent sequences used in the exemplification of the present invention
 X Sequence 56 AA;
 Q

Query Match 95.0%; Score 19; DB 4; Length 56;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 1 VAEF 4

RESULT 59
 BP97126
 D ABP97126 standard; peptide; 56 AA.
 X C ABP97126;
 X T 24-JUN-2003 (first entry)
 X X Human matrix metalloproteinase 7 cleavage region peptide SEQ ID NO:4.
 E Human; matrix metalloproteinase; MMP; anticancer; wound healing;
 W matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
 W vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
 W vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
 W dermatological; metastatic; non-metastatic; vascularised; heart disease;
 W non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
 W macular degeneration; diabetic retinopathy; cleavage region.
 S Homo sapiens.
 X N WO2003018748-A2.
 X N 06-MAR-2003.
 X D 15-AUG-2002; 2002WO-US026319.
 F 16-AUG-2001; 2001US-0312726P.
 X R 21-DEC-2001; 2001US-00032376.
 R R 21-MAY-2002; 2002US-00153185.
 X A (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 X X Quirk S, Weart IF;
 I

DR WPI; 2003-381408/36.
 XX Anti-angiogenic composition comprising peptide inhibitor of matrix
 PT metalloproteinase, useful for decreasing the expression of vascular
 PT endothelial growth factor and treating cancers and tissue injuries.
 XX Claim 17; Page 15; 103pp; English.
 PS
 XX The present invention describes an anti-angiogenic composition (I) for
 CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)
 CC comprises an effective amount of a peptide inhibitor of matrix
 CC metalloproteinase (MMP), where the peptide can inhibit the expression of
 CC VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective,
 CC antidiabetic, ophthalmological and dermatological activities. (I) can be
 CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX Sequence 56 AA;
 SQ

Query Match 95.0%; Score 19; DB 6; Length 56;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Db 31 VAEF 34

RESULT 60
 ABG76312
 ID ABG76312 standard; protein; 56 AA.
 XX AC ABG76312;
 XX 10-MAY-2003 (first entry)
 DT Human matrix metalloproteinase (MMP) peptide inhibitor #4.
 XX Human; peptide inhibitor; matrix metalloproteinase-7; MMP-7;
 XX cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnary.
 XX Homo sapiens.
 OS WO2003016520-A1.
 XX 27-FEB-2003.
 PD 15-AUG-2002; 2002WO-US026198.
 XX 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.
 XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA Quirk S, Malik S, Villanueva JM;
 PI WPI; 2003-289980/28.
 XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.
 XX Claim 1; Page 16; 120pp; English.
 PS

Query Match 95.0%; Score 19; DB 2; Length 58;

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABLN15762 to ABLN27252 encode the human ORFX proteins given in ABLN00010 to ABLN11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with an ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut, protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not

C form part of the printed specification, but was obtained in electronic
 C format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

X Sequence 58 AA;

Q Query Match 95.0%; Score 19; DB 5; Length 58;

Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5

b |||||

30 VAEF 33

ESULT 63

AG60085

D AAG60085 standard; protein; 59 AA.

C AAG60085;

T 18-OCT-2000 (first entry)

X Arabidopsis thaliana protein fragment SEQ ID NO: 77787.

E Arabidopsis thaliana protein fragment SEQ ID NO: 77787.

W Protein identification; signal transduction pathway; metabolic pathway;
 W hybridisation assay; genetic mapping; gene expression control; promoter;
 W termination sequence.

S Arabidopsis thaliana.

X EF1033405-A2.

D 06-SEP-2000.

F 25-FEB-2000; 2000EP-00301439.

X 25-FEB-1999; 99US-0121825P.

R 03-MAR-1999; 99US-0123180P.

R 23-MAR-1999; 99US-0123548P.

R 25-MAR-1999; 99US-0125788P.

R 29-MAR-1999; 99US-0126264P.

R 01-APR-1999; 99US-0126785P.

R 06-APR-1999; 99US-0127462P.

R 08-APR-1999; 99US-0128234P.

R 16-APR-1999; 99US-0128714P.

R 19-APR-1999; 99US-0129845P.

R 21-APR-1999; 99US-0130077P.

R 23-APR-1999; 99US-0130449P.

R 28-APR-1999; 99US-0130510P.

R 30-APR-1999; 99US-0131449P.

R 04-MAY-1999; 99US-0132048P.

R 05-MAY-1999; 99US-0132407P.

R 06-MAY-1999; 99US-0132484P.

R 07-MAY-1999; 99US-0132487P.

R 11-MAY-1999; 99US-0132863P.

R 14-MAY-1999; 99US-0134256P.

R 14-MAY-1999; 99US-0134218P.

R 14-MAY-1999; 99US-0134219P.

R 14-MAY-1999; 99US-0134221P.

R 18-MAY-1999; 99US-0134370P.

R 19-MAY-1999; 99US-0134768P.

R 20-MAY-1999; 99US-0134941P.

R 21-MAY-1999; 99US-0135124P.

R 24-MAY-1999; 99US-0135353P.

R 25-MAY-1999; 99US-0135629P.

R 27-MAY-1999; 99US-0136021P.

R 28-MAY-1999; 99US-0136392P.

R 01-JUN-1999; 99US-0136782P.

R 03-JUN-1999; 99US-0137222P.

R 99US-0137528P.

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PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

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PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

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PR 22-JUN-1999; 99US-0139899P.

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PR 30-JUN-1999; 99US-0141287P.

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PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

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PR 23-JUL-1999; 99US-0145218P.

PR 23-JUL-1999; 99US-0145224P.

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PR 28-JUL-1999; 99US-0145951P.

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PR 02-AUG-1999; 99US-0146388P.

PR 02-AUG-1999; 99US-0146388P.

PR 04-AUG-1999; 99US-0147038P.

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PR 04-AUG-1999; 99US-0147302P.

PR 05-AUG-1999; 99US-0147192P.

PR 05-AUG-1999; 99US-0147260P.

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Query Match 95.0%; Score 19; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 78631.

Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.

05-MAR-1999; 99US-0123180P.

09-MAR-1999; 99US-0123548P.

23-MAR-1999; 99US-0125788P.

25-MAR-1999; 99US-0126264P.

29-MAR-1999; 99US-0126785P.

01-APR-1999; 99US-0127462P.

06-APR-1999; 99US-0128234P.

08-APR-1999; 99US-0128714P.

16-APR-1999; 99US-0129845P.

19-APR-1999; 99US-0130077P.

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30-APR-1999; 99US-0132407P.

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05-MAY-1999; 99US-0132485P.

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24-MAY-1999; 99US-0135629P.

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27-MAY-1999; 99US-0136392P.

28-MAY-1999; 99US-0136782P.

01-JUN-1999; 99US-0137222P.

03-JUN-1999; 99US-0137528P.

04-JUN-1999; 99US-0137502P.

07-JUN-1999; 99US-0137724P.

08-JUN-1999; 99US-0138094P.

10-JUN-1999; 99US-0138540P.

14-JUN-1999; 99US-0138847P.

14-JUN-1999; 99US-0139119P.

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R 30-JUN-1999; 99US-0142887P.
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R 12-AUG-1999; 99US-0148341P.

PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154035P.
PR 22-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 26-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157533P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 95.0%; Score 19; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 45 VAEF 48

RESULT 65

ABB42044
ID ABB42044 standard; peptide; 60 AA.

XX AC ABB42044;
XX DT 04-FEB-2002 (first entry)
XX DE Peptide #9550 encoded by human foetal liver single exon probe.
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX OS Homo sapiens.

XX PN WO200157277-A2.
XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT Gene expression in human foetal liver.
XX FS Claim 27; SEQ ID NO 34679; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
XX CC human gene expression in a sample derived from human foetal liver. The
XX CC single exon nucleic acid probes may be used for predicting, measuring and
XX CC displaying gene expression in samples derived from human foetal liver. The
XX CC present sequence is a peptide encoded by a single exon nucleic acid probe
XX CC of the invention. Note: The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 AA;
Query Match 95.0%; Score 19; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 8 VAEF 11
RESULT 66
AAM35846
ID AAM35846 standard; protein; 60 AA.
XX AC AAM35846;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #9883 encoded by probe for measuring placental gene expression.
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW Genetic disorder.
XX OS Homo sapiens.

XX PN WO200157272-A2.
XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT Gene expression in human placenta.
XX PS Claim 27; SEQ ID NO 36115; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from human placenta. The probes are useful for antenatal diagnosis of
XX CC human genetic disorders
XX SQ Sequence 60 AA;
Query Match 95.0%; Score 19; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 8 VAEF 11
RESULT 67
AAM75737
ID AAM75737 standard; protein; 60 AA.
XX AC AAM75737;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36043.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.

XX PN WO200157276-A2.
XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.

PS Example 4; SEQ ID NO 36043; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a CC protein encoded by one of the probes of the invention

XX Sequence 60 AA;

Query Match 95.0%; Score 19; DB 4; Length 60;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

DB 8 VAEF 11

RESULT 68

AA62925

ID AAM62925 standard; protein; 60 AA.

AC AAM62925;

DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 35030.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;

KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

XX WO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human brains.

PS Example 4; SEQ ID NO 35030; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention

XX Sequence 60 AA;

Query Match 95.0%; Score 19; DB 4; Length 60;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

DB 8 VAEF 11

RESULT 69

ABG57475

ID ABG57475 standard; peptide; 60 AA.

XX AC ABG57475;

XX 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID NO 36123.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

KW hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000664.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488998/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

XX Claim 27; SEQ ID NO 36123; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 60 AA;

Query Match 95.0%; Score 19; DB 4; Length 60;

26-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241825P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251989P.
05-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
26-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241825P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251989P.
05-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX N-PSDB; AAK64028.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 18840; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I/
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent
XX disease and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX Sequence 62 AA;
Query Match 95.0%; Score 19; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. NO. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 25 VAEF 28
RESULT 72
ABM65667
ID ABM65667 standard; protein; 62 AA.
AC ABM65667;
DT 20-OCT-2003 (first entry)
DE Propionibacterium acnes immunogenic polypeptide #30343.
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine; immunogenic.
XX Propionibacterium acnes.
XX WO2003033515-A1.
XX 24-APR-2003.
XX 11-OCT-2002; 2002WO-US032727.
XX 15-OCT-2001; 2001US-00978825.
XX (CORI-) CORIXA CORP.
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallie-Douglass J;
XX WPI; 2003-381789/36.
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the

PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX
 PS Claim 7; SEQ ID NO 30343; 1481pp; English.

XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 XX encoding a Propionibacterium acnes protein. The invention also relates to
 XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 XX immunogenic fragments of P. acnes polypeptides. The invention
 XX additionally encompasses expression vectors and host cells comprising a
 XX polynucleotide of the invention; antibodies against polypeptides of the
 XX invention; fusion proteins comprising a polypeptide of the invention; a
 XX method for stimulating an immune response specific for a P. acnes
 XX polypeptide and an isolated T cell population comprising T cells prepared
 XX via this method; a vaccine composition (comprising P. acnes polypeptides,
 XX polynucleotides, antibodies, fusion proteins), T cell populations, or
 XX antigen-presenting cells that express the polypeptide; a method and kit
 XX for detecting or determining the presence or absence of P. acnes in a
 XX patient; and a method for inhibiting the development of P. acnes in a
 XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 XX proteins, T cell populations or antigen-presenting cells that express the
 XX polypeptides are useful for diagnosing, preventing or treating acne
 XX vulgaris, or for stimulating an immune response specific for a P. acnes
 XX protein. The polynucleotides can also be used as probes or primers for the
 XX nucleic acid hybridisation. The vaccine composition is useful for the
 XX stimulation of an immune response against P. acnes, or for treating acne,
 XX and the kit is useful for performing a diagnostic assay. The present
 XX sequence represents a specifically claimed P. acnes polypeptide which is
 XX thought to contain an immunogenic region. Note: The sequence data for
 XX this patent did not form part of the printed specification, but was
 XX obtained in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 62 AA;

Query Match 95.0%; Score 19; DB 6; Length 62;
 Best Local Similarity 100.0%; Pred. NO. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 8 VAEF 11

RESULT 73
 AA009517
 ID AA009517 standard; protein; 64 AA.

XX AA009517;
 XX
 XX
 XX 06-NOV-2001 (first entry)
 XX
 XX Human polypeptide SEQ ID NO 23409.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 XX tissue growth factor; immunomodulatory; cancer; leukaemia;
 XX nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.
 DR N-PSDB; AA189448.
 XX
 XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 XX Claim 20; SEQ ID NO 23409; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA00010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 64 AA;

Query Match 95.0%; Score 19; DB 4; Length 64;
 Best Local Similarity 100.0%; Pred. NO. 9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 54 VAEF 57

RESULT 74

AA179941
 ID AA179941 standard; protein; 67 AA.

XX AA179941;
 AC AA179941;

XX 08-DEC-1999 (first entry)

XX Human prostate cancer-associated protein 49.

XX Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
 KW cancer; tissue specificity; human.

XX Homo sapiens.

XX DE19811194-A1.

XX 16-SEP-1999.

XX 10-MAR-1998; 98DE-01011194.

XX 10-MAR-1998; 98DE-01011194.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

XX WPI; 1999-519629/44.

XX N-PSDB; AA233499.

XX New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 PT agents.

XX Claim 22; 143; 194pp; German.

XX This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used: (a) for identifying agents for treatment of

C prostatic cancer and (b) for therapy of prostate cancer, optionally where
C expressed by gene therapy methods. (A) is also used to isolate full-
C length genes (for gene therapy) and for recombinant production of (I),
C which can be used to raise specific antibodies. (A) are identified by
C assembly of ESTs (expressed sequence tags) before these are analyzed by
C expression pattern (tissue specificity). This approach eliminates many of
C the false results, as regards tissue specificity, associated with known
C methods that use single (usually short) ESTs. AAY48304-48456 represent
C peptides encoded by the expressed sequence tags described in the method
C of the invention
C
X
Q Sequence 67 AA;

Query Match 95.0%; Score 19; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 18 VAEF 21

RESULT 75
BP31047
D ABP31047 standard; protein; 68 AA.

X C ABP31047;

X T 08-JUL-2002 (first entry)

X E Human ORF20 protein, SEQ ID NO:40.

W Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
W disease monitoring; cytokine; cell proliferation; cell differentiation;
W immune modulation; haematopoiesis regulation; tissue growth;
W angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
W thrombolytic; tumour inhibition; bodily characteristic; fertility;
W behaviour; cancer; proliferative disorder; neurological disorder;
W cardiovascular disease; immune system disorder; organ transplantation;
W tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
W hypothyroidism; cholesterol ester storage disease; infection; vulnery;
W vasotropic; antiporiatic; antidiabetic; cytosolic; neotropic;
W neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
W cardiant; hypotensive; antichyroid; antiinflammatory; immunomodulator;
W dermatological; analgesic; virucide; antibacterial; fungicide.

X S Homo sapiens.

X N WO200190366-A2.

X D 29-NOV-2001.

X F 24-MAY-2001; 2001WO-US017076.

X R 24-MAY-2000; 2000US-0206690P.

X A (CURA-) CURAGEN CORP.

X I Leach MD, Shinkets RA;

X R WPI; 2002-106200/14.

X R N-PSDB; ABN75073.

X T Novel human polypeptides and polynucleotides useful for diagnosing,
X T preventing and treating cardiovascular disease, neurodegenerative,
X T hyperproliferative disorders and disorders related to organ
X T transplantation.

X S Claim 10; Page 280; 2508pp; English.

X C Sequences ABP31028-ABP35561 represent 4534 novel human proteins
C designated ORF (open reading frame) 1-4534, and sequences ABN75054-
C ABN75587 represent cDNAs encoding them. The invention also encompasses

CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC polypeptides, methods of screening for modulators of ORFX expression or
CC activity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cell differentiation, immune modulation, haematopoiesis regulation,
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC nucleic acids and antibodies may be used in the treatment of cancers,
CC other proliferative disorders such as psoriasis and benign tumours,
CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases

XX SQ Sequence 68 AA;

Query Match 95.0%; Score 19; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

Db 3 VAEF 6

Search completed: May 24, 2004, 17:38:05
Job time : 122.786 secs

GenCore version 5.1.6
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M protein - protein search, using sw model

Run on: May 24, 2004, 17:32:13 ; Search time 12.5 seconds
(without alignments)
38.477 Million cell updates/sec

Title: US-09-594-978A-1

Perfect score: 20

Sequence: 1 XVAEF 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	95.0	20	2 S39049	cytotoxin-binding
2	19	95.0	33	2 G64625	hypothetical prote
3	19	95.0	48	2 E64618	hypothetical prote
4	19	95.0	52	2 A42375	hypothetical prote
5	19	95.0	54	2 E85745	unknown protein en
6	19	95.0	59	2 A69386	conserved hypothet
7	19	95.0	59	2 E71349	probable preprotel
8	19	95.0	63	2 JC4002	carboxymycin resist
9	19	95.0	63	2 G64007	hypothetical prote
10	19	95.0	64	2 I51350	transferrin - Atla
11	19	95.0	74	2 D97045	hypothetical prote
12	19	95.0	75	2 S07277	gene D protein - p
13	19	95.0	79	2 T18034	hypothetical prote
14	19	95.0	79	2 T27605	hypothetical prote
15	19	95.0	84	2 F83922	hypothetical prote
16	19	95.0	87	2 A38725	transferrin - shee
17	19	95.0	89	1 H64116	ribosomal protein
18	19	95.0	89	2 F66818	hypothetical prote
19	19	95.0	89	2 T15018	hypothetical prote
20	19	95.0	96	2 AC3053	hypothetical prote
21	19	95.0	97	2 AB1397	conserved hypothet
22	19	95.0	99	2 B83244	conserved hypothet
23	19	95.0	101	2 H90297	conserved hypothet
24	19	95.0	106	2 T10097	nifX protein - Met
25	19	95.0	108	2 G64950	hypothetical prote
26	19	95.0	109	2 E70949	probable regulator
27	19	95.0	111	2 T17582	hypothetical prote
28	19	95.0	112	2 B83431	type III export pr
29	19	95.0	114	2 A55872	kedarcidin [valida

30	19	95.0	114	2 D97414	hypothetical prote
31	19	95.0	115	2 D75218	hypothetical prote
32	19	95.0	116	1 IPAF	insulin precursor
33	19	95.0	118	2 T48682	hypothetical prote
34	19	95.0	119	2 F95327	hypothetical prote
35	19	95.0	122	2 F82861	conjugal transfer
36	19	95.0	125	2 B69129	gamma-carboxymuon
37	19	95.0	125	2 D70790	hypothetical prote
38	19	95.0	126	2 B81368	hypothetical prote
39	19	95.0	127	2 D70799	hypothetical prote
40	19	95.0	127	2 AB1732	hypothetical prote
41	19	95.0	128	2 A54797	ileal lipid-bindin
42	19	95.0	129	2 T02012	probable cathepsin
43	19	95.0	130	2 D72348	conserved hypothet
44	19	95.0	131	2 G75208	hypothetical prote
45	19	95.0	132	2 JQ2270	hypothetical 15-2K
46	19	95.0	132	2 AG1996	hypothetical prote
47	19	95.0	133	2 AH0137	conserved hypothet
48	19	95.0	133	2 H75623	conserved hypothet
49	19	95.0	133	2 A84221	riboflavin synthas
50	19	95.0	134	1 WMS015	ybgC protein - Esc
51	19	95.0	134	2 C90725	hypothetical prote
52	19	95.0	134	2 D85576	hypothetical prote
53	19	95.0	134	2 AD0592	conserved hypothet
54	19	95.0	136	2 S76416	hypothetical prote
55	19	95.0	137	2 F81355	hypothetical prote
56	19	95.0	138	2 F82106	flagellar basal-bo
57	19	95.0	139	2 A69052	riboflavin synthas
58	19	95.0	139	2 A83975	hypothetical prote
59	19	95.0	140	2 B63323	hypothetical prote
60	19	95.0	142	2 JQ2279	low-temperature re
61	19	95.0	142	2 JQ2280	low-temperature re
62	19	95.0	143	2 H69515	riboflavin synthas
63	19	95.0	143	2 T36978	probable transposa
64	19	95.0	145	1 B41715	ribosomal protein
65	19	95.0	145	2 S77043	hypothetical prote
66	19	95.0	146	2 F89837	conserved hypothet
67	19	95.0	147	2 C84294	hypothetical prote
68	19	95.0	147	2 T34803	hypothetical prote
69	19	95.0	148	2 E81788	conserved hypothet
70	19	95.0	148	2 S10655	hypothetical prote
71	19	95.0	149	2 AC1137	ribose 5-phosphate
72	19	95.0	150	2 AB2857	pseudoazurin limpo
73	19	95.0	150	2 AB1089	protein gp35 from
74	19	95.0	150	2 A11452	hypothetical prote
75	19	95.0	151	2 H87263	superoxide dismuta
76	19	95.0	152	2 S04623	hypothetical prote
77	19	95.0	154	2 B90184	hypothetical prote
78	19	95.0	155	2 I64130	PAL cross-reacting
79	19	95.0	156	2 G81283	ankyrin-repeat con
80	19	95.0	159	2 T17848	hypothetical prote
81	19	95.0	161	2 AE0981	probable acetyltra
82	19	95.0	163	2 A24504	salivary glue prot
83	19	95.0	163	2 G70524	hypothetical prote
84	19	95.0	164	2 AD1229	B. subtilis yslB p
85	19	95.0	164	2 A69293	hypothetical prote
86	19	95.0	166	2 S05059	hypothetical prote
87	19	95.0	168	2 S48866	hypothetical 19.5K
88	19	95.0	168	2 AE0192	probable C4-dicarb
89	19	95.0	169	2 T36387	probable acetyltra
90	19	95.0	169	2 AB2739	acetyltransferase
91	19	95.0	170	2 AC2917	invasion protein A
92	19	95.0	172	2 B75041	hypothetical prote
93	19	95.0	172	2 I49449	hemopoietic-specif
94	19	95.0	173	2 T22350	hypothetical prote
95	19	95.0	174	2 D70879	hypothetical prote
96	19	95.0	175	1 G71120	hypothetical prote
97	19	95.0	175	2 AC2648	conserved hypothet
98	19	95.0	175	2 I39055	Bcl-2 related - hu
99	19	95.0	176	2 C27805	ferritin chain M -
100	19	95.0	178	1 E63389	hypothetical prote
101	19	95.0	178	2 A38593	transcription fact
102	19	95.0	178	2 S03629	neurogenic gene co

103	19	95.0	179	2	S34345	hypothetical prote	176	19	95.0	219	2	H69199	conserved hypothet
104	19	95.0	180	2	D87031	probable acetyltra	177	19	95.0	219	2	AF1506	weakly carboxylest
105	19	95.0	180	2	E85358	hypothetical prote	178	19	95.0	220	2	TI0279	protein tyrosine p
106	19	95.0	180	2	A10676	probable exported	179	19	95.0	220	2	B84281	riboflavin-specifi
107	19	95.0	181	2	AG2202	cobinamide kinase	180	19	95.0	221	2	C83947	hypothetical prote
108	19	95.0	183	2	S13186	plasma retinol-bin	181	19	95.0	223	2	D69311	conserved hypothet
109	19	95.0	184	2	A90903	probable ante-term	182	19	95.0	223	2	T35665	hypothetical prote
110	19	95.0	184	2	F90873	probable anti-termi	183	19	95.0	223	2	AC0890	probable lipoprote
111	19	95.0	184	2	D71933	hypothetical prote	184	19	95.0	224	2	S69643	hypothetical prote
112	19	95.0	185	2	S43729	H+-transporting tw	185	19	95.0	224	2	AH1187	hypothetical prote
113	19	95.0	185	2	S39317	replication initia	186	19	95.0	226	2	AG3528	hypothetical prote
114	19	95.0	185	2	S39318	replication initia	187	19	95.0	228	2	A75290	chloramphenicol ac
115	19	95.0	185	2	D75635	resolvase - Deinoc	188	19	95.0	228	2	S48116	integral membrane
116	19	95.0	185	2	B97430	hypothetical prote	189	19	95.0	228	2	AD0693	pyridoxal kinase (
117	19	95.0	187	2	S16314	photosynthetic rea	190	19	95.0	228	2	D30857	hypothetical prote
118	19	95.0	187	2	AG2721	conserved hypothet	191	19	95.0	228	2	TI0399	hypothetical prote
119	19	95.0	187	2	A58896	conserved hypothet	192	19	95.0	228	2	AH0081	probable exported
120	19	95.0	188	2	AB0132	conserved hypothet	193	19	95.0	229	2	F36721	probable glutathio
121	19	95.0	188	2	A71286	conserved hypothet	194	19	95.0	229	2	E70340	glutaredoxin-like
122	19	95.0	188	2	H85713	unknown protein en	195	19	95.0	230	2	E37440	DNA-3-methyladenin
123	19	95.0	189	2	T29159	hypothetical prote	196	19	95.0	230	2	S73229	ribosomal protein
124	19	95.0	189	2	H97633	pseudouridin precu	197	19	95.0	231	2	AF1144	phosphoglycerate m
125	19	95.0	190	2	A29413	ubiquinol-cytochro	198	19	95.0	231	2	AF1503	phosphoglycerate m
126	19	95.0	191	2	A82392	transcription regu	199	19	95.0	231	2	C83179	conserved hypothet
127	19	95.0	192	2	D97503	hypothetical prote	200	19	95.0	231	2	AF3380	hypothetical prote
128	19	95.0	193	1	C64328	conserved hypothet	201	19	95.0	232	2	B70653	hypothetical prote
129	19	95.0	194	1	RPECR5	resolvase - Escher	202	19	95.0	232	2	E87520	hypothetical prote
130	19	95.0	194	2	C84033	hypothetical prote	203	19	95.0	234	2	F96620	hypothetical prote
131	19	95.0	194	2	F97691	hypothetical prote	204	19	95.0	234	2	AC2185	hypothetical prote
132	19	95.0	195	2	B87453	RNA polymerase sig	205	19	95.0	234	2	E91119	hypothetical prote
133	19	95.0	195	2	B86204	hypothetical prote	206	19	95.0	234	2	D85964	hypothetical prote
134	19	95.0	196	1	BVSCAU	transcription regu	207	19	95.0	234	2	S22360	hypothetical prote
135	19	95.0	196	2	A41853	hexose phosphate t	208	19	95.0	235	2	B37753	(p)ppGpp 3-pyropho
136	19	95.0	196	2	AH0963	Two-component syst	209	19	95.0	235	2	C95848	probable transcrip
137	19	95.0	196	2	F91204	transcription regu	210	19	95.0	236	2	A98351	agropine synthesis
138	19	95.0	196	2	H86050	hypothetical prote	211	19	95.0	236	2	AE2931	agropine synthesis
139	19	95.0	196	2	A64888	probable resolvase	212	19	95.0	236	2	B70728	hypothetical prote
140	19	95.0	196	2	D64909	probable resolvase	213	19	95.0	236	2	A84686	hypothetical prote
141	19	95.0	196	2	T21347	hypothetical prote	214	19	95.0	236	2	TS0908	hypothetical prote
142	19	95.0	197	2	C86748	hypothetical prote	215	19	95.0	237	2	F83639	hypothetical prote
143	19	95.0	198	2	S48749	cytochrome P460 pr	216	19	95.0	237	2	C97085	hypothetical prote
144	19	95.0	199	1	VAHU	plasma retinol-bin	217	19	95.0	238	2	C86656	glycerol uptake fa
145	19	95.0	199	2	H90206	amidotransferase h	218	19	95.0	239	2	D81218	conserved periplasm
146	19	95.0	200	2	AB0620	probable bacteriop	219	19	95.0	239	2	F81795	probable periplasm
147	19	95.0	201	1	VA8B	retinol-binding pr	220	19	95.0	239	2	H75195	hypothetical prote
148	19	95.0	201	2	A39486	plasma retinol-bin	221	19	95.0	239	2	S31033	gene 88 protein -
149	19	95.0	201	2	I46257	retinol binding pr	222	19	95.0	240	2	D89281	probable ABC transp
150	19	95.0	201	2	T00799	hypothetical prote	223	19	95.0	240	2	B84606	hypothetical prote
151	19	95.0	202	2	S35126	hypothetical prote	224	19	95.0	241	2	TI4808	hypothetical prote
152	19	95.0	202	2	S77556	hypothetical prote	225	19	95.0	242	2	B70366	hypothetical prote
153	19	95.0	202	2	AH1169	hypothetical prote	226	19	95.0	242	2	G97959	hypothetical prote
154	19	95.0	204	2	C97866	hypothetical prote	227	19	95.0	247	2	S43728	H+-transporting tw
155	19	95.0	204	2	G89753	protein FlilC7.1 [I	228	19	95.0	248	2	AF0177	probable beta-keto
156	19	95.0	205	2	S30739	hypothetical prote	229	19	95.0	248	2	TI2632	water channel prot
157	19	95.0	205	2	H91225	hypothetical prote	230	19	95.0	248	2	TI6648	probable tonoplast
158	19	95.0	205	2	F86072	hypothetical prote	231	19	95.0	248	2	F72604	probable high-affi
159	19	95.0	205	2	G01942	mitotic feedback c	232	19	95.0	248	2	TI8315	hypothetical prote
160	19	95.0	208	2	A86642	hypothetical prote	233	19	95.0	249	2	G81693	serine/threonine p
161	19	95.0	209	2	AH2658	3-methyladenine-DN	234	19	95.0	249	2	B69343	conserved hypothet
162	19	95.0	209	2	H97519	hypothetical prote	235	19	95.0	249	2	TI9088	hypothetical prote
163	19	95.0	212	2	A83521	conserved hypothet	236	19	95.0	250	2	UQ1012	TobR57-18C protein
164	19	95.0	213	2	G82067	hypothetical prote	237	19	95.0	250	2	S13719	probable membrane
165	19	95.0	213	2	AF2551	hypothetical prote	238	19	95.0	250	2	S51781	integral membrane
166	19	95.0	213	2	A84248	transcription regu	239	19	95.0	250	2	D64580	hypothetical prote
167	19	95.0	214	2	T30310	probable GTP bindi	240	19	95.0	251	2	F69494	(R)-hydroxyglutary
168	19	95.0	215	2	AI3072	transcription regu	241	19	95.0	252	2	C90422	hypothetical prote
169	19	95.0	215	2	F84889	hypothetical prote	242	19	95.0	252	2	F87575	hypothetical prote
170	19	95.0	218	2	H83485	conserved hypothet	243	19	95.0	252	2	G44020	hypothetical prote
171	19	95.0	218	2	T03287	osmotin protein ho	244	19	95.0	253	1	SI7711	probable dehydroge
172	19	95.0	218	2	D71392	coat protein - cuc	245	19	95.0	253	2	C65067	2-deoxy-D-gluconat
173	19	95.0	218	2	AB0254	probable fumarylac	246	19	95.0	253	2	C91091	2-deoxy-D-gluconat
174	19	95.0	218	2	T47889	hypothetical prote	247	19	95.0	253	2	F85936	2-deoxy-D-gluconat
175	19	95.0	219	2	T35128	hypothetical prote	248	19	95.0	253	2	AD0210	2-deoxy-D-gluconat

249	19	95.0	253	2	B72552	probable ATP-depen	322	19	95.0	291	2	G59479	methionyl aminopep
250	19	95.0	254	2	F90087	ATP-dependent Clp	323	19	95.0	291	2	E71491	probable geranyl t
251	19	95.0	255	2	T02078	phosphorylase II oxy	324	19	95.0	291	2	H06971	N-terminal CheY re
252	19	95.0	256	2	AB0161	deoxyribose operon	325	19	95.0	292	1	C84503	conserved hypoteth
253	19	95.0	257	2	S12985	phosphoprotein pho	326	19	95.0	292	2	T32000	hypothetical prote
254	19	95.0	258	2	T52130	probable copper/zinc	327	19	95.0	293	2	F71344	hypothetical prote
255	19	95.0	259	2	T35273	probable enoyl coA	328	19	95.0	294	2	H64465	methionyl aminopep
256	19	95.0	260	2	S56108	26S proteasome reg	329	19	95.0	294	2	S48934	nucleic acid-bindi
257	19	95.0	261	2	B82275	conserved hypoteth	330	19	95.0	295	2	D82341	ribosomal protein
258	19	95.0	262	2	F69479	nicotinate-nucleot	331	19	95.0	295	2	A49906	glucose-1-phosphat
259	19	95.0	263	2	T36359	hypothetical prote	332	19	95.0	295	2	C82828	glucose-1-phosphat
260	19	95.0	264	2	S75599	hypothetical prote	333	19	95.0	295	2	C43718	hypothetical prote
261	19	95.0	265	2	G81427	periplasmic protei	334	19	95.0	297	2	A84767	hypothetical prote
262	19	95.0	266	2	AF2054	hypothetical prote	335	19	95.0	297	2	F64470	sulfate permease (
263	19	95.0	267	2	AD2895	short-chain dehydr	336	19	95.0	297	2	AC2002	transposase alr156
264	19	95.0	268	2	G97670	probable oxidoredu	337	19	95.0	297	2	AD1931	transposase alr156
265	19	95.0	269	2	T00100	hypothetical prote	338	19	95.0	297	2	AD2141	transposase alr268
266	19	95.0	270	2	G84010	hypothetical prote	339	19	95.0	297	2	AG2142	transposase alr268
267	19	95.0	271	2	H98213	transcription repr	340	19	95.0	297	2	A12138	transposase alr366
268	19	95.0	272	2	B72333	bacteriocin - Ther	341	19	95.0	297	2	A12228	transposase alr338
269	19	95.0	273	2	AC0132	probable aldo/keto	342	19	95.0	297	2	A12258	transposase alr362
270	19	95.0	274	2	A57490	matrilysin [EC 3.4	343	19	95.0	298	2	H98170	myo-inositol catab
271	19	95.0	275	2	T24397	hypothetical prote	344	19	95.0	298	2	A83116	myo-inositol catab
272	19	95.0	276	2	A87404	ribosomal protein	345	19	95.0	299	2	G82393	transcription regu
273	19	95.0	277	2	A13121	ABC transporter, m	346	19	95.0	300	2	JC4367	NAD(P)-arginine AD
274	19	95.0	278	2	F98165	hypothetical prote	347	19	95.0	301	2	JC5811	osteopontin - rat
275	19	95.0	279	1	R5BVL3	ribosomal protein	348	19	95.0	302	2	A96789	cytochrome-c perox
276	19	95.0	280	2	B44499	major intrinsic pr	349	19	95.0	304	2	G81417	hypothetical prote
277	19	95.0	281	2	A41616	erythrocyte integr	350	19	95.0	305	2	S40927	hypothetical prote
278	19	95.0	282	2	JC1320	water channel prot	351	19	95.0	305	2	G71441	hypothetical prote
279	19	95.0	283	2	I53366	uterine water chan	352	19	95.0	306	2	B98164	hypothetical prote
280	19	95.0	284	2	C71228	hypothetical prote	353	19	95.0	306	2	A83123	glycosyltransferas
281	19	95.0	285	2	A56487	signal recognition	354	19	95.0	307	2	T19582	hypothetical prote
282	19	95.0	286	2	JC2348	water channel prot	355	19	95.0	308	2	D86742	thioredoxin-disulf
283	19	95.0	287	2	B89937	conserved hypoteth	356	19	95.0	309	1	S62835	dnaj protein homol
284	19	95.0	288	2	S37705	amvC protein - The	357	19	95.0	309	2	D90520	conserved hypoteth
285	19	95.0	289	2	H88690	protein p41H10.8 [358	19	95.0	309	2	S76393	hypothetical prote
286	19	95.0	290	2	C83709	hypothetical prote	359	19	95.0	309	2	T09564	glutaminyl-peptide
287	19	95.0	291	2	H97337	acetyl-CoA carboxy	360	19	95.0	310	2	T03566	phosphoprotein pho
288	19	95.0	292	2	B97260	dihydropyrimidin	361	19	95.0	310	2	C90245	conserved hypoteth
289	19	95.0	293	2	AG1842	uroporphyrinogen-I	362	19	95.0	311	2	A95117	dihydrodipicolinat
290	19	95.0	294	2	T19845	hypothetical prote	363	19	95.0	311	2	G97986	dihydrodipicolinat
291	19	95.0	295	2	JW0102	azaarene carbazole	364	19	95.0	311	2	A99196	purine nucleosidas
292	19	95.0	296	2	A72420	conserved hypoteth	365	19	95.0	311	2	B84341	hypothetical prote
293	19	95.0	297	2	E84983	hypothetical prote	366	19	95.0	312	2	S24264	phosphoprotein pho
294	19	95.0	298	2	A81040	conserved hypoteth	367	19	95.0	312	2	S31086	phosphoprotein pho
295	19	95.0	299	2	E71293	probable nicotinam	368	19	95.0	312	2	B3705	cysteine proteinas
296	19	95.0	300	2	S52582	prephenate dehydra	369	19	95.0	312	2	S67052	hypothetical prote
297	19	95.0	301	2	F86842	prephenate dehydra	370	19	95.0	313	2	A26485	dnak-type molecula
298	19	95.0	302	2	T22051	hypothetical prote	371	19	95.0	313	2	S27698	phosphoenolpyruvat
299	19	95.0	303	2	D84185	hypothetical prote	372	19	95.0	313	2	E45509	desiccation-relate
300	19	95.0	304	2	S71506	site-specific DNA-	373	19	95.0	313	2	E35853	hypothetical prote
301	19	95.0	305	2	AC3579	transcription regu	374	19	95.0	313	2	E35853	glycerate dehydrog
302	19	95.0	306	2	C86221	hypothetical prote	375	19	95.0	313	2	AD1285	phosphoprotein pho
303	19	95.0	307	2	E84637	hypothetical prote	376	19	95.0	314	2	AG1656	phosphoprotein pho
304	19	95.0	308	2	F97252	fof1-type ATP synt	377	19	95.0	314	2	S52371	potassium channel
305	19	95.0	309	2	B70200	trNA-pseudouridine	378	19	95.0	314	2	H69458	hypothetical prote
306	19	95.0	310	2	H83651	hypothetical prote	379	19	95.0	314	2	AD2517	phosphoprotein pho
307	19	95.0	311	2	T31275	2-hydroxyoctonate-	380	19	95.0	316	2	S26225	DNA-(apurinic or a
308	19	95.0	312	2	T37996	probable aldose re	381	19	95.0	316	2	S42397	hypothetical prote
309	19	95.0	313	2	B70703	hypothetical prote	382	19	95.0	316	2	T32993	osteopontin precu
310	19	95.0	314	2	A84494	envelope-like prot	383	19	95.0	317	1	A25917	phosphoprotein pho
311	19	95.0	315	2	JC5419	2-hydroxyoctonate-	384	19	95.0	317	2	T03594	DNA-(apurinic or a
312	19	95.0	316	2	A10288	pyridoxal kinase (385	19	95.0	317	2	A39500	ATP sulfurylase, s
313	19	95.0	317	2	S07563	glutamine-tRNA lig	386	19	95.0	317	2	F82672	conserved hypoteth
314	19	95.0	318	2	F64920	probable pyridoxal	387	19	95.0	317	2	D69258	phosphoprotein pho
315	19	95.0	319	2	A90922	pyridoxal kinase 2	388	19	95.0	318	2	S20882	phosphoprotein pho
316	19	95.0	320	2	E85770	pyridoxal kinase 2	389	19	95.0	318	2	T33015	DNA-(apurinic or a
317	19	95.0	321	2	T35229	hypothetical prote	390	19	95.0	318	2	S23550	ubiquitin-activati
318	19	95.0	322	2	A13400	glycine hydroxymet	391	19	95.0	319	2	T05515	protein T12C24.6 [
319	19	95.0	323	1	G64167	hypothetical prote	392	19	95.0	320	2	D86259	unknown protein F2
320	19	95.0	324	2	AD2870	ABC transporter, m	393	19	95.0	320	2	D96750	probable oxidoredu
321	19	95.0	325	2	F97646	probable aliphatic	394	19	95.0	320	2	G96834	

395	19	95.0	320	2	T28992	hypotheical prote	468	19	95.0	352	2	AC1560	two-component sens
396	19	95.0	322	2	D83785	hypotheical prote	469	19	95.0	352	2	AE1202	two-component sens
397	19	95.0	323	2	T09550	phosphoprotein pho	470	19	95.0	353	2	D97295	parvalin-like pept
398	19	95.0	323	2	G84325	hypotheical prote	471	19	95.0	355	2	AG1877	hypotheical prote
399	19	95.0	324	2	E84505	hypotheical prote	472	19	95.0	355	2	AI3624	spemidine/putresc
400	19	95.0	325	2	JC7553	brain mitochondria	473	19	95.0	357	2	AC1276	aminopeptidase hom
401	19	95.0	326	2	G69366	homoserine dehydro	474	19	95.0	357	2	AC1639	aminopeptidase hom
402	19	95.0	326	2	T05094	peroxidase homolog	475	19	95.0	357	2	A84551	hypotheical prote
403	19	95.0	326	2	T13070	hypotheical prote	476	19	95.0	359	2	T02011	probable cathepsin
404	19	95.0	327	2	AC3482	sulfate-binding pr	477	19	95.0	359	2	D95316	probable ABC-trans
405	19	95.0	327	2	E95968	hypotheical expor	478	19	95.0	359	2	H95382	probable ABC trans
406	19	95.0	328	2	E75564	ABC transporter, A	479	19	95.0	360	2	D69025	pleiotropic regula
407	19	95.0	328	2	A89867	hypotheical prote	480	19	95.0	360	2	AB3078	hypotheical prote
408	19	95.0	328	2	C70368	conserved hypotet	481	19	95.0	360	2	G98208	probable ATP-bind
409	19	95.0	328	2	H84548	hypotheical prote	482	19	95.0	361	2	AH3042	hypotheical prote
410	19	95.0	329	2	AD2629	33 kda chaperonin,	483	19	95.0	361	2	D98243	cpuaa (AF234619) [
411	19	95.0	329	2	T50117	mo25 homolog [impo	484	19	95.0	361	2	AE1979	ABC transporter AT
412	19	95.0	329	2	T29218	hypotheical prote	485	19	95.0	361	2	E96743	probable deoxyguan
413	19	95.0	330	1	H64404	hypotheical prote	486	19	95.0	362	2	C97448	hypotheical prote
414	19	95.0	330	2	A83417	probable oxidoredu	487	19	95.0	363	2	B95371	probable oxidoredu
415	19	95.0	331	2	T35499	probable D-lactate	488	19	95.0	363	2	A81134	acyl-CoA dehydrog
416	19	95.0	331	2	AE2928	dehydrogenase Atu3	489	19	95.0	363	2	C81888	probable acyl-CoA
417	19	95.0	331	2	D82972	probable lipolytic	490	19	95.0	364	2	G70364	conserved hypotet
418	19	95.0	331	2	AE2666	divalent cation tr	491	19	95.0	365	2	S76544	hypotheical prote
419	19	95.0	333	2	C71165	probable dehydroge	492	19	95.0	366	1	G49964	photosynthetic rea
420	19	95.0	333	2	C71165	probable dehydroge	493	19	95.0	366	2	T50891	cytochrome subunit
421	19	95.0	334	2	A11881	collagenase PrtC (494	19	95.0	366	2	G84249	NADH-dependent fla
422	19	95.0	334	1	S15318	transcription regu	495	19	95.0	368	2	G70462	succinate-CoA liga
423	19	95.0	334	2	T49195	hypotheical prote	496	19	95.0	368	2	G97291	hypotheical prote
424	19	95.0	335	2	A95951	hypotheical prote	497	19	95.0	368	2	S75652	ABC-type transport
425	19	95.0	335	2	S42807	HSR203J protein -	498	19	95.0	368	2	C83898	response regulator
426	19	95.0	336	2	B95906	probable dehydroge	499	19	95.0	368	2	A97189	lps biosynthesis p
427	19	95.0	336	2	AE0337	probable aspartate	500	19	95.0	369	2	S56638	mitogen-activated
428	19	95.0	336	2	AH3569	ABC transporter AT	501	19	95.0	369	2	A95124	rna polymerase sig
429	19	95.0	336	2	C87623	cobalamin biosynth	502	19	95.0	369	2	C97994	rna polymerase sig
430	19	95.0	336	2	T00571	dolichyl-phosphate	503	19	95.0	369	2	B83571	probable ATP-bind
431	19	95.0	337	2	T35862	probable secreted	504	19	95.0	369	2	S77028	protein kinase, 41
432	19	95.0	337	2	T23757	hypotheical prote	505	19	95.0	369	2	T51477	glutamine-rich pro
433	19	95.0	338	2	AG2938	2-hydroxyacid-fam1	506	19	95.0	370	2	F36819	Cl4 protein - rabb
434	19	95.0	338	2	H98343	hypotheical prote	507	19	95.0	370	2	F95927	probable mandelate
435	19	95.0	338	2	E75301	conserved hypotet	508	19	95.0	370	2	C97998	platelet-derived g
436	19	95.0	339	2	T17930	transcription init	509	19	95.0	371	2	T09622	protein kinase MMK
437	19	95.0	339	2	JC7509	glycoprotein VI-1	510	19	95.0	371	2	F86625	GTP-binding protei
438	19	95.0	339	2	T25630	hypotheical prote	511	19	95.0	371	2	D95000	GTP-binding protei
439	19	95.0	340	2	JC1125	phosphotransferase	512	19	95.0	371	2	D97872	conserved hypotet
440	19	95.0	340	2	T32646	hypotheical prote	513	19	95.0	371	2	AH0686	hypotheical prote
441	19	95.0	340	2	E83146	membrane-bound lyc	514	19	95.0	372	2	AD0075	probable transport
442	19	95.0	340	2	I49451	alpha 4 protein -	515	19	95.0	372	2	AC0253	ribonuclease iii (
443	19	95.0	341	2	S71223	xyloglucan endo-1,	516	19	95.0	375	2	AB3101	dipeptidase [impor
444	19	95.0	342	2	AH0087	sigma-54 transcrip	517	19	95.0	375	2	H98185	membrane dipeptida
445	19	95.0	342	2	S29894	strictosidine synt	518	19	95.0	375	2	T16116	hypotheical prote
446	19	95.0	342	2	AB2258	cobS protein [impo	519	19	95.0	377	2	A48352	genome polypeptin
447	19	95.0	343	2	B86446	probable endoxylg	520	19	95.0	377	2	D95861	probable ABC trans
448	19	95.0	343	2	C88986	protein C50H11.7 [521	19	95.0	378	1	B38178	cella protein pla
449	19	95.0	343	2	D84390	sulfate transport	522	19	95.0	379	2	AF2409	mannosyl transfera
450	19	95.0	344	1	RWRTC2	T-cell surface gly	523	19	95.0	379	2	H82284	queuine tRNA-ribos
451	19	95.0	344	2	A98354	hypotheical prote	524	19	95.0	379	2	G97201	NAD(PAD)-depend
452	19	95.0	344	2	B28967	T-cell surface gly	525	19	95.0	379	2	UC7710	NADH-rubredoxin ox
453	19	95.0	344	2	I49585	CD2 antigen protei	526	19	95.0	379	2	AD3390	pbnM protein [impo
454	19	95.0	344	2	A19502	4-hydroxyphenylpyr	527	19	95.0	379	2	BE3225	ABC transporter, m
455	19	95.0	344	2	S10325	strictosidine synt	528	19	95.0	380	2	D64533	cystathionine gamm
456	19	95.0	345	2	F90239	anthranilate phosp	529	19	95.0	380	2	D71973	probable cystathio
457	19	95.0	345	2	A83927	hypotheical prote	530	19	95.0	381	2	S46583	442K curved dna-bi
458	19	95.0	346	2	A45885	MHC class I histoc	531	19	95.0	383	2	AG3304	pleiotropic regula
459	19	95.0	346	2	C95040	hypotheical prote	532	19	95.0	383	2	G72777	probable S2p metal
460	19	95.0	346	2	C95090	hypotheical prote	533	19	95.0	384	2	D86821	hydroxymethylgluta
461	19	95.0	347	2	D89373	immunogenic protei	534	19	95.0	385	2	T16447	hypotheical prote
462	19	95.0	347	2	AF2645	flagellar motor sw	535	19	95.0	385	2	H84411	phosphoglycerate k
463	19	95.0	347	2	F97427	flagellar motor sw	536	19	95.0	386	2	D64074	hypotheical prote
464	19	95.0	348	2	E69162	sulfate transport	537	19	95.0	386	2	B97411	33k chaperonin (he
465	19	95.0	349	2	H27214	probable O-sialogl	538	19	95.0	387	2	AC3190	hypotheical prote
466	19	95.0	351	2	D84541	hypotheical prote	539	19	95.0	388	2	E70894	probable metB prot
467	19	95.0	352	2	S22464	strictosidine synt	540	19	95.0	388	2	F87208	cystathionine [gam

541	19	95.0	388	2	T23670	hypothetical prote	614	19	95.0	427	2	G98259	methionine gamma-l
542	19	95.0	389	2	T15102	hypothetical prote	615	19	95.0	428	2	F69050	glycine hydroxymet
543	19	95.0	390	2	G84245	NADH dehydrogenase	616	19	95.0	429	2	G72323	phosphopyruvate hy
544	19	95.0	390	2	G84245	conserved hypothet	617	19	95.0	429	2	S30049	transcription fact
545	19	95.0	390	2	H75023	nicotinate phospho	618	19	95.0	429	2	AC2227	hypothetical prote
546	19	95.0	390	2	A84226	farnesyl-diphospha	619	19	95.0	430	2	C83975	O-acetylthioserine
547	19	95.0	390	2	T25996	hypothetical prote	620	19	95.0	430	2	B95892	probable ABC trans
548	19	95.0	390	2	D86291	hypothetical prote	621	19	95.0	431	2	C69087	dihydrolipoamide d
549	19	95.0	391	2	C70972	probable trehalase	622	19	95.0	431	2	G96987	enolase [imported]
550	19	95.0	392	2	B64017	probable RNA methy	623	19	95.0	431	2	T21594	hypothetical prote
551	19	95.0	392	2	S22580	telomere-binding p	624	19	95.0	431	2	D70185	3-hydroxy-3-methyl
552	19	95.0	393	2	E95261	serine proteinase	625	19	95.0	431	2	S37775	filamin, muscle -
553	19	95.0	393	2	C89561	hypothetical prote	626	19	95.0	432	1	S15203	glycine hydroxymet
554	19	95.0	394	2	B70411	fimbrial assembly	627	19	95.0	432	2	S08277	cyclin A - human
555	19	95.0	394	2	C81333	probable efflux pu	628	19	95.0	432	2	A82403	ATP-binding protei
556	19	95.0	394	2	S76331	hypothetical prote	629	19	95.0	433	1	B70677	cytochrome P450 Rv
557	19	95.0	395	2	S38812	cyclin A - chicken	630	19	95.0	433	2	A70465	probable GTP bindi
558	19	95.0	395	2	T20724	hypothetical prote	631	19	95.0	434	2	S30334	glycine hydroxymet
559	19	95.0	397	2	H84225	acyl-CoA dehydroge	632	19	95.0	434	2	D71480	probable flagellum
560	19	95.0	397	2	B98127	serine proteinase	633	19	95.0	436	2	G69466	3-hydroxy-3-methyl
561	19	95.0	397	2	A72315	hypothetical prote	634	19	95.0	437	1	A31752	transcription fact
562	19	95.0	398	2	C95201	hydroxymethylgluta	635	19	95.0	437	2	C64113	tetrahydrofolylpol
563	19	95.0	398	2	A98068	hypothetical prote	636	19	95.0	437	2	JC4988	high-affinity gluc
564	19	95.0	399	2	A84572	nicotinate phospho	637	19	95.0	437	2	S42111	transcription fact
565	19	95.0	399	2	H87342	glycosyl transfera	638	19	95.0	438	2	E95383	probable aminotran
566	19	95.0	399	2	F83796	multidrug-efflux t	639	19	95.0	438	2	A98161	hypothetical prote
567	19	95.0	399	2	AG2221	hypothetical prote	640	19	95.0	438	2	H86006	hypothetical prote
568	19	95.0	400	2	T03460	probable leucine/i	641	19	95.0	438	2	AB0997	high-affinity gluc
569	19	95.0	402	1	A70707	cytochrome P450 Rv	642	19	95.0	439	2	AC0462	glycerol-3-phospha
570	19	95.0	402	2	H82813	cytochrome P450-li	643	19	95.0	439	2	AC2948	hypothetical prote
571	19	95.0	403	2	H82440	ABC transporter, A	644	19	95.0	439	2	G93334	glycerol-3-phospha
572	19	95.0	403	2	G84222	NADH dehydrogenase	645	19	95.0	440	2	AC2985	conserved hypothet
573	19	95.0	405	2	A83084	probable metallope	646	19	95.0	440	2	D98298	probable sugar iso
574	19	95.0	406	2	S24788	cyclin A - bovine	647	19	95.0	441	2	C87233	probable cell inva
575	19	95.0	406	2	F84152	serine proteinase	648	19	95.0	442	2	T44655	O-acetylthioserine
576	19	95.0	406	2	G02022	tryptophan oxygena	649	19	95.0	443	2	A99657	hypothetical prote
577	19	95.0	406	2	T30748	hypothetical prote	650	19	95.0	443	2	A85508	hypothetical prote
578	19	95.0	407	2	B71679	hypothetical prote	651	19	95.0	443	2	T32088	hypothetical prote
579	19	95.0	408	2	T08069	protein kinase, 48	652	19	95.0	444	2	C70444	biotin carboxylase
580	19	95.0	408	2	B97741	hypothetical prote	653	19	95.0	445	2	T16025	hypothetical prote
581	19	95.0	409	2	AD0492	multidrug transloc	654	19	95.0	445	2	S32036	finger protein XFG
582	19	95.0	409	2	T02776	Y4DW protein - Rhi	655	19	95.0	445	2	C82140	undulin 2 - human
583	19	95.0	409	2	F86151	F22M8.10 protein -	656	19	95.0	446	2	C82140	C4-dicarboxylate t
584	19	95.0	410	2	B48585	transcription fact	657	19	95.0	447	2	C96497	glyceraldehyde-3-p
585	19	95.0	410	2	A48585	transcription fact	658	19	95.0	448	2	AF0437	conserved hypothet
586	19	95.0	411	2	H83355	hypothetical prote	659	19	95.0	449	2	D70726	probable gabf - My
587	19	95.0	411	2	AB0199	peptidase T (EC 3.	660	19	95.0	449	2	C70846	probable metC prot
588	19	95.0	412	1	RNECTA	tRNA adenyllytrans	661	19	95.0	449	2	AF2646	chemotaxis motD pr
589	19	95.0	412	2	S51760	ferredoxin reducta	662	19	95.0	449	2	E97428	chemotaxis motD pr
590	19	95.0	412	2	C91121	tRNA nucleotidyl t	663	19	95.0	450	2	T39433	glucoamylase precu
591	19	95.0	412	2	B85966	tRNA nucleotidyl t	664	19	95.0	450	2	F82402	permease VCA0904 l
592	19	95.0	412	2	T21419	hypothetical prote	665	19	95.0	450	2	T21593	hypothetical prote
593	19	95.0	413	2	C69160	phosphoenolpyruvat	666	19	95.0	450	2	C84466	hypothetical prote
594	19	95.0	413	2	T48364	transcription fact	667	19	95.0	453	2	S37935	conserved hypothet
595	19	95.0	415	2	A81920	glutamyl-tRNA redu	668	19	95.0	453	2	C83008	probable purine-bi
596	19	95.0	415	2	C81183	glutamyl-tRNA redu	669	19	95.0	455	2	B71335	hypothetical prote
597	19	95.0	415	2	I51637	cyclin A2 - Africa	670	19	95.0	456	2	T46986	probable chlorohyd
598	19	95.0	416	2	D95321	diaminopimelate de	671	19	95.0	456	2	AH0240	DNA-directed DNA p
599	19	95.0	416	2	F98095	diaminopimelate de	672	19	95.0	458	2	S75328	repSA protein - St
600	19	95.0	418	2	H72203	hypothetical prote	673	19	95.0	459	2	A12218	hypothetical prote
601	19	95.0	418	2	T35993	probable aminotran	674	19	95.0	460	2	A12218	argininosuccinate
602	19	95.0	419	2	B85035	hypothetical prote	675	19	95.0	461	1	WZTRRS	argininosuccinate
603	19	95.0	420	2	S65084	finger protein XFG	676	19	95.0	461	2	E71672	malonate hydratase
604	19	95.0	421	2	A90003	hypothetical prote	677	19	95.0	462	2	A33313	gene XGF 5.1C prot
605	19	95.0	421	2	T47393	hypothetical prote	678	19	95.0	462	2	I51699	gene XGF 5.1C prot
606	19	95.0	422	2	C83063	glutamyl-tRNA redu	679	19	95.0	463	2	D97826	malonate hydratase
607	19	95.0	422	2	S38501	cyclin A2 - mouse	680	19	95.0	464	1	WZMURS	argininosuccinate
608	19	95.0	422	2	S38501	cyclin A - mouse	681	19	95.0	464	2	F70837	probable sulfatase
609	19	95.0	423	2	T37280	hypothetical prote	682	19	95.0	465	2	T36212	replication initia
610	19	95.0	424	2	I39506	citrate (si)-synth	683	19	95.0	466	2	T36212	nicotinamide nucle
611	19	95.0	424	2	H87520	hypothetical prote	684	19	95.0	467	2	A12231	hypothetical prote
612	19	95.0	426	2	H75407	transcription term	685	19	95.0	467	2	G82697	probable phosphopr
613	19	95.0	427	2	AB3025	methionine gamma-l	686	19	95.0	469	1	KCPGI	interstitial colla

587	19	95.0	469	2	S74825	probable Rieske ir	760	19	95.0	513	2	AB5697	Na+/H+ antiporter,
588	19	95.0	470	2	S50083	photolyase - short	761	19	95.0	513	2	G64864	Na+/H+-exchanging
589	19	95.0	471	2	S27676	mannose-1-phosphat	762	19	95.0	514	2	S46733	hypothetical prote
590	19	95.0	472	2	S82917	preprotein translo	763	19	95.0	514	2	T10559	hypothetical prote
591	19	95.0	473	2	T04738	hypothetical prote	764	19	95.0	514	2	AG0723	regulator of intra
592	19	95.0	474	2	E47677	guanosine diphosph	765	19	95.0	514	2	T29852	hypothetical prote
593	19	95.0	475	2	S22621	Phosphomannomutase	766	19	95.0	517	2	T27101	hypothetical prote
594	19	95.0	476	2	D39303	conserved hypothet	767	19	95.0	518	1	A27705	alpha-amylase (EC
595	19	95.0	477	2	T84137	hypothetical prote	768	19	95.0	521	2	T46687	p-cresol methylhyd
596	19	95.0	478	2	S75530	hydrogenase large	769	19	95.0	522	2	A31556	glucose transport
597	19	95.0	479	2	AG3210	proline dipeptidas	770	19	95.0	522	2	B64067	Na+/H+-exchanging
598	19	95.0	480	2	B49681	long-chain-fatty-a	771	19	95.0	524	2	S06920	glucose transport
599	19	95.0	481	2	G72922	hypothetical prote	772	19	95.0	524	1	T40127	IMP dehydrogenase
600	19	95.0	482	2	C64119	starch synthase (G	773	19	95.0	524	2	A31318	glucose transport
601	19	95.0	483	2	C96577	hypothetical prote	774	19	95.0	524	2	T06134	hypothetical prote
602	19	95.0	484	2	S71360	noea protein - Rhi	775	19	95.0	524	2	T09331	hypothetical prote
603	19	95.0	485	2	H95332	Noea host specific	776	19	95.0	526	2	D95205	hypothetical prote
604	19	95.0	486	2	UC4386	adenyl cyclase-a	777	19	95.0	528	2	T31459	proteochlorophyllid
605	19	95.0	487	2	T38409	adenyl cyclase-a	778	19	95.0	528	2	JC4814	Na+/H+-exchanging
606	19	95.0	488	2	T23792	hypothetical prote	779	19	95.0	529	2	AF3059	cytochrome d oxida
607	19	95.0	489	2	S15312	rfbM protein - Sal	780	19	95.0	529	2	B98227	cytochrome d oxida
608	19	95.0	490	2	AH0765	mannose-1-phosphat	781	19	95.0	532	2	T07903	tubulin delta chai
609	19	95.0	491	2	B86367	protein F26P24.16	782	19	95.0	533	2	S52046	deoxyribodipyrimid
610	19	95.0	492	2	H96729	probable alanine a	783	19	95.0	535	2	C82433	methyl-accepting c
611	19	95.0	493	2	A70190	hypothetical prote	784	19	95.0	537	2	T09755	4-coumarate-CoA li
612	19	95.0	494	2	T10095	nifs protein - Met	785	19	95.0	537	2	T09710	2,3-dihydroxybenzo
613	19	95.0	495	2	T14422	cellulase-like pro	786	19	95.0	537	2	AF0575	4-coumarate-CoA li
614	19	95.0	496	2	D82446	probable formate t	787	19	95.0	537	2	H87502	conserved hypothet
615	19	95.0	497	2	T76302	probable 2-dehydro	788	19	95.0	538	2	AD3281	IMP cyclohydrolyase
616	19	95.0	498	2	R86416	unknown protein, 3	789	19	95.0	538	2	AF2923	bifunctional purin
617	19	95.0	499	2	P95238	PTS system, membra	790	19	95.0	540	2	S76584	hypothetical prote
618	19	95.0	500	2	H83131	5-carboxy-2-hydrox	791	19	95.0	543	2	H92282	vibriobactin-speci
619	19	95.0	501	2	C96018	probable starch sy	792	19	95.0	545	2	F83280	probable chemotaxi
620	19	95.0	502	2	T49017	hypothetical prote	793	19	95.0	548	2	AB0591	fumarate hydratase
621	19	95.0	503	2	T39456	zinc finger protei	794	19	95.0	548	2	A81854	glucose-6-phosphat
622	19	95.0	504	2	A95926	probable argininos	795	19	95.0	548	2	C81089	glucose-6-phosphat
623	19	95.0	505	2	T09734	1-aminocyclopropan	796	19	95.0	548	2	T23270	acetyl choline rec
624	19	95.0	506	2	T23055	hypothetical prote	797	19	95.0	549	2	A90253	hypothetical prote
625	19	95.0	507	2	H90423	sugar transport pr	798	19	95.0	549	2	T24508	hypothetical prote
626	19	95.0	508	2	T44576	L-2,4-diaminobuty	799	19	95.0	549	2	JC4083	chaperonin - Caeno
627	19	95.0	509	2	E71486	probable s/t prote	800	19	95.0	550	2	B82330	glucose-6-phosphat
628	19	95.0	510	2	S37053	Glucose-6-phosphat	801	19	95.0	550	2	T24019	hypothetical prote
629	19	95.0	511	2	T11894	NADH2 dehydrogenas	802	19	95.0	550	2	T22557	hypothetical prote
630	19	95.0	512	2	B64642	cell division prot	803	19	95.0	551	2	E84106	hypothetical prote
631	19	95.0	513	2	T01235	hypothetical prote	804	19	95.0	553	2	S03828	regulatory protein
632	19	95.0	514	2	C71873	septum formation p	805	19	95.0	553	2	AG3604	cytochrome d ubiq
633	19	95.0	515	2	H70573	hypothetical prote	806	19	95.0	555	1	SYHQMA	malate synthase (E
634	19	95.0	516	2	S10134	plasmid recombinat	807	19	95.0	556	2	C87472	steroid monooxygen
635	19	95.0	517	2	A33952	58K mobilization p	808	19	95.0	556	2	T16790	hypothetical prote
636	19	95.0	518	2	T27693	hypothetical prote	809	19	95.0	558	2	T29503	serine C-palmitoyl
637	19	95.0	519	2	AD2375	hypothetical prote	810	19	95.0	558	2	A75216	hypothetical prote
638	19	95.0	520	2	S27785	acetyl-CoA acetyl	811	19	95.0	558	2	T28881	hypothetical prote
639	19	95.0	521	2	AG3134	N-ethylameline ch	812	19	95.0	559	2	AB8813	xylian 1,4-beta-xy
640	19	95.0	522	2	T14236	NADH2 dehydrogenas	813	19	95.0	559	2	AB0984	probable membrane
641	19	95.0	523	2	F88359	protein V51H1A.5 {	814	19	95.0	559	2	H82532	conserved hypothet
642	19	95.0	524	2	E98153	N-ethylameline ch	815	19	95.0	561	2	G81842	30S ribosomal prot
643	19	95.0	525	2	B64069	fructose phosphotr	816	19	95.0	561	2	G81099	30S ribosomal prot
644	19	95.0	526	2	R86148	hypothetical prote	817	19	95.0	561	2	H69086	ABC transporter -
645	19	95.0	527	2	C91251	probable tail shea	818	19	95.0	562	2	P97697	hypothetical prote
646	19	95.0	528	2	B81862	exopolysphatase	819	19	95.0	562	2	B82351	hypothetical prote
647	19	95.0	529	2	F81080	exopolysphatase	820	19	95.0	564	2	B72660	probable type III D
648	19	95.0	530	2	G81917	probable ubiquinol	821	19	95.0	567	2	S69779	adenin A65-2 prote
649	19	95.0	531	2	B81184	ubiquinone biosynt	822	19	95.0	567	2	T16105	hypothetical prote
650	19	95.0	532	2	A82193	malonate-CoA decarb	823	19	95.0	567	2	D72359	conserved hypothet
651	19	95.0	533	2	S27113	malonyl-CoA decarb	824	19	95.0	570	2	C90485	beta-glucuronidase
652	19	95.0	534	2	A84244	probable signaling	825	19	95.0	571	2	T06737	hypothetical prote
653	19	95.0	535	2	T16903	hypothetical prote	826	19	95.0	571	1	S33853	hydrogenase (EC 1.
654	19	95.0	536	2	C70468	phosphoribosylamin	827	19	95.0	576	2	B71959	proline-uracil ligas
655	19	95.0	537	2	T31831	hypothetical prote	828	19	95.0	577	2	C69059	acetylacetate synth
656	19	95.0	538	2	AD0475	probable magnesium	829	19	95.0	577	2	F84549	proline-uracil ligas
657	19	95.0	539	2	G98102	hypothetical prote	830	19	95.0	580	2	T30583	probable peptidase
658	19	95.0	540	2	T14638	cytochrome P450 Cy	831	19	95.0	580	2	C86530	31 ribosomal prote
659	19	95.0	541	2	A99839	Na+/H+ antiporter	832	19	95.0	580	2	D72093	ribosomal protein

833	19	95.0	582	2	T16104	hypothetical prote	906	19	95.0	639	2	A56126	peroxisomal target
834	19	95.0	583	2	G86481	Mutator-like trans	907	19	95.0	640	1	A55073	transforming prote
835	19	95.0	583	2	T46177	villin 3 homolog T	908	19	95.0	641	2	F75553	hypothetical prote
836	19	95.0	587	2	R82431	methyl-accepting c	909	19	95.0	642	2	AD3502	dnak protein impo
837	19	95.0	588	2	T25248	hypothetical prote	910	19	95.0	642	2	S55521	beta-fructofuranos
838	19	95.0	588	2	A43740	DG42 protein - Afr	911	19	95.0	644	2	JQ0160	3-isopropylmalate
839	19	95.0	588	2	AB3460	hypothetical cytos	912	19	95.0	644	2	A45635	dnak-type molecula
840	19	95.0	589	2	A46459	macrophage-activat	913	19	95.0	645	2	JC5642	hypothetical prote
841	19	95.0	589	2	S74668	hypothetical prote	914	19	95.0	645	2	T25824	hypothetical prote
842	19	95.0	590	2	B81104	nitrate/nitrite se	915	19	95.0	646	2	B86295	transcription anti
843	19	95.0	590	2	C81911	nitrate/nitrite se	916	19	95.0	647	2	AF1488	probable thiamin p
844	19	95.0	591	2	S43506	hypothetical prote	917	19	95.0	648	2	AG0314	drebrin E (clone g
845	19	95.0	591	2	S70524	guanine nucleotide	918	19	95.0	649	2	UN0809	beta-fructofuranos
846	19	95.0	592	2	S64923	probable membrane	919	19	95.0	650	2	F72540	dnak-type molecula
847	19	95.0	592	2	T45827	pectinesterase-lik	920	19	95.0	651	2	T12083	hypothetical prote
848	19	95.0	598	2	B71095	hypothetical prote	921	19	95.0	651	2	JC4610	beta-fructofuranos
849	19	95.0	598	2	T32430	hypothetical prote	922	19	95.0	652	2	T14763	parasporeal crystal
850	19	95.0	602	2	D89331	probable DNA topoi	923	19	95.0	652	2	I39811	transferrin-bindin
851	19	95.0	602	2	T01360	hypothetical prote	924	19	95.0	654	2	S70905	peptidase (importe
852	19	95.0	603	2	T39674	hypothetical dnaj	925	19	95.0	654	2	AD3183	hypothetical prote
853	19	95.0	604	2	F87936	protein M01G12.12	926	19	95.0	656	1	E70107	transferrin-bindin
854	19	95.0	604	2	T33669	hypothetical prote	927	19	95.0	660	2	S70904	ATP-dependent DNA
855	19	95.0	605	2	I39837	dnak-type molecula	928	19	95.0	669	2	C82984	hypothetical prote
856	19	95.0	605	2	D84687	hypothetical prote	929	19	95.0	669	2	C96630	hypothetical prote
857	19	95.0	605	2	S46833	transfrase - Stre	930	19	95.0	670	2	D86457	hypothetical prote
858	19	95.0	606	2	T35710	dnak protein impo	931	19	95.0	670	2	AH2425	probable chemotaxi
859	19	95.0	607	2	B86744	dnak-type molecula	932	19	95.0	672	2	S61157	bacterio-opsin act
860	19	95.0	607	2	S39342	dnak protein impo	933	19	95.0	673	2	E84300	hypothetical prote
861	19	95.0	607	2	B95060	hypothetical prote	934	19	95.0	674	2	T22733	NADPH-ferrinemopro
862	19	95.0	607	2	G37928	hypothetical prote	935	19	95.0	678	1	RDRT04	growth arrest-spec
863	19	95.0	607	2	A95898	probable sensor ki	936	19	95.0	680	2	A42297	peptidyl-dipeptida
864	19	95.0	610	2	S41315	hypothetical prote	937	19	95.0	680	2	AH0678	dipeptidyl carboxy
865	19	95.0	610	2	C89939	conserved hypotet	938	19	95.0	682	2	AD25602	hypothetical prote
866	19	95.0	610	2	G69130	probable ABC-type	939	19	95.0	684	2	T25602	hypothetical prote
867	19	95.0	612	2	A70756	dnak-type molecula	940	19	95.0	685	2	S64985	hypothetical prote
868	19	95.0	613	2	T43738	class I heat-shock	941	19	95.0	686	2	C64428	hypothetical prote
869	19	95.0	613	2	AE1621	class I heat-shock	942	19	95.0	688	2	E86409	hypothetical prote
870	19	95.0	613	2	A11258	protein kinase pkn	943	19	95.0	688	2	D96930	methyl-accepting c
871	19	95.0	619	2	S77221	hypothetical prote	944	19	95.0	690	2	T11749	transferrin - Atla
872	19	95.0	619	2	A84411	hypothetical prote	945	19	95.0	691	2	T32748	conserved hypotet
873	19	95.0	621	2	T06717	phosphothricin-t	946	19	95.0	691	2	AD2766	hypothetical prote
874	19	95.0	622	2	PT0059	two-component sens	947	19	95.0	691	2	H97546	transferrin precu
875	19	95.0	622	2	E83160	parasporeal crystal	948	19	95.0	694	1	TFRBP	transferrin - pig
876	19	95.0	622	2	S17402	hypothetical prote	949	19	95.0	696	1	S01384	hypothetical prote
877	19	95.0	624	2	C83389	transferrin-bindin	950	19	95.0	696	2	E96831	hypothetical prote
878	19	95.0	625	2	D64107	asparagine synthas	951	19	95.0	696	2	H83024	asmA protein VC103
879	19	95.0	625	2	D86903	probable periplasm	952	19	95.0	698	1	TFHUP	carbonic anhydrase
880	19	95.0	625	2	G96976	carnitine O-acetyl	953	19	95.0	703	2	G32249	phenylalanine ammo
881	19	95.0	627	2	S53369	hypothetical prote	954	19	95.0	704	2	I47228	hypothetical prote
882	19	95.0	627	2	S69958	hypothetical prote	955	19	95.0	705	2	JC5873	transferrin precu
883	19	95.0	627	2	D71974	carbon-monoxide de	956	19	95.0	705	2	D86227	phenylalanine ammo
884	19	95.0	628	1	H64390	hypothetical prote	957	19	95.0	706	2	S33761	transferrin precu
885	19	95.0	628	2	B64534	nucleoside-triphos	958	19	95.0	707	2	S29029	phenylalanine ammo
886	19	95.0	631	1	NPVZ17	nucleoside-triphos	959	19	95.0	707	2	S60588	phenylalanine ammo
887	19	95.0	631	2	H36847	hypothetical prote	960	19	95.0	708	1	TVVPR4	large T antigen -
888	19	95.0	631	2	T28539	Oil protein - vari	961	19	95.0	708	2	T14255	phenylalanine ammo
889	19	95.0	631	2	C72163	nucleoside triphos	962	19	95.0	708	2	T14255	phenylalanine ammo
890	19	95.0	631	2	T37384	transferrin-bindin	963	19	95.0	708	2	T10909	conserved hypotet
891	19	95.0	631	2	S70908	hypothetical prote	964	19	95.0	710	2	JC5872	ATP-dependent DNA
892	19	95.0	634	2	T30702	probable SNF2-type	965	19	95.0	710	2	E83226	phenylalanine ammo
893	19	95.0	634	2	S32349	dnak-type molecula	966	19	95.0	712	2	T03663	phenylalanine ammo
894	19	95.0	635	2	B64112	dnak protein VC085	967	19	95.0	712	2	T01858	hercylisin secretio
895	19	95.0	635	2	B82273	1-deoxy-xylulose 5	968	19	95.0	714	2	A41464	hypothetical prote
896	19	95.0	635	2	AF1881	transforming prote	969	19	95.0	715	1	JX0199	fatty-acid beta-ox
897	19	95.0	636	1	TWMSMB	dnak-type molecula	970	19	95.0	715	1	G83269	transforming prote
898	19	95.0	637	2	A47042	dnak protein PA476	971	19	95.0	715	4	TWMSMY	glycyl-tRNA synthe
899	19	95.0	637	2	B83052	DNA repair helicase	972	19	95.0	716	2	AH2319	conserved hypotet
900	19	95.0	637	2	E75044	heat shock protein	973	19	95.0	716	2	D98855	hypothetical prote
901	19	95.0	638	1	IQECDK	dnak-type molecula	974	19	95.0	716	2	G82627	probable glgX prot
902	19	95.0	638	2	F90630	heat shock protein	975	19	95.0	721	2	A70764	hypothetical prote
903	19	95.0	638	2	F85481	dnak-type molecula	976	19	95.0	722	2	S76367	hypothetical prote
904	19	95.0	638	2	AE0503	hypothetical prote	977	19	95.0				
905	19	95.0	639	2	S72163	methyl-accepting c	978	19	95.0				

979 19 95.0 724 2 B85045 probable calcium c
 980 19 95.0 725 1 Z2BPA4 rapid lysis protei
 981 19 95.0 725 2 S52990 phenylalanine ammo
 982 19 95.0 725 2 G84787 phenylalanine ammo
 983 19 95.0 725 2 A10147 probable ATP-depen
 984 19 95.0 725 2 A91038 hypothetical prote
 985 19 95.0 729 2 A90808 probable membrane
 986 19 95.0 738 2 A87516 dipeptidyl peptida
 987 19 95.0 742 2 D85882 hypothetical prote
 988 19 95.0 744 2 T13048 NADH2 dehydrogenas
 989 19 95.0 746 2 S31816 genome polyprotein
 990 19 95.0 748 2 G96498 hypothetical prote
 991 19 95.0 754 2 T25551 subtilisin-like pr
 992 19 95.0 756 2 T04187 transforming prote
 993 19 95.0 761 1 TVH0MB polysulfide reduct
 994 19 95.0 763 2 S23457 aconitate hydratase
 995 19 95.0 764 2 S49849 sensory box/GGDEF
 996 19 95.0 768 2 H82367 yfeA protein - Esc
 997 19 95.0 768 2 H65013 subtilisin-like pr
 998 19 95.0 772 2 T05838 probable aminopept
 999 19 95.0 774 2 G71308 DNA polymerase B1
 1000 19 95.0 781 2 A69312

ALIGNMENTS

RESULT 1
 S39049
 cytotoxin-binding protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 16-Feb-1997
 C:Accession: S39049
 R:Ruttz, F.; Mohr, M.; Grimmig, M.; Leidl, R.; Linder, D.
 Eur. J. Biochem. 217, 1123-1128, 1993
 A>Title: Pseudomonas aeruginosa cytotoxin-binding protein in rabbit erythrocyte membrane
 A:Reference number: S39049; MUID:94039134; PMID:7693466
 A:Accession: S39049
 A>Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <LUT>
 C:Superfamily: lens fiber membrane major intrinsic protein

Query Match 95.0%; Score 19; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 14 VAEF 17

RESULT 2
 G64625
 hypothetical protein HP0847 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: G64625
 R:Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: G64625
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-33 <TOM>

A:Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07920.1; PID:g231400
 Query Match 95.0%; Score 19; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 88;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 DB 15 VAEF 18

RESULT 3
 B64618
 hypothetical protein HP0789 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: B64618
 R:Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: B64618
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-48 <TOM>

A:Cross-references: GB:AE000591; GB:AE000511; NID:g2313918; PIDN:AAD07847.1; PID:g231392

Query Match 95.0%; Score 19; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 15 VAEF 18

RESULT 4
 A42375
 hypothetical protein (lon 5' region) - Bacillus brevis
 C:Species: Bacillus brevis
 C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 15-Oct-1999
 C:Accession: A42375; I39873
 R:Ito, K.; Uda, S.; Yamagata, H.
 J. Bacteriol. 174, 2281-2287, 1992
 A>Title: Cloning, characterization, and inactivation of the Bacillus brevis lon gene.
 A:Reference number: A42375; MUID:92202157; PMID:1551846
 A:Accession: A42375
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-52 <ITO>
 A:Cross-references: GB:D00863; NID:g216293; PIDN:BA00736.1; PID:g303507

Query Match 95.0%; Score 19; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 47 VAEF 50

RESULT 5
 E85745
 unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain O1
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: E85745
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: E85745
 A>Status: preliminary


```

Molecule type: DNA
;Residues: 1-54 <STO>
;Cross-references: GB:AE005174; NID:g12515374; PIDN:RAG56425.1; GSPDB:GN00145; UWGP:223
;Experimental source: strain O157:H7, substrain EDL933
;Genetics:
;Gene: Z2382

Query Match      95.0%; Score 19; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      |||||
b     32 VAEF 35

RESULT 6
69386
observed hypothetical protein AF1090 - Archaeoglobus fulgidus
;Species: Archaeoglobus fulgidus
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
;Accession: A69386
;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
;Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
ature 390, 364-370, 1997
;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
mith, H.O.; Woese, C.R.; Venter, J.C.
;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
;Reference number: A69250; MUID:98049343; PMID:9389475
;Accession: A69386
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-59 <KLE>
;Cross-references: GB:AE001028; GB:AE000782; NID:G2689351; PIDN:AAB90157.1; PID:G264950
;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975

Query Match      95.0%; Score 19; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      |||||
b     51 VAEF 54

RESULT 7
71349
robable preprotein translocase subunit (secE) - syphilis spirochete
;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
;Accession: E71349
;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McBo
hey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
cience 281, 375-388, 1998
;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
;Reference number: A71250; MUID:9832770; PMID:9665876
;Accession: E71349
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-59 <COL>
;Cross-references: GB:AE001205; GB:AE000520; NID:G3322501; PIDN:AAC65223.1; PID:G332250
;Experimental source: strain Nichols
;Genetics:
;Gene: TP0235

Query Match      95.0%; Score 19; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      |||||

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Db      12 VAEF 15

RESULT 8
JC4002
carbamoyl resistance protein carA - Streptomyces sp. (fragment)
;Species: Streptomyces sp.
;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999
;Accession: JC4002
;Arisawa, A.; Tsunekawa, H.; Okamura, K.; Okamoto, R.
Riosci. Biotechnol. Biochem. 59, 582-588, 1995
;Title: Nucleotide sequence analysis of the carbamoyl biosynthetic genes including the
;Reference number: JC4001; MUID:95290751; PMID:7772821
;Accession: JC4002
;Molecule type: DNA
;Residues: 1-63 <ARI>
;Cross-references: DBJ:D30759; NID:G551628; PIDN:BA06419.1; PID:d1006989; PID:G551629
;Note: the source was designated as Streptomyces thermotolerans
;Genetics:
;Gene: carA
;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
;Keywords: ATP
F:1-55/Domain: ATP-binding cassette homology (fragment) <ABC2>

Query Match      95.0%; Score 19; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      |||||
Db     57 VAEF 60

RESULT 9
G64007
hypothetical protein H10451 - Haemophilus influenzae (strain Rd KW20)
;Species: Haemophilus influenzae
;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
;Accession: G64007
;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
;D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J
;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
;Reference number: A64000; MUID:95350630; PMID:7542800
;Accession: G64007
;Status: nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-63 <TIGR>
;Cross-references: GB:U32728; GB:L42023; NID:g1573425; PIDN:AAC22109.1; PID:g1573437; T]

Query Match      95.0%; Score 19; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      |||||
Db     27 VAEF 30

RESULT 10
IS1350
transferrin - Atlantic salmon (fragment)
;Species: Salmo salar (Atlantic salmon)
;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
;Accession: IS1350
;Kvingedal, A.M.
Gene 150, 335-339, 1994
;Title: Characterization of the 5' region of the Atlantic salmon (Salmo salar) transferr
;Reference number: IS1350; MUID:95121925; PMID:7821802
;Accession: IS1350
;Status: preliminary; translated from GB/EMBL/DBJ

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A:Molecule type: DNA
 A:Residues: 1-64 <KVI>
 A:Cross-references: GB:L26909; NID:G598395; PIDN:AAC42221.1; PID:G598396
 C:Genetics:
 A:Gene: If
 A:Introns: 14/1
 C:Superfamily: transferrin; transferrin repeat homology

Query Match 95.0%; Score 19; DB 2; Length 64;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 45 VAEF 48

RESULT 11

D97045
 Hypothetical protein CAC1179 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: D97045

R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: D97045

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-74 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK79151.1; PID:g15024100; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC624

C:Genetics:

A:Gene: CAC1179

Query Match 95.0%; Score 19; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8

RESULT 12

S07277
 Gene D protein - phage 186 (fragment)

C:Species: phage 186

C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 17-Mar-1999

C:Accession: S07277; S25273

R:Kallionis, B.; Dodd, I.B.; Egan, J.B.

J. Mol. Biol. 191, 199-203, 1986

A:Title: Control of gene expression in the P2-related template coliphages. III. DNA sequ

A:Reference number: S07277; MUID:87112711; PMID:3806670

A:Accession: S07277

A:Molecule type: DNA

A:Residues: 1-75 <KAL>

A:Cross-references: EMBL:X04449; NID:g15549; PID:g15550

R:Dibbens, J.A.; Gregory, S.L.; Egan, J.B.

Mol. Microbiol. 6, 2643-2650, 1992

A:Title: Control of gene expression in the temperate coliphage 186. X. The cI repressor

A:Reference number: S25273; MUID:93078618; PMID:1447973

A:Accession: S25273

A:Molecule type: DNA

A:Residues: 1-75 <DTB>

A:Cross-references: EMBL:X04449; NID:g15549; PID:g15550

Query Match 95.0%; Score 19; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8

RESULT 13

T18034
 Hypothetical protein A532L - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18034

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T18034

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-79 <GRA>

A:Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96899.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: A532L

Query Match 95.0%; Score 19; DB 2; Length 79;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 49 VAEF 52

RESULT 14

T27605
 Hypothetical protein ZC477.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27605

R:Du, Z.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid ZC477.

A:Reference number: Z20392

A:Accession: T27605

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-79 <DUZ>

A:Cross-references: EMBL:U40802; PIDN:AAA81506.1; CESP:ZC477.6

C:Genetics:

A:Gene: CESP:ZC477.6

A:Introns: 51/2

Query Match 95.0%; Score 19; DB 2; Length 79;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 74 VAEF 77

RESULT 15

F83922
 Hypothetical protein BH2182 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: F83922

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83922

A>Status: preliminary

A:Molecule type: DNA

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;Residues: 1-84 <STO>
;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA05901.1; GSPDB:GNO0
;Experimental source: strain C-125
;Genetics:
;Gene: BH2182

Query Match          95.0%; Score 19; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/      2 VAEF 5
      ||||
      38 VAEF 41

RESULT 16
38725
transferrin - sheep (fragments)
;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
;Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 05-Dec-1997
;Accession: A38725
;Tu, G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.
;Biol. Chem. 266, 6201-6208, 1991
;Title: The distribution of cerebral expression of the transferrin gene is species spec
;Reference number: A38725; MUID:91177867; PMID:1848850
;Accession: A38725
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-87 <TUA>
;Cross-references: GB:M64692
;Superfamily: transferrin; transferrin repeat homology
;Keywords: duplication

Query Match          95.0%; Score 19; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/      2 VAEF 5
      ||||
      13 VAEF 16

RESULT 17
34116
ribosomal protein S15 - Haemophilus influenzae (strain Rd KW20)
;Species: Haemophilus influenzae
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: H64116; E64125
;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
;Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
;D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
;Science 269, 496-512, 1995
;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
;Reference number: A64000; MUID:95350630; PMID:7542800
;Accession: H64116
;Status: nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-89 <TIG1>
;Cross-references: GB:U32812; GB:U42023; NID:g1574784; PIDN:AAC22973.1; PID:g1574788; T
;Note: named as homolog to a protein from Escherichia coli
;Accession: E64125
;Status: nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-89 <TIG2>
;Cross-references: GB:U32825; GB:L42023; NID:g1574307; PIDN:AAC23117.1; PID:g1574309; T
;Note: named by homology to a protein from Escherichia coli
;Genetics:
;Superfamily: this gene are found in the Haemophilus influenzae chromosome
;Note: two copies of this gene are found in the Haemophilus influenzae chromosome
;23-99/Domain: eubacterial ribosomal protein S15 homology <BS15>

Query Match          95.0%; Score 19; DB 1; Length 89;

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Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      ||||
      12 VAEF 15

Db

RESULT 18
F86818
hypothetical protein YPjB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
;Species: Lactococcus lactis subsp. lactis
;CDate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
;CAccession: F86818
;R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlic
;Genome Res. 11, 731-753, 2001
;A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
;AReference number: A86625; MUID:21235186; PMID:11337471
;AAccession: F86818
;A>Status: preliminary
;A:Molecule type: DNA
;A:Residues: 1-89 <STO>
;A:Cross-references: GB:AE005176; PID:g12724551; PIDN:AAK05648.1; GSPDB:GNO0146
;A:Experimental source: strain IL1403
;C:Genetics:
;A:Gene: YPjB

Query Match          95.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      ||||
      68 VAEF 71

Db

RESULT 19
T15018
hypothetical protein Y1103 - Yersinia pestis plasmid pMT1
;Species: Yersinia pestis
;CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
;CAccession: T15018
;R;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
;Infect. Immun. 66, 5731-5742, 1998
;A>Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
;AReference number: Z18268; MUID:99043898; PMID:9826348
;AAccession: T15018
;A>Status: preliminary; translated from GB/EMBL/DBD
;A:Molecule type: DNA
;A:Residues: 1-89 <LIN>
;A:Cross-references: EMBL:AF074611; NID:g3883003; PID:g3883101; PIDN:AAC82761.1
;C:Genetics:
;A:Gene: Y1103
;A:Genome: plasmid pMT1

Query Match          95.0%; Score 19; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      ||||
      3 VAEF 6

Db

RESULT 20
AB3053
hypothetical protein Atu4039 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
;Species: Agrobacterium tumefaciens
;CDate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
;CAccession: AB3053
;R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
;Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan
;Karp, P.; Romero, P.; Zhang, S.

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Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Acetobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <KUR>
A:Cross-references: GB:AB008689; PIDN:AA44840.1; PID:g17742484; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4039
A:Map position: linear chromosome

Query Match 95.0%; Score 19; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 55 VAEF 58

RESULT 21
AC1397
conserved hypothetical protein lmo2579 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1397
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 845-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1397
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00657.1; PID:g16412067; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2579

Query Match 95.0%; Score 19; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 15 VAEF 18

RESULT 22
EB3244
conserved hypothetical protein PA3202 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: EB3244
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10384043
A:Accession: EB3244
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <STO>
A:Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001

Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Acetobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AB3053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <KUR>
A:Cross-references: GB:AB008689; PIDN:AA44840.1; PID:g17742484; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu4039
A:Map position: linear chromosome

Query Match 95.0%; Score 19; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 55 VAEF 58

RESULT 21
AC1397
conserved hypothetical protein lmo2579 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AC1397
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 845-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1397
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00657.1; PID:g16412067; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2579

Query Match 95.0%; Score 19; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 15 VAEF 18

RESULT 22
EB3244
conserved hypothetical protein PA3202 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: EB3244
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10384043
A:Accession: EB3244
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <STO>
A:Cross-references: GB:AE004744; GB:AE004091; NID:g9949317; PIDN:AAG06590.1; GSPDB:GN001

A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3202

Query Match 95.0%; Score 19; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 62 VAEF 65

RESULT 23
H90297
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: H90297
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90297
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: GB:AE006641; NID:g13814625; PIDN:AAK41639.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS01404

Query Match 95.0%; Score 19; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 20 VAEF 23

RESULT 24
TI0097
nifX protein - Methanococcus maripaludis
C:Species: Methanococcus maripaludis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: TI0097
R:Kessler, P.S.; McLarnan, J.; Leigh, J.A.
J. Bacteriol. 179, 541-543, 1997
A:Title: Nitrogenase phylogeny and the molybdenum dependence of nitrogen fixation in Met
A:Reference number: Z16944; MUID:97144542; PMID:8990309
A:Accession: TI0097
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-106 <KES>
A:Cross-references: EMBL:U75887; NID:g1666882; PIDN:AAC45519.1; PID:g1666890
A:Experimental source: strain JJ
C:Genetics:
A:Gene: nifX

Query Match 95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 35 VAEF 38

RESULT 25
CG4490
hypothetical protein MJ1524 - Methanococcus jannaschii

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;Species: Methanococcus jannaschii
;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 12-Jun-2003
;Accession: C64490
;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
;Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
;son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
;Science 273, 1058-1073, 1996
;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
;Reference number: A64300; MUID:96337999; PMID:8688087
;Accession: C64490
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-108 <BUL>
;Cross-references: GB:U67593; GB:L77117; NID:G2826427; PIDN:AAB99550.1; PID:G1592154; T
;Genetics:
;Map position: FOR1501406-1501732
;Superfamily: uncharacterized conserved protein MJ1524
Query Match 95.0%; Score 19; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
C 52 VAEF 55

ESULT 26
70949
robable regulator - Mycobacterium tuberculosis (strain H37RV)
;Species: Mycobacterium tuberculosis
;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
;Accession: E70949
;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
;Connor, R.; Davies, R.; Delvin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
;ajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
;ature 393, 537-544, 1998
;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
;Reference number: A70500; MUID:98295987; PMID:9634230
;Accession: E70949
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-109 <COL>
;Cross-references: GB:AL021646; GB:AL123456; NID:G3242278; PIDN:CAA16648.1; PID:G282759
;Experimental source: strain H37RV
;Genetics:
;Gene: Rv3183

Query Match 95.0%; Score 19; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
b 97 VAEF 100

ESULT 27
17582
ypothetical protein A92L - Chlorella virus PBCV-1
;Species: Chlorella virus PBCV-1
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
;Accession: T17582
;Graves, M.V.; Van Etten, J.L.
;submitted to the EMBL Data Library, May 1999
;Reference number: Z18806
;Accession: T17582
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-111 <GRA>
;Cross-references: EMBL:U42580; NID:G4028896; PIDN:AAC96460.1

;Experimental source: specific host Chlorella strain NC64
;Genetics:
;C/Gene: A92L
;C/Superfamily: Chlorella virus PBCV-1 hypothetical protein A92L
Query Match 95.0%; Score 19; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
Db 17 VAEF 20

RESULT 28
B83431
type III export protein Psci PA1722 [imported] - Pseudomonas aeruginosa (strain PA01)
;Species: Pseudomonas aeruginosa
;C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
;C/Accession: B83431
;R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bri
;adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
;Lory, S.; Olson, M.V.
;Nature 406, 959-964, 2000
;A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
;A/Reference number: A82950; MUID:20437337; PMID:10984043
;A/Accession: B83431
;A/Status: preliminary
;A/Molecule type: DNA
;A/Residues: 1-112 <STO>
;A/Cross-references: GB:AE004598; GB:AE004091; NID:G9947687; PIDN:AAG05111.1; GSPDB:GN001;
;A/Experimental source: strain PA01
;Genetics:
;C/Gene: psci: PA1722
;C/Superfamily: Yersinia enterocolitica plasmid pYV virC-region hypothetical protein yscI

Query Match 95.0%; Score 19; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
Db 28 VAEF 31

RESULT 29
A55872
kedarcidin [validated] - Streptoalloteichus sp. (ATCC 53650)
;Alternate names: kedarcidin apoprotein
;C/Species: Streptoalloteichus sp.
;A/Variety: strain L585-6 (ATCC 53650)
;C/Date: 21-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 15-Sep-2000
;C/Accession: A55872
;R/Hofstead, S.J.; Matson, J.A.; Malacko, A.R.; Marquardt, H.
;J. Antibiot. 45, 1250-1254, 1992
;A/Title: Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation, purificati
;A/Reference number: A55872; MUID:93015257; PMID:1399845
;A/Accession: A55872
;A/Molecule type: protein
;A/Residues: 1-114 <HOF>
;A/Note: sequence extracted from NCBI backbone (NCBIP:118354)
;R/Constantine, K.L.; Colson, K.L.; Wittekind, M.; Friedrichs, M.S.; Zein, N.; Tuttle, J.;
;ler, L.
;submitted to the Brookhaven Protein Data Bank, June 1994
;A/Reference number: A52519; PDB:1AKP
;A/Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues
;R/Zein, N.; Casazza, A.M.; Doyle, T.W.; Leet, J.E.; Schroeder, D.R.; Solomon, W.; Nadler,
;Proc. Natl. Acad. Sci. U.S.A. 90, 8009-8012, 1993
;A/Title: Selective proteolytic activity of the antitumor agent kedarcidin.
;A/Reference number: A58601; MUID:93376732; PMID:8367457
;A/Contents: annotation; protein activity
;A/Note: the apoprotein may have proteolytic activity
;C/Superfamily: macromonocin

```

2; Keywords: antibiotic; pigment binding
2; 37-47, 88-95/Disulfide bonds: #status experimental

Query Match 95.0%; Score 19; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 49 VAEF 52

RESULT 30

97414
hypothetical protein AGR_C_804 [imported] - Agrobacterium tumefaciens (strain C58, Cere
2; Species: Agrobacterium tumefaciens
2; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
2; Accession: D97414
2; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A; Reference number: A97359; MUID: 21608551; PMID: 11743194
A; Accession: D97414
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-114 <KUR>
A; Cross-references: GB:AE007869; PIDN:AAK86269.1; PID:g15155379; GSPDB:GN00169
2; Genetics:
A; Gene: AGR_C_804
A; Map position: circular chromosome

Query Match 95.0%; Score 19; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 40 VAEF 43

RESULT 31

975218
hypothetical protein PAB0185 - Pyrococcus abyssi (strain Orsay)
2; Species: Pyrococcus abyssi
2; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
2; Accession: D75218
2; Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A; Reference number: A75001
A; Accession: D75218
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-115 <KAW>
A; Cross-references: GB:AJ249283; GB:AL096836; NID:g5457433; PIDN:CAB49195.1; PID:e151508
A; Experimental source: strain Orsay
2; Genetics:
A; Gene: PAB0185

Query Match 95.0%; Score 19; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 101 VAEF 104

RESULT 32

IPAF
insulin precursor - American goosetish
2; Species: Lophius americanus (American goosetish)

C; Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 16-Jul-1999
A; Accession: A01608
R; Hobart, P.M.; Shen, L.P.; Crawford, R.; Pictet, R.L.; Rutter, W.J.
Science 210, 1360-1363, 1980
A; Title: Comparison of the nucleic acid sequence of anglerfish and mammalian insulin mRN
A; Reference number: A94254; MUID: 81056434; PMID: 7001633
A; Accession: A01608
A; Molecule type: mRNA
A; Residues: 1-116 <HOB>
A; Cross-references: GB:V00634; GB:J00934; NID:g64025; PIDN:CAA23907.1; PID:g64026
C; Superfamily: insulin
C; Keywords: hormone; pancreas
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-54/Domain: insulin chain B #status predicted <SCH>
F; 25-54, 96-116/Product: insulin #status predicted <MAT>
F; 56-93/Domain: connecting peptide #status predicted <CFEP>
F; 95-116/Domain: insulin chain A #status predicted <ACH>
F; 32-102, 44-115, 101-106/Disulfide bonds: #status predicted

Query Match 95.0%; Score 19; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 80 VAEF 83

RESULT 33

T48682
hypothetical protein DKFZp761N05121.1 - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C; Accession: T48682
R; Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24535
A; Accession: T48682
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-118 <AAA>
A; Cross-references: EMBL:AL353932
A; Experimental source: adult amygdala; clone DKFZp761N05121
C; Genetics:
A; Note: DKFZp761N05121.1

Query Match 95.0%; Score 19; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 15 VAEF 18

RESULT 34

F95327
hypothetical protein SMA0974 [imported] - Sinorhizobium meliloti (strain 1021) megaplasm
2; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: F95327
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A; Reference number: A95262; MUID: 21396509; PMID: 11481432
A; Accession: F95327
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-119 <KUR>
A; Cross-references: GB:AE006469; PIDN:AAK65184.1; PID:g14523629; GSPDB:GN00165
A; Experimental source: strain 1021, megaplasmid pSyma
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

la, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 .; Hyman, R.W.; Jones, T.
 :ence 293, 668-672, 2001
 Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, B.; Komp, C.; Lelaure,
 bault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 Reference number: A96039; MUID:21368234; PMID:11474104
 Contents: annotation
 Genetics:
 Gene: SMA0974
 Genome: plasmid

Query Match 95.0%; Score 19; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 26 VAEF 29

RESULT 35
 12861
 njugal transfer protein Xfa0006 [imported] - Xylella fastidiosa (strain 9a5c)
 Species: Xylella fastidiosa
 Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 Accession: F82861
 anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen-
 ture 406, 151-157, 2000
 Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 Reference number: A82515; MUID:20365717; PMID:10910347
 Note: for a complete list of authors see reference number A59328 below
 Accession: F82861
 Status: preliminary
 Molecule type: DNA
 Residues: 1-122 <SIM>
 Cross-references: GB:AB003851; NID:G9112238; PIDN:AAF85575.1; GSPDB:GN00130; XFSC:XFA0
 Experimental source: strain 9a5c
 Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A-
 -Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.F.; Ferreira, A.J.S.
 bmitted to GenBank, June 2000
 Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 ado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H
 Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 drigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 ; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 Reference number: A59328
 Contents: annotation
 Genetics:
 Gene: Xfa0006
 Genome: plasmid
 Note: plasmid pXFS.1

Query Match 95.0%; Score 19; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 32 VAEF 35

RESULT 36
 59129
 nma-carboxymuconolactone decarboxylase - Methanobacterium thermoautotrophicum (strain
 Species: Methanobacterium thermoautotrophicum
 Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
 Accession: B69129
 Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
 Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A>Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functi
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: B69129
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-125 <MTH>
 A:Cross-references: GB:AE000810; GB:AE000666; NID:G2621277; PIDN:AAB94740.1; PID:G262128;
 A:Experimental source: strain Delta H
 C:Genetics:
 C:Gene: MTH234
 C:Superfamily: 4-carboxymuconolactone decarboxylase

Query Match 95.0%; Score 19; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 37 VAEF 40

RESULT 37
 D70730
 hypochemical protein Rv3675 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: D70790
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: D70790
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-125 <COL>
 A:Cross-references: GB:AL022121; GB:AL123456; NID:G3261559; PIDN:CAA17997.1; PID:el26453;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv3675

Query Match 95.0%; Score 19; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 42 VAEF 45

RESULT 38
 B81368
 hypochemical protein Cj0939c [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C:Accession: B81368
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandram, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
 Nature 403, 665-668, 2000
 A>Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
 A:Reference number: A81250; MUID:20150912; PMID:10688204
 A:Accession: B81368
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <PAR>
 A:Cross-references: GB:AL139076; GB:AL111168; NID:G6968128; PIDN:CAB73196.1; PID:G6968376;
 A:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:

```

i;Gene: Cj0939c
  Query Match          95.0%; Score 19; DB 2; Length 126;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Y 2 VAEF 5
  b 83 VAEF 86

RESULT 39
>70799
  hypothetical protein RV3747 - Mycobacterium tuberculosis (strain H37RV)
  ;Species: Mycobacterium tuberculosis
  ;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
  ;Accession: D70799
  ;Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
  ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.;
  ; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.;
  ; Nature 393, 537-544, 1998
  ;Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
  ;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
  ;Reference number: A70500; MUID:98295987; PMID:9634230
  ;Accession: D70799
  ;Status: preliminary; nucleic acid sequence not shown; translation not shown
  ;Molecule type: DNA
  ;Residues: 1-127 <COL>
  ;Cross-references: GB:AL022121; GB:AL123456; NID:G3261559; PIDN:CA118069.1; PID:G296017
  ;Experimental source: strain H37RV
  ;Genetics:
  ;Gene: RV3747

  Query Match          95.0%; Score 19; DB 2; Length 127;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Y 2 VAEF 5
  b 80 VAEF 83

RESULT 40
>AB1732
  hypothetical protein lin2399 [imported] - Listeria innocua (strain Clip11262)
  ;Species: Listeria innocua
  ;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
  ;Accession: AB1732
  ;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
  ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
  ; Jones, L.M.; Karet, U.
  ;Science 294, 849-852, 2001
  ;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
  ; C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
  ;Title: Comparative genomics of Listeria species
  ;Reference number: AB1077; MUID:21537279; PMID:11679669
  ;Accession: AB1732
  ;Status: preliminary
  ;Molecule type: DNA
  ;Residues: 1-127 <GLA>
  ;Cross-references: GB:AL592022; PIDN:CAC97626.1; PID:gi61414922; GSPDB:GN00178
  ;Genetics:
  ;Gene: lin2399

  Query Match          95.0%; Score 19; DB 2; Length 127;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Y 2 VAEF 5
  b 71 VAEF 74

us-09-594-978a-1.rpr
  ileal lipid-binding protein - mouse
  ;Species: Mus musculus (house mouse)
  ;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
  ;Accession: A54797
  ;Crossman, M.W.; Hauff, S.M.; Gordon, J.I.
  ;J. Cell Biol. 126, 1547-1564, 1994
  ;Title: The mouse ileal lipid-binding protein gene: a model for studying axial patterni
  ;Reference number: A54797; MUID:94375529; PMID:8089185
  ;Accession: A54797
  ;Status: preliminary
  ;Molecule type: mRNA
  ;Residues: 1-128 <CRO>
  ;Cross-references: GB:U00938; NID:G507143; PIDN:AAC27352.1; PID:G507144
  ;Genetics:
  ;C;Superfamily: myelin P2 protein

  Query Match          95.0%; Score 19; DB 2; Length 128;
  Best Local Similarity 100.0%; Pred. No. 3.6e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Y 2 VAEF 5
  b 92 VAEF 95

RESULT 42
>T02012
  probable cathepsin B-like cysteine proteinase (EC 3.4.22.-) T15B16.17b - Arabidopsis tha
  ;Species: Arabidopsis thaliana (mouse-ear cress)
  ;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
  ;Accession: T02012
  ;Stonking, T.; Smith, R.
  ;Submitted to the EMBL Data Library, November 1998
  ;Description: The sequence of A. thaliana T15B16.
  ;Reference number: Z14488
  ;Accession: T02012
  ;Status: translated from GB/EMBL/DBJ
  ;Molecule type: DNA
  ;Residues: 1-129 <STO>
  ;Cross-references: EMBL:AF104919; NID:G3859590; PIDN:AAC72873.1; PID:G3859607
  ;Experimental source: cultivar Columbia
  ;Genetics:
  ;Map position: 4
  ;Introns: 26/3; 44/3; 71/3
  ;Note: T15B16.17b
  ;Superfamily: papain
  ;Keywords: cysteine proteinase; hydrolase

  Query Match          95.0%; Score 19; DB 2; Length 129;
  Best Local Similarity 100.0%; Pred. No. 3.7e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Y 2 VAEF 5
  b 72 VAEF 75

RESULT 43
>D72348
  conserved hypothetical protein - Thermotoga maritima (strain MSB8)
  ;Species: Thermotoga maritima
  ;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
  ;Accession: D72348
  ;R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
  ; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
  ; C.M.
  ;Nature 399, 323-329, 1999
  ;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
  ;Reference number: A72200; MUID:199287316; PMID:10360571

```


Accession: D72348
 Status: preliminary
 Molecule type: DNA
 Residues: 1-130 <ARN>
 Cross-references: GB:AE001739; GB:AE000512; NID:g4981176; PID:RAD35739.1; PID:g498117
 Experimental source: strain MSB8
 Gene: TM0655
 Superfamily: conserved hypothetical protein MU0315

Query Match 95.0%; Score 19; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 9 VAEF 12

RESULT 44
 75208
 hypothetical protein PAB2224 - Pyrococcus abyssi (strain Oresay)
 Species: Pyrococcus abyssi
 Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 06-Jan-2003
 Accession: G75208
 anonymous, Genoscope
 Submitted to the EMBL Data Library, July 1999
 Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
 Reference number: A75001
 Accession: G75208
 Status: preliminary
 Molecule type: DNA
 Residues: 1-131 <KAW>
 Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49118.1; PID:g545762
 Experimental source: strain Orsay
 Genetics:
 Gene: PAB2224
 Superfamily: uncharacterized conserved protein

Query Match 95.0%; Score 19; DB 2; Length 131;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 4 VAEF 7

RESULT 45
 22270
 hypothetical 15.2K protein - Anabaena sp.
 Species: Anabaena sp.
 Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Sep-1998
 Accession: JQ2270
 Larimer, F.W.; Soper, T.S.
 ene 126, 85-92, 1993
 Title: Overproduction of Anabaena 7120 ribulose-bisphosphate carboxylase/oxygenase in
 Reference number: JQ2270; MUID:93231541; PMID:8472962
 Accession: JQ2270
 Molecule type: DNA
 Residues: 1-132 <LAR>
 Cross-references: DDBJ:J01540
 Experimental source: strain 7120
 Genetics:
 Gene: rbcX
 Superfamily: rbcX protein

Query Match 95.0%; Score 19; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||

Db 81 VAEF 84

RESULT 46
 AG1996
 hypothetical protein alr1525 [imported] - Nostoc sp. (strain PCC 7120)
 Species: Nostoc sp. PCC 7120
 Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 Accession: AG1996
 R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat
 AReference number: AB1807; MUID:21595285; PMID:11759840
 Accession: AG1996
 Status: preliminary
 Molecule type: DNA
 Residues: 1-132 <KUR>
 Cross-references: GB:BA000019; PIDN:BA077891.1; PID:g17135345; GSPDB:GN00179
 Experimental source: strain PCC 7120
 Genetics:
 Gene: alr1525
 Superfamily: rbcX protein

Query Match 95.0%; Score 19; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 81 VAEF 84

Db 81 VAEF 84

RESULT 47
 AH0137
 conserved hypothetical protein YP01120 [imported] - Yersinia pestis (strain CO92)
 Species: Yersinia pestis
 Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 Accession: AH0137
 R.Paithill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
 ll, M.; Rutherford, K.; Simmons, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
 Nature 413, 523-527, 2001
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 AReference number: AB0001; MUID:21470413; PMID:11586360
 Accession: AH0137
 Status: preliminary
 Molecule type: DNA
 Residues: 1-133 <KUR>
 Cross-references: GB:AL590842; PIDN:CAC89963.1; PID:g15979187; GSPDB:GN00175
 Genetics:
 Gene: YP01120
 Superfamily: 15.5K protein (tolAB operon 5' region)

Query Match 95.0%; Score 19; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 129 VAEF 132

Db 129 VAEF 132

RESULT 48
 H75623
 conserved hypothetical protein - Deinococcus radiodurans (strain R1)
 Species: Deinococcus radiodurans
 Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 Accession: H75623
 R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A;Accession: G64809
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-134 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73830.1; PID:g1786957;
A;Experimental source: strain K-12, substrain MG1655
C;Comment: This is one of the proteins, encoded by the *fli-tolAB* gene cluster, that is i
C;Genetics:
A;Gene: *ybgC*
A;Map position: 17 min
A;Start codon: GTG
C;Superfamily: 15.5K protein (tolAB operon 5' region)

Query Match 95.0%; Score 19; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 129 VAEF 132

RESULT 51
C90725
hypothetical protein ECs0771 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: C90725
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90725
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <RAY>
A;Cross-references: GB:BA000007; PIDN:BA34194.1; PID:g13360230; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0771
C;Superfamily: 15.5K protein (tolAB operon 5' region)

Query Match 95.0%; Score 19; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||
DB 129 VAEF 132

RESULT 52
D85576
hypothetical protein ybgC [imported] - Escherichia coli (strain O157:H7, substrain EDL933
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85576
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grothbeck, E.J.; Davis, N.W.; Llim, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <STO>
A;Cross-references: GB:AE005174; NID:g12513669; PIDN:AAG55072.1; GSPDB:GN00145; UNGP:Z09
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: *ybgC*
C;Superfamily: 15.5K protein (tolAB operon 5' region)

Query Match 95.0%; Score 19; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
129 VAEF 132

SULT 53
0592
nsered hypothetical protein STY0790 [imported] - Salmonella enterica subsp. enterica
Species: Salmonella enterica subsp. enterica serovar Typhi
Note: this species has also been called Salmonella typhi
Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
Accession: AD0592
Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
S.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
ture 413, 848-852, 2001
Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: AD0592
Status: preliminary
Molecule type: DNA
Residues: 1-134 <PAR>
Cross-references: GB:ALU513382; PIDN:CAD05206.1; PID:gl6501976; GSPDB:GN00176
Genetics:
Gene: STY0790
Superfamily: 15.5K protein (tolAB operon 5' region)

Query Match 95.0%; Score 19; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
129 VAEF 132

SULT 54
6416
potheical protein - Synecocystis sp. (strain PCC 6803)
Species: Synecocystis sp.
Variety: PCC 6803
Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
Accession: S76416
Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
IA Res. 3, 109-136, 1996
Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

Reference number: S74322; MUID:97061201; PMID:8905231

Accession: S76416
Status: preliminary
Molecule type: DNA
Residues: 1-136 <KAN>
Cross-references: EMBL:D90915; GB:AB001339; NID:g1653604; PIDN:BAAL18545.1; PID:gl65363
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 95.0%; Score 19; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
88 VAEF 91

SULT 55
1355
potheical protein Cj0829c [imported] - Campylobacter jejuni (strain NCTC 11168)

Query Match 95.0%; Score 19; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
33 VAEF 36

RESULT 56
F82106
flagellar basal-body rod protein FlgC VC2199 [imported] - Vibrio cholerae (strain N16961
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: F82106
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, B.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: F82106
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-138 <HEI>
A/Cross-references: GB:AE004292; GB:AE003852; NID:g9656760; PIDN:AAF95344.1; GSPDB:GN001;
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2199
A/Map position: 1

Query Match 95.0%; Score 19; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
79 VAEF 82

RESULT 57
A69052
riboflavin synthase beta subunit - Methanobacterium thermoautotrophicum (strain Delta H)
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000
C/Accession: A69052
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
K4, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: A69052
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

```

;Residues: 1-139 <MTH>
;Cross-references: GB:AE000092; GB:AE000666; NID:G2622500; PIDN:AAB85867.1; PID:G2622500
;Experimental source: strain Delta H
;Genetics:
;Gene: MTH1390
;Superfamily: riboflavin synthase beta chain

Query Match      95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 10 VAEF 13

RESULT 58
;Hypothetical protein BH2601 [imported] - Bacillus halodurans (strain C-125)
;Species: Bacillus halodurans
;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
;Accession: AB3975
;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
;Nucleic Acids Res. 28, 4317-4331, 2000
;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
;Reference number: A83650; MUID:20512582; PMID:11058132
;Accession: AB3975
;Status: preliminary
;Molecule type: DNA
;Residues: 1-139 <STO>
;Cross-references: GB:AF001516; GB:BA000004; NID:G10175192; PIDN:BA806320.1; GSPDB:GN00
;Experimental source: strain C-125
;Genetics:
;Gene: BH2601
;Superfamily: Bacillus subtilis hypothetical protein ylbD

Query Match      95.0%; Score 19; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 11 VAEF 14

RESULT 59
;Hypothetical protein AF0586 - Archaeoglobus fulgidus
;Species: Archaeoglobus fulgidus
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Nov-1999
;Accession: B69323
;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
;Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
;Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
;ature 390, 364-370, 1997
;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
;Smith, H.O.; Woese, C.R.; Venter, J.C.
;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
;Reference number: A69250; MUID:98049343; PMID:9389475
;Accession: B69323
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-140 <KLE>
;Cross-references: GB:AE001064; GB:AE000782; NID:G2689387; PIDN:AAB90658.1; PID:G265004
;Superfamily: Archaeoglobus fulgidus hypothetical protein AF0586

Query Match      95.0%; Score 19; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 65 VAEF 68

;Residues: 1-142 <WER>
;Cross-references: GB:S68726; NID:G544693; PIDN:AAB29482.1; PID:G544694
;Comment: This protein is a low-temperature-related protein.

Query Match      95.0%; Score 19; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 125 VAEF 128

RESULT 61
;Low-temperature regulated protein BN19 - rape
;Species: Brassica napus (rape)
;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 28-May-1999
;Accession: JQ2280
;Weretilnyk, E.; Orr, W.; White, T.C.; Iu, B.; Singh, J.
;Plant Physiol. 101, 171-177, 1993
;Title: Characterization of three related low-temperature-regulated cDNAs from winter B
;Reference number: JQ2279; MUID:94105287; PMID:7904076
;Accession: JQ2279
;Molecule type: mRNA
;Residues: 1-142 <WER>
;Cross-references: GB:S68726; NID:G544693; PIDN:AAB29482.1; PID:G544694
;Comment: This protein is a low-temperature-related protein.

Query Match      95.0%; Score 19; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 125 VAEF 128

RESULT 62
;riboflavin synthase, subunit beta (ribs) homolog - Archaeoglobus fulgidus
;Species: Archaeoglobus fulgidus
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
;Accession: H69515
;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
;Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
;Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
;ature 390, 364-370, 1997
;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
;Smith, H.O.; Woese, C.R.; Venter, J.C.
;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
;Reference number: A69250; MUID:98049343; PMID:9389475
;Accession: H69515
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA
;Residues: 1-143 <KLE>
;Cross-references: GB:AE000957; GB:AE000782; NID:G2689280; PIDN:AAB89124.1; PID:G2648400
;Superfamily: riboflavin synthase beta chain

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Query Match          95.0%; Score 19; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

f      2 VAEF 5
      ||||
g     10 VAEF 13

RESULT 63
16978
;robable transposase, truncated section 1 [imported] - Streptomyces coelicolor (fragment
;Species: Streptomyces coelicolor
;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
;Accession: T36978
;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
;Submitted to the EMBL Data Library, August 1999
;Reference number: Z21618
;Accession: T36978
;Status: preliminary; translated from GB/EMBL/DBJ
;Molecule type: DNA
;Residues: 1-143 <OLI>
;Cross-references: EMBL:AL109949; PIDN:CBAS2892.1; GSPDB:GN00070; SCOEDB:SCJ11.07c
;Experimental source: strain A3(2)
;Comment: A complete transposase sequence can be assembled from three adjacent orfs (PI
;Genetics:
;Gene: SCOEDB:SCJ11.07c

Query Match          95.0%; Score 19; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y      2 VAEF 5
      ||||
g     113 VAEF 116

RESULT 64
41715
;ribosomal protein L13 [similarity] - Haloarcula marismortui
;Species: Haloarcula marismortui
;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 14-Apr-2003
;Accession: B41715
;Kroemer, W.J.; Arndt, E.
;Biochem. J. 266, 24573-24579, 1991
;Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with g
;acterium) marismortui.
;Reference number: A41715; MUID:92105119; PMID:1840597
;Accession: B41715
;Status: preliminary
;Molecule type: DNA
;Residues: 1-145 <KRO>
;Cross-references: GB:M76567; NID:gl48775; PIDN:AAA73097.1; PID:gl48777
;Superfamily: ribosomal protein L13

Query Match          95.0%; Score 19; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y      2 VAEF 5
      ||||
b      3 VAEF 6

RESULT 65
77043
;ypothetical protein sll0678 - Synechocystis sp. (strain PCC 6803)
;Species: Synechocystis sp.
;Variety: PCC 6803
;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
;Accession: S77043
;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
;K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77043
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-145 <KAN>
A;Cross-references: EMBL:D64005; GB:AB001339; NID:gl001779; PIDN:BAAL0735.1; PID:gl000658;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein sll0678

Query Match          95.0%; Score 19; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
DB     35 VAEF 38

RESULT 66
F89837
;conserved hypothetical protein SA0624 [imported] - Staphylococcus aureus (strain N315)
;Species: Staphylococcus aureus
;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
;Accession: F89837
;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
;Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
;Lancet 357, 1285-12840, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: X89758; MUID:21311952; PMID:11418146
A;Accession: F89837
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <KUR>
A;Cross-references: GB:BA000018; PID:gl3700560; PIDN:BAB41857.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0624

Query Match          95.0%; Score 19; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
DB     102 VAEF 105

RESULT 67
CB4294
;hypothetical protein Vngl1398c [imported] - Halobacterium sp. NRC-1
;Species: Halobacterium sp. NRC-1
;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
;Accession: CB4294
;K'ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
;Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
;Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A>Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: CB4294
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <STO>
A;Cross-references: GB:AE004437; NID:gl0580903; PIDN:AAG19719.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1398C
C;Superfamily: hypothetical protein yjcf

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Query Match          95.0%; Score 19; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y      2 VAEF 5
      |||||
Db      117 VAEF 120

RESULT 68
T34803
Hypothetical protein SC2E1.35 - Streptomyces coelicolor
Species: Streptomyces coelicolor
Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 04-Mar-2000
Accession: T34803
Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
Reference number: Z21557
Accession: T34803
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: DNA
Residues: 1-147 <MUR>
Cross-references: EMBL:AL023797; PIDN:CAA19410.1; GSPDB:GN00070; SCOPDB:SC2E1.35
Experimental source: strain A3(2)
Genetics:
Gene: SCOPDB:SC2E1.35
Superfamily: Streptomyces coelicolor hypothetical protein SC2E1.35

Query Match          95.0%; Score 19; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y      2 VAEF 5
      |||||
Db      125 VAEF 128

RESULT 69
B81788
conserved hypothetical protein NMA2160 [imported] - Neisseria meningitidis (strain Z2491)
Species: Neisseria meningitidis
Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
Accession: B81788
Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
Reference number: B81775; MUID:20222556; PMID:10761919
Accession: B81788
Status: preliminary
Molecule type: DNA
Residues: 1-148 <PAR>
Cross-references: GB:AL157959; NID:g7380672; PIDN:CAB85372.1; PID:g738078
Experimental source: serogroup A, strain Z2491
Genetics:
Gene: NMA2160
Superfamily: hypothetical protein ytwi

Query Match          95.0%; Score 19; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      |||||
Db      77 VAEF 80

RESULT 70
S10655
Hypothetical protein X - Pyrococcus woesei (fragment)
Species: Pyrococcus woesei
Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1993
Accession: S10655

R;Zwickl, P.; Fabry, S.; Bogedain, C.; Haas, A.; Hensel, R.
J. Bacteriol. 172, 4329-4338, 1990
Title: Glyceraldehyde-3-phosphate dehydrogenase from the hyperthermophilic archaeobacte
scherichia coli.
Reference number: S10650; MUID:90330536; PMID:2165475
Accession: S10655
Molecule type: DNA
Residues: 1-148 <ZWI>
Note: the authors translated the codon GGT for residue 54 as Glu

Query Match          95.0%; Score 19; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      |||||
Db      115 VAEF 118

RESULT 71
AC1137
ribose 5-phosphate isomerase homolog lmo0498 [imported] - Listeria monocytogenes (strain
Species: Listeria monocytogenes
Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Accession: AC1137
Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Authors: Kreft, J.; Kuhn, M.; Kunat, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ck, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A.; Title: Comparative genomics of Listeria species.
Reference number: AB1077; MUID:21537279; PMID:11679669
Accession: AC1137
Status: preliminary
Molecule type: DNA
Residues: 1-149 <GLA>
Cross-references: GB:NC_003210; PIDN:CAC98577.1; PID:g16409874; GSPDB:GN00177
Experimental source: strain EGD-e
Genetics:
Gene: lmo0498
Superfamily: galactoside O-acetyltransferase

Query Match          95.0%; Score 19; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      |||||
Db      124 VAEF 127

RESULT 72
AB2857
pseudouridine [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
Accession: AB2857
Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCIell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Reference number: AB2577; MUID:21608550; PMID:11743193
Accession: AB2857
Status: preliminary
Molecule type: DNA
Residues: 1-150 <KUR>
Cross-references: GB:AB008688; PIDN:AAL43272.1; PID:g17740759; GSPDB:GN00186
Experimental source: strain C58 (Dupont)
Genetics:

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;Gene: Atu2283
;Map position: circular chromosome
;Superfamily: plastocyanin

Query Match      95.0%; Score 19; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5      |||||
b      78 VAEF 81    |||||

RESULT 73
BI089
rotein gp35 from Bacteriophage A118 homolog lmo0113 [imported] - Listeria monocytogenes
;Species: Listeria monocytogenes
;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
;Accession: AB1089
;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
; Jones, L.M.; Karst, U.
; Science 294, 849-852, 2001
; Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
; C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
; Title: Comparative Genomics of Listeria species.
; Reference number: AB1077; MUID:21537279; PMID:11679669
; Accession: AB1089
; Status: preliminary
; Molecule type: DNA
; Residues: 1-150 <GLA>
; Cross-references: GB:NC_003210; PID:NCAC98328.1; PID:gl6409472; GSPDB:GN00177
; Experimental source: strain EGD-e
; Genetics:
; Gene: lmo0113

Query Match      95.0%; Score 19; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5      |||||
b      105 VAEF 108  |||||

3SULT 74
II452
rotein gp35 from Bacteriophage A118 homolog lin0160 [imported] - Listeria innocua (stra
;Species: Listeria innocua
;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
;Accession: AII452
;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
; Jones, L.M.; Karst, U.
; Science 294, 849-852, 2001
; Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
; C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehländ,
; Title: Comparative Genomics of Listeria species.
; Reference number: AB1077; MUID:21537279; PMID:11679669
; Accession: AII452
; Status: preliminary
; Molecule type: DNA
; Residues: 1-150 <GLA>
; Cross-references: GB:AL592022; PID:NCAC95393.1; PID:gl6412579; GSPDB:GN00178
; Experimental source: strain Clp11262
; Genetics:
; Gene: lin0160

Query Match      95.0%; Score 19; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5      |||||
b      105 VAEF 108  |||||

;Db      105 VAEF 108  |||||

RESULT 75
H87263
hypothetical protein CC0121 [imported] - Caulobacter crescentus
;Species: Caulobacter crescentus
;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
;Accession: H87263
;Rieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
; Title: Complete Genome Sequence of Caulobacter crescentus.
; Reference number: AB7249; MUID:21173698; PMID:11259647
; Accession: H87263
; Status: preliminary
; Molecule type: DNA
; Residues: 1-151 <STO>
; Cross-references: GB:AE005673; NID:gl3421228; PID:AAK22108.1; GSPDB:GN00148
; Genetics:
; Gene: CC0121

Query Match      95.0%; Score 19; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5      |||||
b      73 VAEF 76     |||||

Search completed: May 24, 2004, 17:38:36
Job time : 66.5 secs

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GenCore version 5.1.6
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M protein - protein search, using sw model

run on: May 24, 2004, 17:33:28 ; Search time 8.57143 Seconds
(without alignments)

30.374 Million cell updates/sec

title: US-09-594-978A-1

effect score: 20

sequence: 1 XVAEF 5

coring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 141681 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SwissProt_42.1*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	19	95.0	19	NS2_MYCTU	P81136 mycobacteri
2	19	95.0	19	SECE_TREPA	O83263 treponema p
3	19	95.0	59	YA90_ARCFU	O39175 archaeoglob
4	19	95.0	63	Y451_HAEIN	P43998 haemophilus
5	19	95.0	88	RS15_HAEIN	P44389 haemophilus
6	19	95.0	93	ALR2_METKA	O82766 methanopyru
7	19	95.0	108	YF24_METIA	O89919 methanococc
8	19	95.0	114	KED4_ACTSL	P41249 actinomycet
9	19	95.0	115	INS_VERMO	Q9w7r2 verasper mo
10	19	95.0	116	INS_LOPPI	P01341 lophius pis
11	19	95.0	119	U279_DROME	Q9v8f3 drosophila
12	19	95.0	120	GTR2_PIG	O62786 sus scrofa
13	19	95.0	122	R18E_PYRAF	Q8zyq2 pyrobaculum
14	19	95.0	124	Y670_PASMU	Q8cm00 pasteurella
15	19	95.0	127	ILBP_MOUSE	P51162 mus musculu
16	19	95.0	130	SPEH_THEMA	Q9wzc3 thermotoga
17	19	95.0	131	Y194_PYRAB	Q9v280 pyrococcus
18	19	95.0	133	R18B_HALN1	Q8hrm5 halobacteri
19	19	95.0	134	YBSC_ECOLI	P08999 escherichia
20	19	95.0	139	R18B_WETH	O27443 methanobact
21	19	95.0	140	Y586_ARCFU	O39669 archaeoglob
22	19	95.0	143	R18B_ARCFU	O8152 archaeoglob
23	19	95.0	145	RL13_HALMA	P29198 haloarcula
24	19	95.0	148	CLM4_MOUSE	Q9jlm3 mus musculu
25	19	95.0	148	YORX_PYRWO	P20298 pyrococcus
26	19	95.0	150	R18B_PYRAF	Q8zte3 pyrobaculum
27	19	95.0	152	SODC_PRIGL	P11418 prionace gl
28	19	95.0	154	R18B_SULSO	Q960B5 sulfolobus
29	19	95.0	155	PCP_HAEIN	P10325 haemophilus
30	19	95.0	157	RAP_TAROF	O49065 taraxacum o
31	19	95.0	157	R18B_SULTO	Q975m5 sulfolobus
32	19	95.0	163	SGS5_DROME	P07701 drosophila
33	19	95.0	166	UTR5_YEAST	P32630 saccharomyc

19	95.0	169	1	SSB_RHOBA	P59932 rhodopirell
19	95.0	172	1	BFL1_MOUSE	Q07440 mus musculu
19	95.0	175	1	BFL1_HUMAN	Q16548 homo sapien
19	95.0	176	1	FR12_RANCA	P07798 rana catesb
19	95.0	177	1	RL10_THETN	Q8r7u4 thermocanae
19	95.0	178	1	DSBB_PASMU	Q916b3 pasteurella
19	95.0	178	1	ESMS_DROME	P13096 drosophila
19	95.0	178	1	YB18_ARCFU	O29147 archaeoglob
19	95.0	179	1	APT_HAEDU	Q7vkg4 haemophilus
19	95.0	183	1	RTTB_BOVIN	P18902 bos taurus
19	95.0	186	1	DNAA_WOLSP	P35907 wolbachia s
19	95.0	190	1	UCGI_PARDE	P05417 paracoccus
19	95.0	193	1	NTPA_METJA	Q57619 methanococc
19	95.0	194	1	HAM2_EACHD	Q9K8G9 bacillus na
19	95.0	194	1	TNR0_ECOLI	P05823 escherichia
19	95.0	196	1	PINQ_ECOLI	P77170 escherichia
19	95.0	196	1	PINR_ECOLI	P77574 escherichia
19	95.0	196	1	UHPA_ECOLI	P10940 escherichia
19	95.0	196	1	UHPA_SALTY	P27667 salmonella
19	95.0	198	1	AICD_MOUSE	Q3wve0 mus musculu
19	95.0	199	1	RHS_SULSO	Q37777 sulfolobus
19	95.0	201	1	RETB_HORSE	Q28369 equus cabal
19	95.0	201	1	RETB_HUMAN	P02753 homo sapien
19	95.0	201	1	RETB_PIG	P27485 sus scrofa
19	95.0	201	1	RETB_RABIT	P06912 oryctolagus
19	95.0	204	1	YIGZ_ECOLI	P27862 escherichia
19	95.0	205	1	MD21_HUMAN	Q13257 homo sapien
19	95.0	205	1	MD21_MOUSE	Q21B5 mus musculu
19	95.0	208	1	YAC1_LEGPN	P37033 legionella
19	95.0	215	1	HMUO_CORDI	Q66120 cucumber mo
19	95.0	218	1	COAT_CMVIX	Q66120 cucumber mo
19	95.0	220	1	PTP1_NPVOP	O10274 orgyia pseu
19	95.0	223	1	ECR1_ARCFU	O29758 archaeoglob
19	95.0	223	1	RAN_TETPY	P41914 tetrahymena
19	95.0	223	1	VATD_THETH	O87880 thermus the
19	95.0	225	1	RAN_TETTH	P41915 tetrahymena
19	95.0	228	1	Y132_NPVOP	P24080 orgyia peeu
19	95.0	230	1	NADD_PSRPK	Q88d15 pseudomonas
19	95.0	230	1	RR3_FORPU	P51308 porphyra pu
19	95.0	230	1	UBIE_COREF	Q8feb3 corynebacte
19	95.0	230	1	UBIE_CORGL	Q8nt39 corynebacte
19	95.0	234	1	YIGB_ECOLI	P24195 escherichia
19	95.0	236	1	PUR7_WOLSU	Q7m9x5 wolfinella s
19	95.0	236	1	YPS8_MYCTU	Q50740 mycobacteri
19	95.0	238	1	Y437_STAEP	Q8ctk9 staphylococ
19	95.0	238	1	Y669_STAAM	Q8nx12 staphylococ
19	95.0	238	1	YH89_STRMU	Q8ds14 streptococc
19	95.0	239	1	RLPA_NEIMA	Q9jnm7 neisseria m
19	95.0	239	1	RLPA_NEIMB	Q9k1a0 neisseria m
19	95.0	239	1	VG88_BPML5	Q05305 mycobacteri
19	95.0	240	1	ATP7_ARATH	Q9ej12 arabidopsis
19	95.0	240	1	KDKA_PASPI	P58551 pasteurella
19	95.0	241	1	PCYA_PROMP	Q93tl5 prochloroco
19	95.0	242	1	V755_AQURE	O66957 aquifex aeo
19	95.0	244	1	COMB_SYNEL	Q8dl85 synechococc
19	95.0	247	1	ATPD_SORBI	Q07300 sorghum bic
19	95.0	247	1	CYSZ_VIBPA	Q87rj6 vibrio para
19	95.0	249	1	AQP_AEDAE	P21h67 aedes aegyp
19	95.0	250	1	TIP1_TOBAC	Q9nhw3 nicotiana t
19	95.0	250	1	TIP2_TOBAC	P24422 nicotiana t
19	95.0	250	1	TIP2_ANTWA	P23778 brassica na
19	95.0	253	1	KDUD_ECOLI	Q9clc2 pasteurella
19	95.0	253	1	KDUD_ERWCH	P48556 homo sapien
19	95.0	255	1	PF1_BRANA	Q9c5x6 mus musculu
19	95.0	255	1	TRMB_PASMU	O28439 archaeoglob
19	95.0	257	1	PSD8_HUMAN	O15400 homo sapien
19	95.0	257	1	PSD8_MOUSE	O70439 mus musculu
19	95.0	258	1	NADC_ARCFU	O70439 mus musculu
19	95.0	261	1	STX7_HUMAN	O70439 mus musculu
19	95.0	261	1	STX7_MOUSE	O70439 mus musculu
19	95.0	261	1	STX7_RAT	O70439 mus musculu
19	95.0	266	1	TRPA_SYNEL	Q8dlm9 synechococc
19	95.0	267	1	APHC_MOUSE	Q9d099 mus musculu

107	19	95.0	267	1	DKGB_YERPE	Q8zh36 yersinia pe	180	19	95.0	325	1	UCP5_MOUSE	Q9z2b2 mus musculus
108	19	95.0	267	1	GNPI_CAEEL	Q9xvj2 caenorhabdi	181	19	95.0	326	1	PE46_ARATH	O81772 arabidopsis
109	19	95.0	267	1	NM07_RAT	P50280 rattus norv	182	19	95.0	326	1	Y077_CAEEL	Q09444 caenorhabdi
110	19	95.0	269	1	AQ01_HUMAN	P29972 homo sapien	183	19	95.0	328	1	AIPL_RAT	Q911g9 rattus norv
111	19	95.0	269	1	AQ01_MOUSE	Q02013 mus musculu	184	19	95.0	328	1	Y778_AQUAE	O66974 aquifex aeo
112	19	95.0	269	1	R003_YEAST	P29975 rattus norv	185	19	95.0	329	1	YFV6_SCHPO	Q927q8 schizosacch
113	19	95.0	269	1	R003_YEAST	P33334 saccharomyc	186	19	95.0	330	1	PRC2_FORGI	P33437 porphyromon
114	19	95.0	269	1	SRPB_MOUSE	P47758 mus musculu	187	19	95.0	330	1	Y840_METUA	Q58250 methanococc
115	19	95.0	269	1	YS13_STAAU	O05337 staphylococ	188	19	95.0	334	1	CCPA_BACSU	P25144 bacillus su
116	19	95.0	271	1	AQ01_BOVIN	P47865 bos taurus	189	19	95.0	334	1	PRC1_FORGI	P59916 porphyromon
117	19	95.0	271	1	SRPB_HUMAN	Q9v5m8 homo sapien	190	19	95.0	334	1	YH33_RHIME	Q92v44 rhizobium m
118	19	95.0	272	1	AQ01_SHEEP	P56401 ovis aries	191	19	95.0	337	1	OPCM_CHICK	Q98892 gallus gall
119	19	95.0	272	1	YF63_STAMP	Q98rt3 staphylococ	192	19	95.0	338	1	O4XL_RHISN	P55704 rhizobium s
120	19	95.0	274	1	AMYC_THETU	P37729 thermansaer	193	19	95.0	339	1	HRDC_STROO	P18184 streptomyce
121	19	95.0	277	1	Y087_THEMA	Q9cux2 thermotoga	194	19	95.0	339	1	IGB1_HUMAN	P78318 homo sapien
122	19	95.0	279	1	PHEA_LACLA	Q9cux2 lactococcus	195	19	95.0	340	1	HUR_STRAU	Q00923 streptomyce
123	19	95.0	279	1	PHEA_LACLA	P43909 lactococcus	196	19	95.0	340	1	IGB1_MOUSE	Q61249 mus musculu
124	19	95.0	282	1	TRUEB_BORBU	O51743 borrelia bu	197	19	95.0	340	1	IGB1_RAT	O08836 rattus norv
125	19	95.0	284	1	Y3G4_SHEON	Q8eae2 shewanella	198	19	95.0	343	1	MO2M_ARATH	Q9m0m4 arabidopsis
126	19	95.0	284	1	YN13_MYCTU	P71899 mycobacteri	199	19	95.0	343	1	MO2M_ARATH	Q9fgk3 arabidopsis
127	19	95.0	285	1	YB45_HAEIN	P45071 haemophilus	200	19	95.0	343	1	XT30_ARATH	Q38908 arabidopsis
128	19	95.0	287	1	PDXV_ECOLI	P71150 escherichia	201	19	95.0	344	1	CD2_MOUSE	P05920 mus musculu
129	19	95.0	287	1	SYQ_DICDI	P14325 dictyostell	202	19	95.0	344	1	CD2_RAT	P08921 rattus norv
130	19	95.0	288	1	Y169_PASMU	Q9cp85 pasteurella	203	19	95.0	344	1	STSY_RAUSE	P15324 raoultia s
131	19	95.0	291	1	AMPM_ARCFU	O28438 archaeoglob	204	19	95.0	345	1	TRPD_SULSO	P50384 sulfolobus
132	19	95.0	292	1	YG29_METJA	Q59023 methanococc	205	19	95.0	347	1	FLIG_AGRTS	Q44458 agrobacteri
133	19	95.0	294	1	AMPM_METJA	Q58725 methanococc	206	19	95.0	352	1	CYCR_ROSDE	P26278 roseobacter
134	19	95.0	294	1	SSB1_YEAST	P10080 saccharomyc	207	19	95.0	352	1	STSY_CATRO	P18417 catharanthu
135	19	95.0	295	1	PRMA_VIECH	Q9kv64 vibrio chol	208	19	95.0	354	1	DCD1_HUMAN	P59894 homo sapien
136	19	95.0	295	1	RFBA_XANCP	P55256 xanthomonas	209	19	95.0	362	1	MURG_SHEON	Q8ck35 shewanella
137	19	95.0	295	1	YDH2_XANAU	P22644 xanthobacte	210	19	95.0	364	1	DDL_CHLTE	Q8kcr8 chlorobium
138	19	95.0	297	1	YD67_METJA	Q58762 methanococc	211	19	95.0	364	1	DHLE_BACLI	Q53560 bacillus li
139	19	95.0	299	1	T2R1_HUMAN	Q9nyw7 homo sapien	212	19	95.0	364	1	MRP_AQUAE	Q66946 aquifex aeo
140	19	95.0	300	1	NARE_CHICK	Q92080 gallus gall	213	19	95.0	365	1	MURG_SHEVI	Q9f1n0 shewanella
141	19	95.0	304	1	CYSD_XYLPA	Q9pd79 xyella fas	214	19	95.0	366	1	CYCR_RHOGE	P51758 rhodocyclu
142	19	95.0	304	1	CYSD_XYLPA	Q8cdg8 xyella fas	215	19	95.0	369	1	RPSD_STRPN	O03388 streptococc
143	19	95.0	305	1	E2BA_CAEEL	P34604 caenorhabdi	216	19	95.0	378	1	KLAS_ECOLI	Q52328 escherichia
144	19	95.0	308	1	CPP3_ENTHI	Q06964 entamoeba h	217	19	95.0	379	1	TGT_VIECH	Q9kty9 vibrio chol
145	19	95.0	308	1	KSGA_BIFLO	Q8g6i3 b dimethyla	218	19	95.0	380	1	METB_HELPY	Q92mw7 helicobacte
146	19	95.0	309	1	DNJL_MYCOP	Q50312 mycoplasma	219	19	95.0	380	1	METB_HELPY	P56069 helicobacte
147	19	95.0	309	1	NTCB_SYNY3	P74422 synchocyst	220	19	95.0	381	1	CD84_SCHPO	O09184 schizosacch
148	19	95.0	310	1	MIAA_CLOPE	Q84185 clostridium	221	19	95.0	383	1	CYCR_CHRVI	O82947 chromatium
149	19	95.0	310	1	PP12_TOBAC	O04857 nicotiana t	222	19	95.0	384	1	AIPL_HUMAN	Q95mm3 pan paniscu
150	19	95.0	310	1	SIR5_HUMAN	Q9nx48 homo sapien	223	19	95.0	384	1	AIPL_PANPA	Q20701 caenorhabdi
151	19	95.0	310	1	SIR5_MOUSE	Q8k2c6 mus musculu	224	19	95.0	385	1	GBA5_CAEEL	P43702 haemophilus
152	19	95.0	310	1	Y942_SULSO	Q97zh1 sulfolobus	225	19	95.0	385	1	PGK_HAEIN	P10312 bacterioph
153	19	95.0	311	1	DAPA_STRPN	Q97r25 streptococc	226	19	95.0	387	1	VPD_BPP2	P10312 bacterioph
154	19	95.0	311	1	DAPA_STRPN	Q8dp29 streptococc	227	19	95.0	388	1	METB_MYCLE	P46807 mycobacteri
155	19	95.0	311	1	MIAA_LACPL	Q88wp5 lactobacill	228	19	95.0	388	1	METB_MYCLE	O53427 mycobacteri
156	19	95.0	311	1	OSL1_HUMAN	Q8ng12 homo sapien	229	19	95.0	389	1	RFIM_CAEEL	O44568 caenorhabdi
157	19	95.0	311	1	OSL2_HUMAN	Q8ng10 homo sapien	230	19	95.0	389	1	VPD_BF186	P21679 bacterioph
158	19	95.0	312	1	O6N1_HUMAN	Q8ngy5 homo sapien	231	19	95.0	390	1	Y181_ARCFU	O30056 archaeoglob
159	19	95.0	312	1	PP12_ARATH	P48482 arabidopsis	232	19	95.0	392	1	TEBB_STYMY	P29548 stylonichia
160	19	95.0	312	1	PP15_ARATH	P48485 arabidopsis	233	19	95.0	392	1	YBGF_HAEIN	P44083 haemophilus
161	19	95.0	313	1	DRPE_CRAPL	P22242 craterostig	234	19	95.0	394	1	DXR_SYNY3	Q55663 synchocyst
162	19	95.0	313	1	PEPM_STRHY	P29247 streptomyce	235	19	95.0	395	1	CGA2_CHICK	P43449 gallus gall
163	19	95.0	314	1	LUNE_CRIFA	Q27546 crithidia f	236	19	95.0	397	1	Y929_THEMA	P56727 thermotoga
164	19	95.0	314	1	PP1_FHAVU	P48490 phaseolus v	237	19	95.0	398	1	PNGB_BUCAP	Q8k9i6 buchnera ap
165	19	95.0	315	1	O3A2_HUMAN	P47893 homo sapien	238	19	95.0	399	1	PNGB_BUCAL	P57442 buchnera ap
166	19	95.0	315	1	O3A2_PANTR	Q9tu97 pan troglod	239	19	95.0	400	1	ER19_HUMAN	P53602 homo sapien
167	19	95.0	315	1	O3A3_HUMAN	P47888 homo sapien	240	19	95.0	401	1	ER19_MOUSE	Q99jfs mus musculu
168	19	95.0	315	1	O3A3_PANTR	Q9tua0 pan troglod	241	19	95.0	401	1	ER19_RAT	Q62967 rattus norv
169	19	95.0	316	1	APEI_MOUSE	P28352 mus musculu	242	19	95.0	402	1	C123_MYCTU	P77902 mycobacteri
170	19	95.0	316	1	APEI_RAT	P43138 rattus norv	243	19	95.0	402	1	C13B_XYLF	Q9pgc5 xyella fas
171	19	95.0	316	1	PP1_BRAOL	P48487 brassica ol	244	19	95.0	402	1	C13B_XYLF	Q97ax5 xyella fas
172	19	95.0	317	1	APEI_HUMAN	P27695 homo sapien	245	19	95.0	406	1	CGA2_BOVIN	P30274 bos taurus
173	19	95.0	317	1	OSTP_RAT	P08721 rattus norv	246	19	95.0	406	1	T230_HUMAN	P87775 homo sapien
174	19	95.0	317	1	PP11_TOBAC	O04856 nicotiana t	247	19	95.0	407	1	RPF2_HUMAN	O60858 homo sapien
175	19	95.0	318	1	PP11_ARATH	P30366 arabidopsis	248	19	95.0	409	1	Y4DM_RHISN	P55412 rhizobium s
176	19	95.0	322	1	PP15_ARATH	P48486 arabidopsis	249	19	95.0	410	1	TDPI_HUMAN	Q14186 homo sapien
177	19	95.0	324	1	ADD_RHIME	Q92L48 rhizobium m	250	19	95.0	410	1	TDPI_MOUSE	Q08639 mus musculu
178	19	95.0	324	1	PP18_ARATH	P28734 arabidopsis	251	19	95.0	411	1	PBPT_YERPE	Q8xfro yersinia pe
179	19	95.0	325	1	UCP5_HUMAN	Q95258 homo sapien	252	19	95.0	412	1	CCA_ECOLI	P06961 escherichia

253	19	95.0	415	1	CGA2_XENLA	P47827 xenopus lae	326	19	95.0	477	1	CAP2_HUMAN	P40123 homo sapien
254	19	95.0	415	1	HEM1_NEIO	Q3hd6 neisseria g	327	19	95.0	477	1	CAP2_RAT	P52481 rattus norv
255	19	95.0	415	1	HEM1_NEIO	Q3hd6 neisseria g	328	19	95.0	479	1	RFBM_SALTY	P26404 salmonella
256	19	95.0	415	1	HEM1_NEIO	P56994 neisseria m	329	19	95.0	479	1	YS02_CAEEL	Q09357 caenorhabdi
257	19	95.0	417	1	HEM1_OCEIH	Q8elt8 oceanobacil	330	19	95.0	483	1	NIFE_MEIMP	P71528 methanococ
258	19	95.0	417	1	HEM1_CHRVO	P6ely3 chromobacte	331	19	95.0	486	1	GLG2_RHIME	P58394 rhizobium m
259	19	95.0	418	1	CSD_STPCO	Q9xads streptomyc	332	19	95.0	488	1	ARL2_RHIME	Q92vms rhizobium m
260	19	95.0	419	1	MURD_CHLCV	Q821s1 chlamydophi	333	19	95.0	490	1	ARLY_BIFLO	C8G5f3 bifidobacte
261	19	95.0	420	1	CGA2_CHLVR	P15986 chlorohydra	334	19	95.0	491	1	AP2A_SHEEP	C9n0n3 ovis aries
262	19	95.0	421	1	CGA2_MESAU	P37881 mesocricetu	335	19	95.0	491	1	G6PD_ERWCH	P37986 erwina chr
263	19	95.0	421	1	MUAI_STAMU	Q39sf8 staphylococ	336	19	95.0	491	1	GCSB_COXBU	Q83b09 coxiella bu
264	19	95.0	421	1	MUAI_STAPB	Q8crn8 staphylococ	337	19	95.0	491	1	NU4M_MEISE	Q47497 metridium s
265	19	95.0	422	1	CGA2_MOUSE	P51943 mus musculu	338	19	95.0	492	1	FTSA_HELPF	O25629 helicobacte
266	19	95.0	422	1	HEM1_PSEAE	P42807 pseudomonas	339	19	95.0	493	1	FTSA_HELPF	Q9zkm3 helicobacte
267	19	95.0	423	1	CISY_ACIAN	P20902 acinetobact	340	19	95.0	493	1	GLYM_CANAL	O13425 candida alb
268	19	95.0	423	1	GLYA_METHH	O77433 methanobact	341	19	95.0	494	1	PRE_STRAG	P13925 streptococ
269	19	95.0	423	1	GBA4_CAEEL	Q09453 caenorhabdi	342	19	95.0	498	1	NU4C_PSINU	O8whx8 psilotom nu
270	19	95.0	424	1	GLA2_BALSO	Q8xttd1 ralstonia s	343	19	95.0	499	1	PTFA_HABIN	P44715 h pts syste
271	19	95.0	426	1	RHO_DEIRA	P521s3 deinococcus	344	19	95.0	500	1	CATA_NEIGO	O59602 neisseria g
272	19	95.0	429	1	ENO_THEMA	P42848 thermotoga	345	19	95.0	500	1	DNAA_BIFLO	O896K0 bifidobacte
273	19	95.0	430	1	SVH_CHLTE	Q8kft6 chlorobium	346	19	95.0	503	1	AMPA_RHILO	Q98481 rhizobium l
274	19	95.0	431	1	ENO_CLOAB	Q971s2 clostridium	347	19	95.0	503	1	UBIB_NEIMA	O9jvd5 neisseria m
275	19	95.0	431	1	HNDH_BORBU	O51628 borrelia bu	348	19	95.0	503	1	UBIB_NEIMB	O9K0n0 neisseria m
276	19	95.0	432	1	CGA2_HUMAN	P20248 homo sapien	349	19	95.0	504	1	DCMC_ANSAN	P12617 anser anser
277	19	95.0	432	1	GLYA_BRAUA	P24060 bradyrhizob	350	19	95.0	504	1	YO93_CAEEL	P41843 caenorhabdi
278	19	95.0	433	1	C125_MYCTU	P71856 mycobacteri	351	19	95.0	506	1	PUR9_AQUAE	O67775 a bifunctio
279	19	95.0	433	1	ENGA_AQUAE	O67749 aquifex aeo	352	19	95.0	512	1	C981_SORBI	O48956 sorghum bic
280	19	95.0	434	1	GLYA_HYPME	P34895 rhychomicrob	353	19	95.0	513	1	NHAB_ECOLI	P27377 escherichia
281	19	95.0	434	1	GLYA_METEX	P50435 methyllobact	354	19	95.0	514	1	YHK8_YEAST	P38776 saccharomy
282	19	95.0	436	1	HNDH_ARCTU	O28538 archaeoglob	355	19	95.0	518	1	AMT6_BACS7	P19571 bacillus sp
283	19	95.0	437	1	AP2A_HUMAN	P55549 homo sapien	356	19	95.0	520	1	BCHB_HEIMO	O92958 helicobacil
284	19	95.0	437	1	AP2A_MOUSE	P34056 mus musculu	357	19	95.0	520	1	DHAC_PSPPU	P09788 pseudomonas
285	19	95.0	437	1	AP2A_RAT	P58197 rattus norv	358	19	95.0	521	1	SYE_LEPIN	O8eym3 leptospira
286	19	95.0	437	1	FOLC_HABIN	P43775 haemophilus	359	19	95.0	522	1	GTR2_RAT	P12336 rattus norv
287	19	95.0	437	1	GNTT_ECOLI	P39835 escherichia	360	19	95.0	522	1	NHAB_HABIN	P44706 haemophilus
288	19	95.0	438	1	G3PB_TORAB	P09044 nicotiana t	361	19	95.0	523	1	GTR2_MOUSE	P14246 mus musculu
289	19	95.0	438	1	GLYA_BRUME	Q8ygg7 bruceella me	362	19	95.0	524	1	IMDH_SCHPO	P11168 homo sapien
290	19	95.0	438	1	GLYA_BRUSU	Q9511a bruceella su	363	19	95.0	524	1	IMDH_SCHPO	P11168 homo sapien
291	19	95.0	445	1	NHRI_CAEEL	Q18187a caenorhabdi	364	19	95.0	525	1	UBIB_RALSO	O14344 schizosacch
292	19	95.0	445	1	ZGS_XENLA	P18725 xenopus lae	365	19	95.0	530	1	RNP2_HUMAN	O8y275 ralstonia s
293	19	95.0	446	1	DTA2_RALSO	Q8xub6 ralstonia s	366	19	95.0	530	1	RNP2_MOUSE	O1498 homo sapien
294	19	95.0	446	1	SYE_AZOB	P45631 azospirillum	367	19	95.0	532	1	PUR_POTTR	O8vhs1 mus musculu
295	19	95.0	447	1	G3PE_ARATH	P5857 arabidopsis	368	19	95.0	536	1	PUR_RHIME	Q28811 potorus tr
296	19	95.0	448	1	YX43_CAEEL	P34255 caenorhabdi	369	19	95.0	537	1	4CL_PINTA	O92Kx6 r bifunctio
297	19	95.0	449	1	G64F_DROME	P32297 drosophila	370	19	95.0	538	1	PUR9_AGR15	P41636 pinus taeda
298	19	95.0	449	1	GABT_MYCTU	Q50632 mycobacteri	371	19	95.0	538	1	PUR9_BRUME	O8ubm8 a bifunctio
299	19	95.0	450	1	AMYG_SCHPO	O60087 schizosacch	372	19	95.0	539	1	Z173_HUMAN	O8y153 b bifunctio
300	19	95.0	450	1	SYN_ENTFA	Q831x4 enterococcu	373	19	95.0	540	1	VIBE_VIBCH	O12899 homo sapien
301	19	95.0	453	1	YKX8_YEAST	Q9er04 mus musculu	374	19	95.0	543	1	G6PI_CORGL	Q08991 corynebacte
302	19	95.0	455	1	TMS5_MOUSE	P57909 pasteurella	375	19	95.0	547	1	TCPA_TETPY	O07899 vibrio chol
303	19	95.0	457	1	ARLY_PASMU	Q9h343 homo sapien	376	19	95.0	548	1	TCPA_NEIMA	O15891 tetrahymena
304	19	95.0	457	1	TMS5_HUMAN	Q9ns44 homo sapien	377	19	95.0	548	1	G6PI_NEIMB	O9jtw1 neisseria m
305	19	95.0	458	1	Z275_HUMAN	Q9ns44 homo sapien	378	19	95.0	548	1	PPAC_THEMEA	O9jyx3 neisseria m
306	19	95.0	459	1	REPS_STRAM	P36891 streptomyc	379	19	95.0	548	1	G6PI_PASMU	O9wz56 thermotoga
307	19	95.0	460	1	FUMC_CHLCV	Q822d5 chlamydophi	380	19	95.0	549	1	RSL_HABIN	Q48082 haemophilus
308	19	95.0	461	1	ARLY_RAT	P20673 rattus norv	381	19	95.0	549	1	TCPA_CAEEL	P41988 caenorhabdi
309	19	95.0	461	1	FUMC_RICPR	Q9zcg4 rickettsia	382	19	95.0	549	1	TCPA_CAEEL	Q9kyu4 vibrio chol
310	19	95.0	461	1	FUMC_RICCN	Q92gW0 rickettsia	383	19	95.0	550	1	YKX8_CAEEL	O21802 caenorhabdi
311	19	95.0	464	1	ARLY_HUMAN	P04424 homo sapien	384	19	95.0	550	1	YKX8_CAEEL	Q8d8v3 vibrio vuln
312	19	95.0	464	1	ARLY_MOUSE	Q1y140 mus musculu	385	19	95.0	553	1	HCP_VIBU	P09434 rhodobacter
313	19	95.0	465	1	SELA_DESBA	P56372 desulfovibr	386	19	95.0	553	1	SYR_STAPB	Q8ctn9 staphylococ
314	19	95.0	468	1	P2C3_YEAST	P34221 saccharomyc	387	19	95.0	555	1	MASY_PICAN	P21360 pichia angu
315	19	95.0	469	1	MM01_HORSE	Q9xsz5 equus cabal	388	19	95.0	555	1	TP6B_AERPE	Q9y64 aeropyrum p
316	19	95.0	469	1	MM01_PIG	P21692 sus scrofa	389	19	95.0	574	1	PT1_LACSK	O07126 lactobacill
317	19	95.0	471	1	MANC_SALMO	Q01410 salmonella	390	19	95.0	575	1	MBHL_WOLSU	P31883 wolfinella s
318	19	95.0	473	1	ARLY_STRLC	P50988 streptomyc	391	19	95.0	575	1	MSPA_TREMA	Q24433 treponema m
319	19	95.0	473	1	RFBM_SALMU	Q00473 salmonella	392	19	95.0	576	1	DD34_HUMAN	O14147 homo sapien
320	19	95.0	474	1	DCDA_MYCSM	Q9x5m1 mycobacteri	393	19	95.0	576	1	SYP_HELPF	Q9zmk6 helicobacte
321	19	95.0	475	1	ARLY_STRCO	Q911b1 streptomyc	394	19	95.0	577	1	PT1_STRBO	Q9wxk3 screptococ
322	19	95.0	475	1	ECHE_RAT	Q50587 rattus norv	395	19	95.0	577	1	SYP_HELPF	P56124 helicobacte
323	19	95.0	476	1	CAP2_MOUSE	Q5cyl6 mus musculu	396	19	95.0	578	1	V02Z_FOWPV	Q9j5h9 fowpox vir
324	19	95.0	476	1	GLGA_HABIN	P45179 haemophilus	397	19	95.0	579	1	FUMA_SALTY	P40720 salmonella
325	19	95.0	476	1	NOEA_RHIME	Q28892 rhizobium m	398	19	95.0	579	1		

399	19	95.0	580	1	RS1_CHLPH	Q928m3 chlamydia p	472	19	95.0	649	1	INVA_PHAU	P29001 phaseolus a
400	19	95.0	587	1	CO8B_ONCMY	Q90x85 oncorhynchu	473	19	95.0	651	1	INVA_PHAU	Q24509 phaseolus v
401	19	95.0	588	1	HAS1_XENLA	P13563 xenopus lae	474	19	95.0	652	1	C3BB_BACTU	Q06117 bacillus th
402	19	95.0	589	1	GBP1_MOUSE	Q01514 mus musculu	475	19	95.0	660	1	FDL_DROME	Q8w5f3 drosophila
403	19	95.0	589	1	GBP2_MOUSE	Q92066 mus musculu	476	19	95.0	660	1	TP6B_METJA	Q58434 methanococc
404	19	95.0	589	1	GBP2_MOUSE	Q63663 rattus norv	477	19	95.0	670	1	NICA_ARATH	Q8gum5 arabidopsis
405	19	95.0	591	1	GBP2_MOUSE	P32456 homo sapien	478	19	95.0	677	1	NCPR_MOUSE	P37040 mus musculu
406	19	95.0	592	1	ALAM_YEAST	P52893 saccharomyc	479	19	95.0	677	1	NCPR_MOUSE	P00388 rattus norv
407	19	95.0	592	1	ALAM_YEAST	P50342 homo sapien	480	19	95.0	680	1	DCP_SALTY	P27236 salmonella
408	19	95.0	602	1	PEX5_HUMAN	P05605 archaeoglob	481	19	95.0	685	1	CSD_MYCPA	Q9x116 mycobacteri
409	19	95.0	604	1	TP6B_ARCFU	P05646 bacillus me	482	19	95.0	690	1	TRF1_SALSA	P80426 salmo salar
410	19	95.0	604	1	DNAK_BACME	Q8b114 mus musculu	483	19	95.0	691	1	TRF2_SALSA	P80429 salmo salar
411	19	95.0	605	1	APM2_MOUSE	Q8b114 mus musculu	484	19	95.0	692	1	HEXA_ANOGA	Q17020 anopheles g
412	19	95.0	607	1	BKL3_MOUSE	Q8b114 mus musculu	485	19	95.0	693	1	RECG_PASMU	Q9cmb4 pasteurella
413	19	95.0	607	1	DNAK_FUSIN	Q8r005 fusobacteri	486	19	95.0	695	1	TRPE_PABIT	P19134 cryptolagus
414	19	95.0	607	1	DNAK_LACLA	P42368 lactococcus	487	19	95.0	696	1	TRPE_PABIT	P03571 sus scrofa
415	19	95.0	607	1	DNAK_STRP3	Q8k624 streptococc	488	19	95.0	698	1	TRPE_PIG	P02787 homo sapien
416	19	95.0	607	1	DNAK_STRPN	P95829 streptococc	489	19	95.0	704	1	ICA_FIG	Q29545 sus scrofa
417	19	95.0	607	1	DNAK_STRPN	P95831 streptococc	490	19	95.0	705	1	TRFE_BOVIN	Q29443 bos taurus
418	19	95.0	608	1	DNAK_STRPN	Q8cwt3 streptococc	491	19	95.0	705	1	TRFE_BOVIN	Q8a474 bacteroides
419	19	95.0	609	1	BKL3_HUMAN	Q8ab22 homo sapien	492	19	95.0	705	1	TRFE_BOVIN	Q49836 lithospermu
420	19	95.0	610	1	DNAK_ENTFA	Q835r7 enterococcu	493	19	95.0	706	1	TRFE_MOUSE	Q9x86 mus musculu
421	19	95.0	610	1	DNAK_BACSH	Q69268 bacillus sp	494	19	95.0	706	1	TRFE_MOUSE	Q8f983 leptospira
422	19	95.0	610	1	DNAK_STRPN	Q99tr7 staphylococ	495	19	95.0	706	1	TRFE_MOUSE	P27425 equus cabal
423	19	95.0	610	1	DNAK_STRPN	P45554 staphylococ	496	19	95.0	707	1	TRFE_MOUSE	Q07266 rattus norv
424	19	95.0	611	1	DNAK_BACAA	Q81182 bacillus an	497	19	95.0	707	1	TRFE_MOUSE	P14166 ipomoea bat
425	19	95.0	611	1	DNAK_BACCR	Q818e9 bacillus ce	498	19	95.0	708	1	TRFE_MOUSE	Q23865 daucus caro
426	19	95.0	612	1	DNAK_LISIN	Q92bn8 listeria in	499	19	95.0	708	1	TRFE_MOUSE	Q42858 ipomoea bat
427	19	95.0	612	1	DNAK_LISMO	Q955a4 listeria mo	500	19	95.0	708	1	TRFE_MOUSE	P03070 simian viru
428	19	95.0	612	1	ILVD_XANAC	Q8p910 xanthomonas	501	19	95.0	710	1	TRFE_MOUSE	Q49835 lithospermu
429	19	95.0	612	1	ILVD_XANCP	Q8p910 xanthomonas	502	19	95.0	712	1	TRFE_MOUSE	P35513 nicotiana t
430	19	95.0	614	1	YC81_MYCTU	Q11040 mycobacteri	503	19	95.0	712	1	TRFE_MOUSE	P45733 nicotiana t
431	19	95.0	614	1	DNAK_LACSN	Q8km16 lactobacill	504	19	95.0	714	1	TRFE_MOUSE	Q44219 drosophila
432	19	95.0	614	1	SPKE_SYNY3	P73515 synchocyst	505	19	95.0	715	1	TRFE_MOUSE	P28793 p fatty oxi
433	19	95.0	621	1	TP6B_METAC	Q8tcf7 methanocarc	506	19	95.0	716	1	TRFE_MOUSE	Q8ypt0 anabaena sp
434	19	95.0	621	1	TP6B_METFA	Q8p9b8 methanocarc	507	19	95.0	721	1	TRFE_MOUSE	Q10767 mycobacteri
435	19	95.0	622	1	C2AC_BACTU	Q45743 bacillus th	508	19	95.0	722	1	TRFE_MOUSE	Q55690 synchocyst
436	19	95.0	624	1	COOS_METJA	Q58138 methanococc	509	19	95.0	725	1	TRFE_MOUSE	P35510 arabidopsis
437	19	95.0	625	1	P2L2_HUMAN	Q9nm6 homo sapien	510	19	95.0	725	1	TRFE_MOUSE	P3690 bacterioph
438	19	95.0	625	1	TP22_HAEN	Q9q814 myxoma viru	511	19	95.0	729	1	TRFE_MOUSE	P23842 escherichia
439	19	95.0	627	1	TP22_HAEN	Q9q822 Shope fibro	512	19	95.0	759	1	TRFE_MOUSE	Q8kd17 chlorobium
440	19	95.0	627	1	CACP_CANTR	P43736 haemophilus	513	19	95.0	763	1	TRFE_MOUSE	P31075 wolinsella s
441	19	95.0	631	1	CACP_CANTR	P52826 columba liv	514	19	95.0	764	1	TRFE_MOUSE	Q42669 cucumis mel
442	19	95.0	631	1	NTPL_VACCA	Q57214 vaccinia vi	515	19	95.0	781	1	TRFE_MOUSE	Q29753 archaeoglob
443	19	95.0	631	1	NTPL_VACCV	P20637 vaccinia vi	516	19	95.0	781	1	TRFE_MOUSE	Q9pke3 chlamydia m
444	19	95.0	631	1	NTPL_VACCV	P05807 vaccinia vi	517	19	95.0	787	1	TRFE_MOUSE	Q84253 chlamydia t
445	19	95.0	632	1	NTPL_VACV	P33066 variola vir	518	19	95.0	787	1	TRFE_MOUSE	Q10313 schizosacch
446	19	95.0	632	1	NTPL_VACV	Q9q814 myxoma viru	519	19	95.0	804	1	TRFE_MOUSE	Q9hr31 halobacteri
447	19	95.0	632	1	NTPL_SFVKA	Q9q822 Shope fibro	520	19	95.0	807	1	TRFE_MOUSE	Q91w96 mus musculu
448	19	95.0	634	1	DNAK_HASIN	P43736 haemophilus	521	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
449	19	95.0	634	1	NTPL_MCV1	Q98267 molluscum c	522	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
450	19	95.0	635	1	DNAK_VIRCH	Q34241 vibrio chol	523	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
451	19	95.0	635	1	DNAX_ANASP	Q8y280 anabaena sp	524	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
452	19	95.0	636	1	DNAX_VIRVY	Q8d166 vibrio vuln	525	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
453	19	95.0	636	1	DNAX_VIRVY	Q7ma85 vibrio vuln	526	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
454	19	95.0	637	1	MYB_MOUSE	P06876 mus musculu	527	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
455	19	95.0	637	1	DNAX_BRUME	Q8y876 bruceella me	528	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
456	19	95.0	637	1	DNAX_BRUOV	Q50981 bruceella ov	529	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
457	19	95.0	637	1	DNAX_BRUSU	Q8fx22 bruceella su	530	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
458	19	95.0	637	1	DNAX_ECOLI	P04475 escherichia	531	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
459	19	95.0	637	1	DNAX_PSEAE	Q9hw43 pseudomonas	532	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
460	19	95.0	637	1	DNAX_SALT1	Q8z9r1 salmonella	533	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
461	19	95.0	637	1	DNAX_SALT2	Q56073 salmonella	534	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
462	19	95.0	637	1	DNAX_VIRPA	Q87rx3 vibrio para	535	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
463	19	95.0	637	1	DNAX_VIRPB	Q91721 vibrio para	536	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
464	19	95.0	637	1	DNAX_VIRPB	Q91721 vibrio para	537	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
465	19	95.0	638	1	DNAX_BUCBP	P59565 buchnera ap	538	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
466	19	95.0	638	1	DNAX_BUCBP	Q3328 rhizobium	539	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
467	19	95.0	638	1	DNAX_RHILE	Q83mns shigella fl	540	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
468	19	95.0	638	1	DNAX_SHIFL	Q87384 vibrio harv	541	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
469	19	95.0	640	1	DNAX_VIRHA	P46200 bos taurus	542	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
470	19	95.0	640	1	MYB_BOVIN	P10242 homo sapien	543	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
471	19	95.0	642	1	INVA_VICFA	Q43857 vicia faba	544	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
472	19	95.0	644	1	H570_BRUMA	P27541 bugia mala	545	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
473	19	95.0	644	1	LSU2_RHIRA	P17279 rhizomucor	546	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu
474	19	95.0	649	1	DREB_HUMAN	Q16643 homo sapien	547	19	95.0	808	1	TRFE_MOUSE	Q91w96 mus musculu

545	19	95.0	916	1	SVI_STARP	O8cxsl	staphylococ	618	19	95.0	2236	1	POLG_HPAV4	P26581	hepatitis a
546	19	95.0	919	1	Y893_HUMAN	O94967	homo sapien	619	19	95.0	2226	1	POLG_HPAV8	P26582	hepatitis a
547	19	95.0	920	1	DMF1_SCHPO	P78953	schizosacch	620	19	95.0	2227	1	POLG_HPAV8	P06617	hepatitis a
548	19	95.0	920	1	PMN1_NEUCR	P707038	neurospora	621	19	95.0	2227	1	POLG_HPAV8	P06441	hepatitis a
549	19	95.0	921	1	SVI_BACSU	O45477	bacillus eu	622	19	95.0	2230	1	POLG_HPAV8	P14553	simian hepa
550	19	95.0	922	1	DPO1_RICFE	O9raa9	rickettsia	623	19	95.0	2314	1	PTP2_HUMAN	P23471	homo sapien
551	19	95.0	929	1	YDM6_SCHPO	P87137	schizosacch	624	19	95.0	2316	1	PTP2_RAT	Q62656	rattus norv
552	19	95.0	937	1	MSH2_ARATH	O24617	arabidopsis	625	19	95.0	2649	1	P285_HUMAN	Q9byk8	homo sapien
553	19	95.0	937	1	SVL_METH	O27552	methanobact	626	19	95.0	2725	1	FLNC_HUMAN	Q14115	homo sapien
554	19	95.0	942	1	MSH2_MALZE	Q9xgc9	zea mays (m	627	19	95.0	2774	1	MAPA_RAT	P34926	rattus norv
555	19	95.0	952	1	LYAG_HUMAN	P10253	homo sapien	628	19	95.0	2805	1	MAPA_HUMAN	P78559	homo sapien
556	19	95.0	953	1	SVY_VIBCH	O8kp73	vibrio chol	629	19	95.0	3412	1	POLG_TBVEV	P07720	t genome po
557	19	95.0	966	1	VIL3_ARATH	O81645	arabidopsis	630	19	95.0	3414	1	POLG_LANVT	P29837	l genome po
558	19	95.0	969	1	SVL_MYCTU	P71698	mycobacteri	631	19	95.0	3414	1	POLG_TBVEV	Q01299	t genome po
559	19	95.0	971	1	ANPN_HASCO	O10737	haemonchus	632	19	95.0	3414	1	POLG_TBVEV	P14336	t genome po
560	19	95.0	972	1	MTRA_YEAST	Q99189	saccharomyc	633	19	95.0	3415	1	POLG_POWVL	Q04538	t genome po
561	19	95.0	973	1	UDV3_RHILU	Q98m36	rhizobium l	634	19	95.0	3803	1	TRAL_DROME	Q8i8u7	drosophila
562	19	95.0	974	1	POD7_CAUUC	Q92988	caulobacter	635	19	95.0	3859	1	TRAP_HUMAN	Q9y4a5	homo sapien
563	19	95.0	976	1	VIL2_ARATH	O81644	arabidopsis	636	19	95.0	4447	1	PKSK_BACSU	P40803	bacillus su
564	19	95.0	980	1	POLG_LIV	P22338	louping ill	637	19	95.0	5179	1	MUC2_HUMAN	Q02817	homo sapien
565	19	95.0	987	1	UVRA_XANCP	O8pn26	xanthomonas	638	19	95.0	5217	1	HTS1_COCCA	Q01886	cochliobolu
566	19	95.0	988	1	UVRA_XANCP	O8pbh3	xanthomonas	639	19	95.0	5262	1	MLL2_HUMAN	O14686	homo sapien
567	19	95.0	992	1	UVRA_MICLU	P13567	micrococcus	640	19	95.0	5596	1	MDN1_HUMAN	Q9nu22	homo sapien
568	19	95.0	997	1	CBF_HUMAN	P53569	mus musculus	641	19	95.0	12	1	CALM_TETH	Q05055	tetrahymena
569	19	95.0	998	1	CBF_HUMAN	O03701	homo sapien	642	18	90.0	58	1	YOZD_BACSU	O31863	bacillus su
570	19	95.0	1012	1	DPOG_PICPA	O01941	pichia past	643	18	90.0	71	1	EX7S_STRA3	Q8em0	streptococc
571	19	95.0	1021	1	MAPA_PICPA	O9qvr6	mus musculus	644	18	90.0	79	1	DLTC_STRA3	Q8vm65	streptococc
572	19	95.0	1063	1	PRL1_YEAST	P12383	saccharomyc	645	18	90.0	79	1	EX7S_LACLA	Q9ch83	lactococcus
573	19	95.0	1065	1	SNCS_SCHPO	O13110	schizosacch	646	18	90.0	81	1	YKJA_ECOLI	P76036	escherichia
574	19	95.0	1086	1	RNC_CAEEL	O01326	caenorhabdi	647	18	90.0	88	1	RS15_PHOLU	P41120	photorhabdu
575	19	95.0	1095	1	AT9B_HUMAN	O43861	homo sapien	648	18	90.0	94	1	YFCL_ECOLI	P76496	escherichia
576	19	95.0	1095	1	AT9B_MOUSE	P98195	mus musculus	649	18	90.0	94	1	SELK_HUMAN	Q9y6d0	homo sapien
577	19	95.0	1117	1	CVT4_NEUCR	P47950	neurospora	650	18	90.0	94	1	SELK_MOUSE	Q9j1j1	mus musculus
578	19	95.0	1123	1	V120_HSV11	P10221	herpes simp	651	18	90.0	94	1	SELK_RAT	P59798	rattus norv
579	19	95.0	1125	1	MAP4_MOUSE	P27546	mus musculus	652	18	90.0	95	1	RS6_BACHD	Q9k5n8	bacillus ha
580	19	95.0	1144	1	FLNC_MOUSE	O8vnx6	mus musculus	653	18	90.0	98	1	YCII_ECOLI	P31070	escherichia
581	19	95.0	1146	1	YHC3_YEAST	P38742	saccharomyc	654	18	90.0	101	1	CYAV_HAEIN	P71358	haemophilus
582	19	95.0	1155	1	IFP2_METJA	O57710	methanococc	655	18	90.0	108	1	PRIB_NITEU	O82xq7	nitrosomona
583	19	95.0	1167	1	CAGA_HELPJ	Q92lt1	helicobacte	656	18	90.0	110	1	VAG1_TOBAC	O82702	nicotiana t
584	19	95.0	1173	1	MOB4_MOUSE	O9800	mus musculus	657	18	90.0	111	1	VAG2_TOBAC	O82703	nicotiana t
585	19	95.0	1200	1	MOG5_CAEEL	O09530	caenorhabdi	658	18	90.0	117	1	RNPA_LACLA	Q9CJ73	lactococcus
586	19	95.0	1211	1	DP3A_HELPJ	O92if9	helicobacte	659	18	90.0	133	1	S3AD_BACSU	P49781	bacillus su
587	19	95.0	1211	1	DP3A_HELPJ	P56157	helicobacte	660	18	90.0	134	1	YK49_STRCO	P16251	streptomyce
588	19	95.0	1239	1	TOP2_CRIFA	P27570	crithidia f	661	18	90.0	136	1	CDD_BACPY	Q9s3m0	bacillus ps
589	19	95.0	1302	1	UB4B_HUMAN	O95155	homo sapien	662	18	90.0	136	1	RL19_XYLFA	Q9ph26	xyella fas
590	19	95.0	1311	1	SPR4_CAEEL	O17582	caenorhabdi	663	18	90.0	136	1	RL19_XYLFA	Q87f53	xyella fas
591	19	95.0	1331	1	CVAB_LEIDO	O25463	leishmania	664	18	90.0	141	1	ALL2_TYRPU	O02380	tyrophagus
592	19	95.0	1355	1	DP3A_SYNY3	P74750	synchocyst	665	18	90.0	141	1	RISB_METJA	Q57751	methanococc
593	19	95.0	1371	1	VCAP_HSVSA	Q00999	herpesvirus	666	18	90.0	144	1	Y991_METJA	Q58398	methanococc
594	19	95.0	1423	1	ALBU_PETMA	Q91274	petromyzon	667	18	90.0	145	1	YK14_VIBVU	Q8db14	vibrio vuln
595	19	95.0	1426	1	NEPH4_HUMAN	O75161	homo sapien	668	18	90.0	147	1	CALM_KLULA	O60041	kluyveromyc
596	19	95.0	1444	1	DPO3_LISIN	Q92634	listeria in	669	18	90.0	147	1	CALM_YEAST	P06787	saccharomyc
597	19	95.0	1450	1	DPO3_LISMO	O8y7g1	listeria mo	670	18	90.0	147	1	YESE_BACSU	O31511	bacillus su
598	19	95.0	1477	1	YORI_YEAST	P53049	saccharomyc	671	18	90.0	148	1	CAL2_PETHY	P27163	petunia hyb
599	19	95.0	1515	1	YCFI_YEAST	P39109	saccharomyc	672	18	90.0	148	1	CALM_DROME	P49258	drosophila
600	19	95.0	1522	1	MRP3_RAT	O88563	rattus norv	673	18	90.0	148	1	CALM_ACHKL	P15094	achlya kleb
601	19	95.0	1524	1	Y133_HUMAN	Q14146	homo sapien	674	18	90.0	148	1	CALM_ACHKL	Q9hfy6	blastoclad
602	19	95.0	1527	1	MRP3_HUMAN	O15438	homo sapien	675	18	90.0	148	1	CALM_DROME	P07181	drosophila
603	19	95.0	1535	1	LML1_CAEEL	P18823	caenorhabdi	676	18	90.0	148	1	CALM_ELEEL	P02594	electrophor
604	19	95.0	1538	1	LHR_ECOLI	Q30015	escherichia	677	18	90.0	148	1	CALM_EUGGR	P11118	euglena gra
605	19	95.0	1609	1	CTPI_MYLE	O53114	mycobacteri	678	18	90.0	148	1	CALM_HORVU	P13565	hordeum vul
606	19	95.0	1679	1	GCC2_MOUSE	O8cbg3	mus musculus	679	18	90.0	148	1	CALM_HUMAN	P02593	homo sapien
607	19	95.0	1906	1	YPAO_ANASP	O8vmd0	anabaena ep	680	18	90.0	148	1	CALM_LYCES	P27161	lycopersico
608	19	95.0	1961	1	MYH9_RAT	Q62812	rattus norv	681	18	90.0	148	1	CALM_MALZE	P41040	zea mays (m
609	19	95.0	2027	1	DOC3_MOUSE	Q8ciq7	mus musculus	682	18	90.0	148	1	CALM_METSE	P02596	metridium s
610	19	95.0	2030	1	DOC3_HUMAN	O8ixd9	homo sapien	683	18	90.0	148	1	CALM_ORISA	P07463	paramecium
611	19	95.0	2039	1	TEGU_HSVJ7	P52362	human herpe	684	18	90.0	148	1	CALM_PATSP	P02595	patinopecte
612	19	95.0	2061	1	MYOF_HUMAN	O9nmz1	homo sapien	685	18	90.0	148	1	CALM_PATSP	P27165	phytophthor
613	19	95.0	2165	1	RPL1_HRSVA	P28887	human respi	686	18	90.0	148	1	CALM_PATSP	P11121	pyridae sp
614	19	95.0	2208	1	POIN_MANCV	O69014	manchester	687	18	90.0	148	1	CALM_PYUSP	P13868	solanum tub
615	19	95.0	2210	1	RPO_TACV	P20430	tacaribe vl	688	18	90.0	148	1	CALM_SOLTU	P04353	spinacia ol
616	19	95.0	2222	1	DPOE_YEAST	P21951	saccharomyc	689	18	90.0	148	1	CALM_SRIOL	P21251	stichopus j
617	19	95.0	2226	1	POLG_HPAV2	P26580	hepatitis a	690	18	90.0	148	1	CALM_STIJA		

691	18	90.0	148	1	CALM STYLE	P27166 stylonychia	764	18	90.0	229	1	RADB THEAC	Q9hjd3 thermoplasm
692	18	90.0	148	1	CALM TETPY	P02598 tetrahymena	765	18	90.0	230	1	ISPD SYNVC	P74323 synechocyst
693	18	90.0	148	1	CALM CHICK	P03597 gallus gall	766	18	90.0	231	1	FP CRIMI	P15697 cricetus
694	18	90.0	149	1	CALM CANAL	P23286 candida alb	767	18	90.0	234	1	SAMP MESAU	P07629 mesocricetu
695	18	90.0	149	1	CALM WHEAT	P04464 triticum ae	768	18	90.0	235	1	ICLN CANFA	P35521 canis famil
696	18	90.0	149	1	MLE3 HUMAN	P06741 homo sapien	769	18	90.0	236	1	PUR7 HELHP	Q7viq6 helicobacte
697	18	90.0	149	1	MLE3 RABIT	P03603 cryptoglagus	770	18	90.0	237	1	PUR7 METAC	Q8ti89 methanosarc
698	18	90.0	149	1	MLE3 RAT	P02601 rattus norv	771	18	90.0	237	1	PUR7 METWA	Q8pyk6 methanosarc
699	18	90.0	150	1	CALM SCHPO	P05933 schizosacch	772	18	90.0	238	1	RL1 ANASP	Q8ylj7 anabaena sp
700	18	90.0	150	1	V351 METJA	P05797 methanococc	773	18	90.0	238	1	Y538 CHLTR	O84543 chlamydia t
701	18	90.0	151	1	CALM DICDI	P03599 dictyosteli	774	18	90.0	238	1	Y825 CHLNU	Q8pjka clamydia m
702	18	90.0	151	1	CP2B DROME	P13486 rhizobium m	775	18	90.0	240	1	PUR7 COXBU	Q83ca8 coxiella bu
703	18	90.0	151	1	Y4G6 RHIME	P50858 enterobacte	776	18	90.0	242	1	MTGA KLEOX	P46022 escherichia
704	18	90.0	152	1	AAC6 ENTAE	P53440 naegleria g	777	18	90.0	242	1	MTGA KLEOX	Q84665 klebsiella
705	18	90.0	155	1	CALF NAAGR	Q8X955 fusobacteri	778	18	90.0	242	1	NPDI THETN	Q9rgn6 thermoanaer
706	18	90.0	155	1	Y463 FUSNG	P03585 homo sapien	779	18	90.0	242	1	PDJX NEIMA	Q9rgv9 neisseria m
707	18	90.0	159	1	TPCS HUMAN	P026801 mus musculu	780	18	90.0	244	1	RRPO SCVLA	P23172 saccharomyc
708	18	90.0	159	1	TPCS MOUSE	P02587 sus scrofa	781	18	90.0	244	1	TRCB HUMAN	Q99426 homo sapien
709	18	90.0	159	1	TPCS PIG	P02586 cryptoglagus	782	18	90.0	244	1	Y132 ARCTU	O82148 archaeoglob
710	18	90.0	159	1	TPCS RABIT	P81660 anguilla an	783	18	90.0	245	1	YCDX ECOLI	P75914 escherichia
711	18	90.0	160	1	TPCS ANGAN	Q9ceul lactococcus	784	18	90.0	246	1	AQPM METTH	O8206 methanobact
712	18	90.0	162	1	AROK LACLA	P04352 chlamydomon	785	18	90.0	246	1	AQPM METTH	Q9C425 methanobact
713	18	90.0	162	1	CALM CHLRE	P03588 gallus gall	786	18	90.0	246	1	HEM4 CHLVI	Q59335 chlorobium
714	18	90.0	162	1	TPCS CHICK	P10246 meleagris g	787	18	90.0	246	1	MTGA HAEIN	P44890 haemophilus
715	18	90.0	162	1	TPCS MELGA	P02589 rana esculu	788	18	90.0	246	1	TRPC SULFO	Q972a1 sulfolobus
716	18	90.0	162	1	TPCS RANES	Q50uW6 sulfolobus	789	18	90.0	248	1	Y4EL RHISN	P55435 rhizobium s
717	18	90.0	166	1	Y551 SULSO	Q80uW6 sulfolobus	790	18	90.0	251	1	TPIS PSESM	P87wq1 pseudomonas
718	18	90.0	166	1	Y628 METJA	Q50445 methanococc	791	18	90.0	251	1	TPIS PSESY	P95576 pseudomonas
719	18	90.0	169	1	IPVR ANASP	P80562 anabaena sp	792	18	90.0	252	1	RECO CHLPN	Q927W5 chlamydia p
720	18	90.0	169	1	IPVR SYN3	P80507 synechocyst	793	18	90.0	252	1	TRPC THENA	Q56319 thermotoga
721	18	90.0	171	1	NSG2 HUMAN	P94328 homo sapien	794	18	90.0	253	1	YTBQ BACSU	P33560 bacillus su
722	18	90.0	171	1	NSG2 MOUSE	P47759 mus musculu	795	18	90.0	254	1	AROD NEIMB	Q9iytc neisseria m
723	18	90.0	171	1	YBP2 ACIAM	P32986 acidianus a	796	18	90.0	254	1	PMW YEAST	P07283 saccharomyc
724	18	90.0	172	1	IPVR SYNEL	Q8dhr2 synechococc	797	18	90.0	257	1	UXUR ECOLI	Q9K5J6 bacillus an
725	18	90.0	173	1	TCPA ANEME	P50157 ambystoma m	798	18	90.0	257	1	UXUR ECOLI	P39161 escherichia
726	18	90.0	174	1	MLRN DROME	P40423 drosophila	799	18	90.0	258	1	EXUR ECOLI	P42608 escherichia
727	18	90.0	177	1	IPVR HALN1	Q9hef3 halobacteri	800	18	90.0	259	1	EXUR ERWCH	Q9x9e0 erwinia chr
728	18	90.0	181	1	PYRE THEAQ	P96078 thermus aqu	801	18	90.0	260	1	RS3 ANASP	Q8ypis anabaena sp
729	18	90.0	184	1	Y803 CHLPN	Q927a3 chlamydia p	802	18	90.0	260	1	TRPC BACTN	Q8aad6 bacteroides
730	18	90.0	185	1	CBX1 HUMAN	P23197 homo sapien	803	18	90.0	261	1	RP8B BACSU	P06574 bacillus su
731	18	90.0	185	1	DPI HUMAN	Q60870 mus musculu	804	18	90.0	264	1	YIN6 YEAST	P33563 saccharomyc
732	18	90.0	185	1	DPI MOUSE	Q60870 mus musculu	805	18	90.0	265	1	GIR2 YEAST	P33768 saccharomyc
733	18	90.0	185	1	NSGI HUMAN	P42857 homo sapien	806	18	90.0	266	1	UXUR HAEIN	P44487 haemophilus
734	18	90.0	185	1	NSGI MOUSE	Q62092 mus musculu	807	18	90.0	267	1	APHC HUMAN	Q9nun7 homo sapien
735	18	90.0	185	1	RFBC ECOLI	P37745 escherichia	808	18	90.0	267	1	RL4 SULSO	Q8uxa6 sulfolobus
736	18	90.0	185	1	Y56A THEMA	P58008 thermotoga	809	18	90.0	267	1	Y955 HAEIN	Q48215 haemophilus
737	18	90.0	189	1	KTHV THEAC	Q9hlz2 thermoplasm	810	18	90.0	268	1	HIS9 BACSU	O34411 bacillus su
738	18	90.0	197	1	Y249 METTH	O26351 methanobact	811	18	90.0	268	1	THIM ARCTU	Q38204 archaeoglob
739	18	90.0	199	1	TDX2 BRUMA	Q17172 brugia mala	812	18	90.0	269	1	TRPA BACST	P19867 bacillus st
740	18	90.0	200	1	ESTE VIBMI	Q00792 vibrio mimi	813	18	90.0	270	1	RPNC SCHPO	P50524 schizosacch
741	18	90.0	201	1	RETE MOUSE	Q00724 mus musculu	814	18	90.0	270	1	YCB7 METJA	Q59087 acinetobact
742	18	90.0	201	1	RETE RAT	P04916 rattus norv	815	18	90.0	272	1	3DHQ ACICA	Q59087 acinetobact
743	18	90.0	202	1	COAE CHLTR	O84499 chlamydia t	816	18	90.0	272	1	AQPA RANES	P50501 rana esculu
744	18	90.0	202	1	HIS5 METAC	Q8ce91 methanosarc	817	18	90.0	275	1	SC65 CANAL	O14415 candida alb
745	18	90.0	202	1	HIS5 METMA	Q8pvd5 methanosarc	818	18	90.0	277	1	Y154 ARCTU	Q30083 archaeoglob
746	18	90.0	202	1	YC55 MYCTU	Q11063 mycobacteri	819	18	90.0	278	1	P128 ARATH	Q32vX8 arabidopsis
747	18	90.0	206	1	CNC2 MOUSE	Q9db76 mus musculu	820	18	90.0	279	1	YD15 STAAW	Q9nu62 staphylococ
748	18	90.0	208	1	CNC2 HUMAN	Q9v3b6 homo sapien	821	18	90.0	279	1	YE25 STAAW	Q9nu62 staphylococ
749	18	90.0	208	1	RL1 PEA	P43208 pium sativ	822	18	90.0	280	1	P127 ARATH	P33004 arabidopsis
750	18	90.0	208	1	RR3 GRATE	P16631 gracilaria	823	18	90.0	281	1	GLPF ECOLI	P11244 escherichia
751	18	90.0	209	1	TRPE METKA	Q8cx29 methanopyru	824	18	90.0	281	1	GLPF SHIFL	P31140 shigella fl
752	18	90.0	216	1	DEF1 BIFLO	Q8G534 bifidobacte	825	18	90.0	282	1	P1P1 ATRCA	P42767 atrilex ca
753	18	90.0	217	1	RECA ARTAU	Q9re16 arthrobacte	826	18	90.0	283	1	LGT_HELPU	P44420 haemophilus
754	18	90.0	221	1	MLR DROME	P18432 drosophila	827	18	90.0	283	1	TSYV PASMU	P57808 pasteurilla
755	18	90.0	223	1	DEOC MYCGE	P47296 mycoplasma	828	18	90.0	283	1	TSYV PASMU	O25609 helicobacte
756	18	90.0	223	1	SAMP CAVPO	P49255 cavia porce	829	18	90.0	284	1	LGT_HELPY	Q8tvh1 methanopyru
757	18	90.0	223	1	SAMP HUMAN	P02743 homo sapien	830	18	90.0	284	1	NADE METKA	P59594 sulfolobus
758	18	90.0	224	1	DEOC MYCPN	P03924 mycoplasma	831	18	90.0	284	1	Y066 SULSO	P43287 arabidopsis
759	18	90.0	224	1	SAMP PIG	O19063 sus scrofa	832	18	90.0	285	1	P122 ARATH	P30302 arabidopsis
760	18	90.0	226	1	ORGO SALTU	P58654 salmonella	833	18	90.0	285	1	P123 ARATH	P3285 arabidopsis
761	18	90.0	228	1	ISPD ANASP	Q8ylx9 anabaena sp	834	18	90.0	286	1	P111 ARATH	Q06611 arabidopsis
762	18	90.0	228	1	IPYR METTH	O26232 methanobact	835	18	90.0	286	1	P112 ARATH	Q08733 arabidopsis
763	18	90.0	228	1	SAMP_RAT	P23680 rattus norv	836	18	90.0	286	1	P113 ARATH	

837	1	P125 ARATH	Q9sv31 arabidopsis	910	18	90.0	363	1	LEU3_BUCAP	085064 buchnera ap
838	1	P126 ARATH	Q9sv31 arabidopsis	911	18	90.0	363	1	MURG_ENTFA	007109 enterococcus
839	1	P127 ARATH	Q9sv31 arabidopsis	912	18	90.0	364	1	AAT_PVRKO	Q93744 pyrococcus
840	1	P128 ARATH	Q9sv31 arabidopsis	913	18	90.0	364	1	YH2B_MYCTU	Q10512 mycobacteri
841	1	P129 ARATH	Q9sv31 arabidopsis	914	18	90.0	365	1	HI82_BORER	Q7wgy3 bordetella
842	1	P130 ARATH	Q9sv31 arabidopsis	915	18	90.0	365	1	HI82_BORER	Q7wgy3 bordetella
843	1	P131 ARATH	Q9sv31 arabidopsis	916	18	90.0	365	1	HI82_BORER	Q7wgy3 bordetella
844	1	P132 ARATH	Q9sv31 arabidopsis	917	18	90.0	365	1	HI82_BORER	Q7wgy3 bordetella
845	1	P133 ARATH	Q9sv31 arabidopsis	918	18	90.0	365	1	HI82_BORER	Q7wgy3 bordetella
846	1	P134 ARATH	Q9sv31 arabidopsis	919	18	90.0	366	1	RECA_SPIPL	P48293 spirulina p
847	1	P135 ARATH	Q9sv31 arabidopsis	920	18	90.0	366	1	RECA_SPIPL	P48293 spirulina p
848	1	P136 ARATH	Q9sv31 arabidopsis	921	18	90.0	366	1	RECA_SPIPL	P48293 spirulina p
849	1	P137 ARATH	Q9sv31 arabidopsis	922	18	90.0	369	1	RECA_SPIPL	P48293 spirulina p
850	1	P138 ARATH	Q9sv31 arabidopsis	923	18	90.0	369	1	RECA_SPIPL	P48293 spirulina p
851	1	P139 ARATH	Q9sv31 arabidopsis	924	18	90.0	371	1	Y1B0_CIOAB	Q04354 clostridium
852	1	P140 ARATH	Q9sv31 arabidopsis	925	18	90.0	372	1	Y1B0_CIOAB	Q04354 clostridium
853	1	P141 ARATH	Q9sv31 arabidopsis	926	18	90.0	372	1	Y1B0_CIOAB	Q04354 clostridium
854	1	P142 ARATH	Q9sv31 arabidopsis	927	18	90.0	376	1	RECA_COREF	P58694 methanococ
855	1	P143 ARATH	Q9sv31 arabidopsis	928	18	90.0	376	1	RECA_COREF	P58694 methanococ
856	1	P144 ARATH	Q9sv31 arabidopsis	929	18	90.0	376	1	RECA_COREF	P58694 methanococ
857	1	P145 ARATH	Q9sv31 arabidopsis	930	18	90.0	380	1	RECA_COREF	P58694 methanococ
858	1	P146 ARATH	Q9sv31 arabidopsis	931	18	90.0	380	1	RECA_COREF	P58694 methanococ
859	1	P147 ARATH	Q9sv31 arabidopsis	932	18	90.0	386	1	RECA_COREF	P58694 methanococ
860	1	P148 ARATH	Q9sv31 arabidopsis	933	18	90.0	386	1	RECA_COREF	P58694 methanococ
861	1	P149 ARATH	Q9sv31 arabidopsis	934	18	90.0	387	1	RECA_COREF	P58694 methanococ
862	1	P150 ARATH	Q9sv31 arabidopsis	935	18	90.0	387	1	RECA_COREF	P58694 methanococ
863	1	P151 ARATH	Q9sv31 arabidopsis	936	18	90.0	387	1	RECA_COREF	P58694 methanococ
864	1	P152 ARATH	Q9sv31 arabidopsis	937	18	90.0	387	1	RECA_COREF	P58694 methanococ
865	1	P153 ARATH	Q9sv31 arabidopsis	938	18	90.0	387	1	RECA_COREF	P58694 methanococ
866	1	P154 ARATH	Q9sv31 arabidopsis	939	18	90.0	387	1	RECA_COREF	P58694 methanococ
867	1	P155 ARATH	Q9sv31 arabidopsis	940	18	90.0	394	1	RECA_COREF	P58694 methanococ
868	1	P156 ARATH	Q9sv31 arabidopsis	941	18	90.0	394	1	RECA_COREF	P58694 methanococ
869	1	P157 ARATH	Q9sv31 arabidopsis	942	18	90.0	395	1	RECA_COREF	P58694 methanococ
870	1	P158 ARATH	Q9sv31 arabidopsis	943	18	90.0	397	1	RECA_COREF	P58694 methanococ
871	1	P159 ARATH	Q9sv31 arabidopsis	944	18	90.0	397	1	RECA_COREF	P58694 methanococ
872	1	P160 ARATH	Q9sv31 arabidopsis	945	18	90.0	401	1	RECA_COREF	P58694 methanococ
873	1	P161 ARATH	Q9sv31 arabidopsis	946	18	90.0	404	1	RECA_COREF	P58694 methanococ
874	1	P162 ARATH	Q9sv31 arabidopsis	947	18	90.0	404	1	RECA_COREF	P58694 methanococ
875	1	P163 ARATH	Q9sv31 arabidopsis	948	18	90.0	405	1	RECA_COREF	P58694 methanococ
876	1	P164 ARATH	Q9sv31 arabidopsis	949	18	90.0	405	1	RECA_COREF	P58694 methanococ
877	1	P165 ARATH	Q9sv31 arabidopsis	950	18	90.0	406	1	RECA_COREF	P58694 methanococ
878	1	P166 ARATH	Q9sv31 arabidopsis	951	18	90.0	406	1	RECA_COREF	P58694 methanococ
879	1	P167 ARATH	Q9sv31 arabidopsis	952	18	90.0	408	1	RECA_COREF	P58694 methanococ
880	1	P168 ARATH	Q9sv31 arabidopsis	953	18	90.0	408	1	RECA_COREF	P58694 methanococ
881	1	P169 ARATH	Q9sv31 arabidopsis	954	18	90.0	410	1	RECA_COREF	P58694 methanococ
882	1	P170 ARATH	Q9sv31 arabidopsis	955	18	90.0	411	1	RECA_COREF	P58694 methanococ
883	1	P171 ARATH	Q9sv31 arabidopsis	956	18	90.0	411	1	RECA_COREF	P58694 methanococ
884	1	P172 ARATH	Q9sv31 arabidopsis	957	18	90.0	414	1	RECA_COREF	P58694 methanococ
885	1	P173 ARATH	Q9sv31 arabidopsis	958	18	90.0	416	1	RECA_COREF	P58694 methanococ
886	1	P174 ARATH	Q9sv31 arabidopsis	959	18	90.0	417	1	RECA_COREF	P58694 methanococ
887	1	P175 ARATH	Q9sv31 arabidopsis	960	18	90.0	420	1	RECA_COREF	P58694 methanococ
888	1	P176 ARATH	Q9sv31 arabidopsis	961	18	90.0	425	1	RECA_COREF	P58694 methanococ
889	1	P177 ARATH	Q9sv31 arabidopsis	962	18	90.0	425	1	RECA_COREF	P58694 methanococ
890	1	P178 ARATH	Q9sv31 arabidopsis	963	18	90.0	425	1	RECA_COREF	P58694 methanococ
891	1	P179 ARATH	Q9sv31 arabidopsis	964	18	90.0	426	1	RECA_COREF	P58694 methanococ
892	1	P180 ARATH	Q9sv31 arabidopsis	965	18	90.0	429	1	RECA_COREF	P58694 methanococ
893	1	P181 ARATH	Q9sv31 arabidopsis	966	18	90.0	430	1	RECA_COREF	P58694 methanococ
894	1	P182 ARATH	Q9sv31 arabidopsis	967	18	90.0	433	1	RECA_COREF	P58694 methanococ
895	1	P183 ARATH	Q9sv31 arabidopsis	968	18	90.0	434	1	RECA_COREF	P58694 methanococ
896	1	P184 ARATH	Q9sv31 arabidopsis	969	18	90.0	434	1	RECA_COREF	P58694 methanococ
897	1	P185 ARATH	Q9sv31 arabidopsis	970	18	90.0	438	1	RECA_COREF	P58694 methanococ
898	1	P186 ARATH	Q9sv31 arabidopsis	971	18	90.0	440	1	RECA_COREF	P58694 methanococ
899	1	P187 ARATH	Q9sv31 arabidopsis	972	18	90.0	444	1	RECA_COREF	P58694 methanococ
900	1	P188 ARATH	Q9sv31 arabidopsis	973	18	90.0	446	1	RECA_COREF	P58694 methanococ
901	1	P189 ARATH	Q9sv31 arabidopsis	974	18	90.0	451	1	RECA_COREF	P58694 methanococ
902	1	P190 ARATH	Q9sv31 arabidopsis	975	18	90.0	455	1	RECA_COREF	P58694 methanococ
903	1	P191 ARATH	Q9sv31 arabidopsis	976	18	90.0	456	1	RECA_COREF	P58694 methanococ
904	1	P192 ARATH	Q9sv31 arabidopsis	977	18	90.0	460	1	RECA_COREF	P58694 methanococ
905	1	P193 ARATH	Q9sv31 arabidopsis	978	18	90.0	462	1	RECA_COREF	P58694 methanococ
906	1	P194 ARATH	Q9sv31 arabidopsis	979	18	90.0	465	1	RECA_COREF	P58694 methanococ
907	1	P195 ARATH	Q9sv31 arabidopsis	980	18	90.0	467	1	RECA_COREF	P58694 methanococ
908	1	P196 ARATH	Q9sv31 arabidopsis	981	18	90.0	469	1	RECA_COREF	P58694 methanococ
909	1	P197 ARATH	Q9sv31 arabidopsis	982	18	90.0	473	1	RECA_COREF	P58694 methanococ

Q8xyd8 pyrobaculum
P42590 escherichia
P19487 xanthomonas
P21885 bacillus su
O52351 mycoplasma
P57693 thermoplasma
Q956t2 caenorhabdi
P28288 arabidopsis
Q8yej2 anabaena sp
O46051 drosophila
P72245 rhodobacter
P40051 saccharomyc
Q92d12 rickettsia
Q9aby4 c.bifunctio
P26334 trypanosoma
P38140 saccharomyc
P49109 cavia porce
Q8xbv3 escherichia

18 90.0 474 1 SYC PYRAE
18 90.0 477 1 YGJI ECOLI
18 90.0 484 1 GUNA XANCP
18 90.0 490 1 DCLY BACSU
18 90.0 498 1 SECY MYCGA
18 90.0 499 1 SYPA THEAC
18 90.0 500 1 GALT CAEEL
18 90.0 500 1 NU4C ARATH
18 90.0 506 1 PUR9 ANASP
18 90.0 507 1 C4DE DROME
18 90.0 509 1 ATPA RHOC
18 90.0 511 1 YE08 YEAST
18 90.0 513 1 Y538 RICPR
18 90.0 519 1 PUR9 CAUCR
18 90.0 529 1 VSM6 TRYBB
18 90.0 529 1 YB83 YEAST
18 90.0 532 1 FM03 CAVPO
18 90.0 536 1 ENTE ECO57

NS2_MYCTU STANDARD; PRT; 19 AA.
P81136;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 2 (fragment).
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
[1]
SEQUENCE.

ALIGNMENTS

RESULT 1
NS2_MYCTU STANDARD; PRT; 19 AA.
P81136;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 2 (fragment).
Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
[1]
SEQUENCE.

Query Match 95.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 11 VAEF 14

RESULT 2
ECF_TREPA STANDARD; PRT; 59 AA.
C 083263;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
E Preprotein translocase secE subunit.
N SECE OR TP0235.
S Treponema pallidum.
C Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
X NCBI_TaxID=160;
[1]
SEQUENCE FROM N.A.
C STAIN=NICHOLS;
MEDLINE=98332770; PubMed=9655876;
A Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,

RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.,
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.",
RL Science 281:375-388 (1998).
CC -I- FUNCTION: Essential for protein export.
CC -I- SUBCELLULAR LOCATION: Tail-anchored membrane protein (Potential).
CC -I- SIMILARITY: Belongs to the SECE/SEC61-gamma family.
CC
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CC
CC
CC ENBL; AE001205; AAC65223.1; -.
DR PIR; E71349; E71349.
DR TIGR; TP0235; -.
DR InterPro; IPR001901; SecE.
DR InterPro; IPR005807; SecE_bac.
DR Pfam; PF0584; SecE; 1.
DR TIGRFAMs; TIGR00964; 3a0501s06; 1.
DR PROSITE; PS01667; SECE_SEC61G; 1.
KW Protein transport; Translocation; Transmembrane; Complete proteome.
FT TRANSMEM 39 59 POTENTIAL.
SQ SEQUENCE 59 AA; 6789 MW; 9AC35BA8F48B2A7F CRC64;
Query Match 95.0%; Score 19; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 12 VAEF 15

RESULT 3
Y90_ARCFU STANDARD; PRT; 59 AA.
ID Y90_ARCFU
AC O29175;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0165 protein AF1090.
GN AF1090.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artisch P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.",
RL Nature 390:364-370 (1997).

-!- SIMILARITY: Belongs to the UPF0165 family.

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EMBL; AE001028; AAB90157.1; -.

PIR; A69386; A69386.

TIGR; AF1090; -.

InterPro; IPR008203; DUF104.

InterPro; IPR008204; DUF104_N.

Pfam; PF01954; DUF104; 1.

ProDom; PD005964; DUF104_N; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 59 AA; 6887 MW; B7E847382B6B6 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 59;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5

|||||

51 VAEF 54

SULT 4

51 HAEIN

STANDARD; PRT;

Y451 HAEIN 63 AA.

P43998;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Hypothetical protein HI0451.

HI0451.

Haemophilus influenzae.

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Haemophilus.

NCBI_TaxID=727;

[1]

SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae

Rd.";

Science 269:496-512(1995).

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EMBL; U32728; AAC22109.1; -.

PIR; G64007; G64007.

TIGR; HI0451; -.

Hypothetical protein; Complete proteome.

SEQUENCE 63 AA; 7047 MW; 36B14B60AC306B67 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

|||||

Db 27 VAEF 30

RESULT 5

RS15 HAEIN

STANDARD; PRT;

AC P44389; 88 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 30S ribosomal protein S15.

GN (RPSO-A OR RPS15-A OR H11328) AND (RPSO-B OR RPS15-B OR H11468).

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OK NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RC MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae

Rd.";

RL Science 269:496-512(1995).

CC -!- FUNCTION: This protein is one of the 16S ribosomal RNA binding

CC proteins (by similarity).

CC -!- SIMILARITY: Belongs to the S15P family of ribosomal proteins.

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CC -----

CC EMBL; U32812; AAC22973.1; -.

CC EMBL; U32825; AAC23117.1; -.

CC PIR; H64116; H64116.

CC HGSP; P05766; 1A32.

CC TIGR; H11328; -.

CC TIGR; H11468; -.

CC InterPro; IPR000589; Ribosomal_S15.

CC InterPro; IPR005290; Ribosomal_S15_b.

CC Pfam; PF00312; Ribosomal_S15; 1.

CC ProDom; PD157043; RS15_bact; 1.

CC TIGRfams; TIGR00952; S15_bact; 1.

CC PROSITE; PS00362; RIBOSOMAL_S15; 1.

CC Ribosomal protein; rRNA-binding; Complete proteome.

FT INIT_MET 0 0 BY SIMILARITY.

SO SEQUENCE 88 AA; 10064 MW; 563BAD2B8B8A7043 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 88;

Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

|||||

Db 11 VAEF 14


```
RESULT 6
LB2_METKA
D_ALB2_METKA STANDARD; PRT; 93 AA.
C Q8TW6;
Y 10-OCT-2003 (Rel. 42, Created)
Y 10-OCT-2003 (Rel. 42, Last sequence update)
Y 10-OCT-2003 (Rel. 42, Last annotation update)
E ALB2 OR MK1089.
N Methanopyrus kandleri.
X Archaea; Euryarchaeota; Methanopyri; Methanopyraxes; Methanopyracace;
X Methanopyrus.
X NCBI_TaxID=2320;
N [1]
N "Complete genome sequence of the methanogenic archaeon, Methanococcus
N jannaschii".
N Science 273:1058-1073(1996).
N -----
N -!- SIMILARITY: BELONGS TO THE UPF0166 FAMILY.
N -----
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N between the Swiss Institute of Bioinformatics and the EMBL outstation -
N the European Bioinformatics Institute. There are no restrictions on its
N use by non-profit institutions as long as its content is in no way
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N or send an email to license@isb-sib.ch).
N -----
N EMBL; U67593; AAB99550.1;
N PIR; C64490; C64490.
N TIGR; MJ1524;
N InterPro: IPR003793; DUF190.
N Pfam; PF02641; DUF190; 1.
N KW Hypothetical protein; Complete proteome.
N SQ SEQUENCE 108 AA; 12398 MW; D3E286AFB9D4AF8B CRC64;

Query Match 95.0%; Score 19; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 52 VAEF 55

RESULT 8
KEDA_ACTSL STANDARD; PRT; 114 AA.
AC P41249;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apokedarcidin.
DE Actinomycete sp. (strain L585-6 / ATCC 53650).
DE Bacteri; Actinobacteria; Actinobacteridae; Actinomycetales.
OX NCBI_TaxID=38989;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 53650 / L585-6;
RX Hofstead S.J., Matson J.A., Malacko A.R., Marguardt H.,
RT "Kedarcidin, a new chromoprotein antitumor antibiotic. II. Isolation,
RL purification and physico-chemical properties.";
RL J. Antibiot. 45:1250-1254(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93376732; PubMed=8367457;
RX Zein N., Casazza A.M., Doyle T.W., Leet J.E., Schoeder D.R.,
RA Solomon W., Nadler S.G.;
RT "Selective proteolytic activity of the antitumor agent kedarcidin.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8009-8012(1993).
RN [3]
```

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STRUCTURE BY NMR.
STRAIN=ATCC 53650 / L585-6;
MEDLINE=95001848; PubMed=7918358;
Constantine K.L., Colson K.L., Wittekind M., Friedrichs M.S.,
Zein N., Tuttle J., Langley D.R., Leet J.E., Schroeder D.R., Lam K.S.,
Farmer B.T. II, Metzler W.J., Bruccoleri R.E., Mueller L.,
"Sequential 1H, 13C, and 15N NMR assignments and solution
conformation of apokadarcidin.";
Biochemistry 33:11438-11452(1994).
-!- FUNCTION: BINDS NON-COVALENTLY TO AN ENEDIYNE CHROMOPHORE WHICH IS
THE CYTOTOXIC AND MUTAGENIC COMPONENT OF THE ANTIBIOTIC. THE
CHROMOPHORE CLEAVES DUPLEX DNA SITE-SPECIFICALLY IN A SINGLE-
STRANDED MANNER. THE APOPROTEIN CLEAVES PROTEINS SELECTIVELY, IN
PARTICULAR HIGHLY BASIC HISTONES, WITH H1 PROTEINS BEING CLEAVED
THE MORE READILY.
-!- DOMAIN: THIS PROTEIN CONSISTS OF AN IMMUNOGLOBULIN-LIKE SEVEN-
STRANDED ANTIPARALLEL BETA-BARREL DOMAIN LINKED TO A SUBDOMAIN
COMPOSED OF TWO BETA-HAIRPIN RIBBONS.
-!- SIMILARITY: Belongs to the neocarzinostatatin family.
PDB; JAKP; 3I-AUG-94.
InterPro; IPR002186; Neocarzinostat.
Pfam; PF00960; Neocarzinostat; 1.
ProDom; PPO12709; Neocarzinostat; 1.
Antibiotic; DNA-binding; 3D-structure.
DISULFID 37 47
STRAND 4 7
TURN 11 13
STRAND 15 16
STRAND 18 18
STRAND 21 24
STRAND 32 33
STRAND 36 39
STRAND 46 47
TURN 50 51
STRAND 55 55
STRAND 61 61
STRAND 64 64
STRAND 67 67
STRAND 71 74
TURN 77 79
STRAND 84 87
STRAND 94 97
STRAND 100 100
STRAND 109 110
STRAND 112 114
SEQUENCE 114 AA; 10969 MW; 1901E2B14E4197B4 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
49 VAEF 52

SULT 9
S_VERMO
INS VERMO STANDARD; PRT; 115 AA.
Q9W7R2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Insulin precursor.
INS.
Verasper moseri (Barfin flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Verasper.
NCBI_TaxID=98923;
[1]

SEQUENCE FROM N.A.
RA Andoh T., Nagasawa H.;
RT "Two molecular forms of insulin from barfin flounder, Verasper moseri,
RL are derived from a single gene.";
Zool. Sci. 15:931-937(1998).
-!- FUNCTION: Insulin decreases blood glucose concentration. It
CC increases cell permeability to monosaccharides, amino acids and
CC fatty acids. It accelerates glycolysis, the pentose phosphate
CC cycle, and glycogen synthesis in liver.
CC -!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
CC disulfide bonds.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the insulin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB029318; BA82315.1; -.
DR HSSP; P01315; INPJ.
DR InterPro; IPR004825; Ins/IGF/relax.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00277; INSULIN.
DR SMART; SM00078; IIGF; 1.
DR PROSITE; PS00262; INSULIN; 1.
DR Insulin family; Hormone; Glucose metabolism; Signal.
FT SIGNAL 1 22
FT CHAIN 23 53
FT PROPEP 56 92
FT CHAIN 95 115
FT DISULFID 32 101
FT DISULFID 44 114
FT DISULFID 100 105
FT SEQUENCE 115 AA; 12608 MW; 7BA2A5B568DEDDBB CRC64;

Query Match 95.0%; Score 19; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
79 VAEF 82

Db

RESULT 10
INS_LOPPI STANDARD; PRT; 116 AA.
AC P01341;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Insulin precursor.
GN INS.
OS Lophius piscatorius (Allmouth goosefish) (Anglerfish), and
OS Lophius americanus (American goosefish) (Anglerfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=8074, 8073;
[1]
RN NCBI_SEQUENCE FROM N.A.
RP SPECIES=L. americanus;
RC MEDLINE=91056434; PubMed=7001633;
RX Hobart P.M., Shen L.-F., Crawford R., Pictet R.L., Rutter W.J.;
RT "Comparison of the nucleic acid sequence of anglerfish and mammalian
RL insulin mRNA's from cloned cDNA's.";
Science 210:1360-1363(1980).
[2]
RN
RP SEQUENCE OF 25-54 AND 96-116.

```

C SPECIES=L.piscatorius;
 X MEDLINE=70036620; PubMed=539299;
 A Neumann P.A., Koldenhof M., Humbel R.E.;
 T "Amino acid sequence of insulin from the angler fish (Lophius
 T piscatorius)".
 L Hoppe-Seyler's Z. Physiol. Chem. 350:1286-1288 (1969).
 C -1- FUNCTION: Insulin decreases blood glucose concentration. It
 C increases cell permeability to monosaccharides, amino acids and
 C fatty acids. It accelerates glycolysis, the pentose phosphate
 C cycle, and glycogen synthesis in liver.
 C -1- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
 C disulfide bonds.
 C -1- SUBCELLULAR LOCATION: Secreted.
 C -1- SIMILARITY: Belongs to the insulin family.
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 C or send an email to license@isb-sib.ch).
 C -----
 R EMBL; V00634; CAA23907.1; --
 R PIR; A01608; IPAF.
 R HSP; P01308; ILPH.
 R InterPro; IPR004825; Ins/IGF/relax.
 R Pfam; PF00049; Insulin; 1.
 R PRINTS; PR00277; INSULIN.
 R SMART; SM00078; ILGF; 1.
 R PROSITE; PS00262; INSULIN; 1.
 R Insulin family; Hormone; Glucose metabolism; Signal.
 T SIGNAL 1 24
 T CHAIN 1 24 INSULIN B CHAIN.
 T PROPEP 25 53 C PEPTIDE.
 T CHAIN 56 93
 T CHAIN 96 116 INSULIN A CHAIN.
 T DISULFID 32 102 INTERCHAIN.
 T DISULFID 44 115
 T DISULFID 101 106
 T SEQUENCE 116 AA; 12737 MW; C685F8F8183BEFE CRC64;
 Y Query Match 95.0%; Score 19; DB 1; Length 116;
 Y Best Local Similarity 100.0%; Pred.No. 2.le+02;
 Y Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 Y ||||
 Y 80 VAEF 83
 RESULT 11
 D U279 DROME STANDARD; PRT; 119 AA.
 C Q9V8F3;
 T 10-OCT-2003 (Rel. 42, Created)
 T 10-OCT-2003 (Rel. 42, Last sequence update)
 T 10-OCT-2003 (Rel. 42, Last annotation update)
 E UPF0279 protein CGI4505.
 N CGI4505.
 S Drosophila melanogaster (Fruit fly).
 C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 C Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 C Ephydroidea; Drosophilidae; Drosophila.
 X NCBI_TaxID=7227;
 X [1]
 N SEQUENCE FROM N.A.
 P STRAIN=Berkley;
 C MEDLINE=20196006; PubMed=10731132;
 X Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 A Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 A Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
 RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Fezzaz C., Ferrera S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorteli J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jaimai M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RC MEDLINE=22426066; PubMed=12537569;
 RX Medline=22426066;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guerin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A Drosophila full-length cDNA resource";
 RL Genome Biol. 3:RESEARCH080.1-RESEARCH080.8(2002).
 CC -1- SIMILARITY: Belongs to the UPF0279 family.
 CC -----
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 CC -----
 CC EMBL; AE003800; AAF57714.1; --
 DR EMBL; AY084100; AAL89838.1; --
 DR FlyBase; FBgn0034327; CGI4505.
 DR InterPro; IPR007967; DUF727.
 DR Pfam; PF05503; DUF727; 1.
 SQ SEQUENCE 119 AA; 13534 MW; 83FA23FCCCE389AA CRC64;
 Query Match 95.0%; Score 19; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred.No. 2.le+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 QY ||||
 QY 33 VAEF 36
 Db
 RESULT 12
 GTR_PIG STANDARD; PRT; 120 AA.
 ID GTR_PIG
 AC G62786;
 DT 28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 2
(Glucose transporter type 2, liver) (Fragment).
SLC2A2 OR GLUT2.

Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]

SEQUENCE FROM N.A.

Canty J.M., Young R.F., Fallavollita J.A.;

Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Facilitative glucose transporter. This isoform likely
mediates the bidirectional transfer of glucose across the plasma
membrane of hepatocytes and is responsible for uptake of glucose

by the beta cells; may comprise part of the glucose-sensing
mechanism of the beta cell. May also participate with the
Na(+)/glucose cotransporter in the transcellular transport of
glucose in the small intestine and kidney (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to the sugar transporter family. Glucose
transporter subfamily.

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EMBL; AF054835; AAC12737.1; -.

InterPro; IPR007114; MFS.

InterPro; IPR005828; Sub transporter.

InterPro; IPR005829; Sug transporter.

InterPro; IPR003663; Sug transprt.

Pfam; PF00083; sugax tr; 1.

PRINTS; PR00171; SUGTRNSPT.

PROSITE; PS00850; MFS; 1.

PROSITE; PS00216; SUGAR TRANSPORT 1; PARTIAL.

PROSITE; PS00217; SUGAR TRANSPORT 2; PARTIAL.

Transmembrane; Sugar transport; Transport; Multigene family.

NON TER 1 1

TRANSMEM 2 22

DOMAIN 23 26

TRANSMEM 27 47

DOMAIN 48 56

TRANSMEM 57 77

DOMAIN 78 84

TRANSMEM 85 105

DOMAIN 106 120

NON TER 120 120

SEQUENCE 120 AA; 13503 MW; DSF73168DBF03203 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 120;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5

46 VAEF 49

RESULT 13

18E_PYPRAE STANDARD; PRT; 122 AA.

Q8ZYQ2;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

50S ribosomal protein L18e.

RPL18E OR PAE0672.

Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
[1]

SEQUENCE FROM N.A.

STRAIN=IM2 / ATCC 51768 / DSM 7523;

MEDLINE=21664397; PubMed=11792869;

Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

Miller J.H.;

"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum

aerophilum".

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.

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EMBL; AE009779; AAL62941.1; -.

HMAP; MF 00329; -; 1.

InterPro; IPR001196; Ribosomal L15.

InterPro; IPR000039; Ribosomal_L18e.

Pfam; PF00256; L15; 1.

PROSITE; PS01106; RIBOSOMAL_L18E; FALSE NEG.

Ribosomal protein; Complete proteome.

SEQUENCE 122 AA; 88F3DB732C4E0394 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 122;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

35 VAEF 38

RESULT 14

Y670_PASMU

ID Y670_PASMU STANDARD; PRT; 124 AA.

AC Q9CWF0;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Hypothetical protein PM0670 precursor.

PM0670.

Pasteurella multocida.

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

Pasteurellaceae; Pasteurella.

NCBI_TaxID=747;

[1]

SEQUENCE FROM N.A.

STRAIN=Pm70;

MEDLINE=21145866; PubMed=11248100;

May B.J., Zhang Q., Li L.I., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-!- SIMILARITY: Belongs to the cytochrome b562 family.

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EMBL; AE006103; AAK02754.1; -.

PIRSF; PIRSF000029; Cytochrome_b562; 1.

W Hypothetical protein; Signal; Complete proteome.
T SIGNAL 1 23 POTENTIAL
T CHAIN 24 124 HYPOTHETICAL PROTEIN PM0670.
Q SEQUENCE 124 AA; 13746 MW; D7B2B485C7B51B9A CRC64;

Query Match 95.0%; Score 19; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 45 VAEF 48
|||||
45 VAEF 48

RESULT 15
LBP_MOUSE
D _LBP_MOUSE STANDARD; PRT; 127 AA.
IC PS1162;
IT 01-OCT-1996 (Rel. 34, Created)
IT 01-OCT-1996 (Rel. 34, Last sequence update)
IT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Gastrin (GR) (ileal lipid-binding protein) (ILBP).
DE FASP6 OR ILBP.
MS Mus musculus (Mouse).
XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
XN NCBI_TaxID=10090;
XN [1]
IP SEQUENCE FROM N.A.
IC STRAIN=DNA/2J; TISSUE=Liver;
IC MEDLINE=94375529; PubMed=9089185;
IA Crossman M.W., Haut S.M., Gordon J.I.;
IA "The mouse ileal lipid-binding protein gene: a model for studying
IL axial patterning during gut morphogenesis."; J. Cell Biol. 126:1547-1564 (1994).
XC -!- FUNCTION: ILEAL PROTEIN WHICH STIMULATES GASTRIC ACID AND
XC PEPSINOGEN SECRETION. SEEMS TO BE ABLE TO BIND TO BILE SALTS AND
XC BILIURINS.
XC -!- SUBCELLULAR LOCATION: Cytoplasmic.
XC -!- SIMILARITY: Belongs to the fatty-acid binding protein (FABP)
XC family.

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XR EMBL; U00938; AAC27352.1; --
XR PIR; A54797; A54797.
XR HSSP; P10289; 1EAL.
XR MGD; MGI:96565; Fabp6.
XR InterPro; IPR000463; Fatty acid BP.
XR InterPro; IPR000566; Lipocalin_cyFABP.
XR Pfam; PF00061; Lipocalin; 1.
XR PRINTS; PR00178; FATTYACIDBP.
XR PROSITE; PS00214; FABP; 1.
CW Transport; Lipid-binding; Acetylation.
FT INIT MET 0
FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD RES 1 1 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 127 AA; 14355 MW; 0690BDD0A9CD922 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
b 91 VAEF 94
|||||

RESULT 16
SPEH_THEME STANDARD; PRT; 130 AA.
AC Q9WZC3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC)
DE (SambC) [Contains: S-adenosylmethionine decarboxylase beta chain; S-
DE adenosylmethionine decarboxylase alpha chain].
GN SPEH OR TM0655.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
XN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=MSB8 / DSM 3109 / ATCC 43589;
RC MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."; Nature 399:323-329 (1999).
RL Nature 399:323-329 (1999).
CC -!- FUNCTION: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine biosynthesis from
CC putrescine (By similarity).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
CC adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
CC -!- COFACTOR: Pyruvoyl group (By similarity).
CC -!- SIMILARITY: Belongs to the prokaryotic AdoMetDC family. Subfamily
CC 1.

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XC or send an email to license@sib-sib.ch).

XR EMBL; AE001739; AAD35739.1; --
XR PIR; D72348; D72348.
XR TIGR; TM0655; --
XR HAMAP; MF_00464; -- 1.
XR InterPro; IPR003826; SAMDC.
XR Pfam; PF02675; AdoMetDC; 1.
XR Spermidine biosynthesis; Lyase; Decarboxylase; Zymogen; Pyruvate;
KW Complete proteome.
KW CHAIN 1 62 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
FT CHAIN (BY SIMILARITY).
FT CHAIN 63 130 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
FT SITE 62 63 CHAIN (BY SIMILARITY).
FT MOD_RES 63 63 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
FT MOD_RES 63 63 CONVERTED TO A PYRUVOL GROUP (BY
FT SIMILARITY).
SQ SEQUENCE 130 AA; 14785 MW; 7659FE20A2019928 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 9 VAEF 12
|||||

RESULT 17
Y194_PYRAB
ID Y194_PYRAB STANDARD; PRT; 131 AA.

Q9V280;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HYPOTHETICAL UPF0146 protein PYRAB01940.
PYRAB01940 OR PAB2224.
Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
Pyrococcus.
NCBI_TaxID=29292;
[1]
SEQUENCE FROM N.A.
STRAIN=GES / Orsay;
MEDLINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
Poch O., Priet D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.,
"An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).
-!- SIMILARITY: Belongs to the UPF0146 family.

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EMBL; AJ248283; CAB49118.1; --
PIR; G75208; G75208.
HAWAP; MF_00341; --; 1.
InterPro; IPR005353; UPF0146.
Pfam; PF03686; UPF0146; 1.
PIRSF; PIRSF016725; UCP016725; 1.
ProDom; PD021130; UPF0146; 1.
HYPOTHETICAL PROTEIN; Complete proteome.
SEQUENCE 131 AA; 14629 MW; D13F37818F932C3 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
4 VAEF 7

RESULT 18
ISB_HALM1 STANDARD; PRT; 133 AA.
O9HRM5;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
(lumazine synthase) (Riboflavin synthase beta chain).
R1BH OR R1BE OR VNG0630G.
X Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
[1]
SEQUENCE FROM N.A.
MEDLINE=20504483; PubMed=11016950;
Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir J., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angelvine C.M., Dale H.,
Tsenbarger T.A., Peck R.F., Pohlshocher M., Spudis J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
ribityl-amino-2,4-(1H,3H)-pyrimidinedione and L-3,4-dihydroxy-2-
butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-
2,4-(1H,3H)-pyrimidinedione with L-3,4-dihydroxy-2-butanone-4-
phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
CC riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
CC -!- PATHWAY: Riboflavin biosynthesis; last step.
CC -!- SIMILARITY: Belongs to the DMRL synthase family.

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EMBL; AE005011; AAC19133.1; --
PIR; A84221; A84221.
HAWAP; MF_00178; --; 1.
InterPro; IPR002180; DMRL synthase.
Pfam; PF00885; DMRL synthase; 1.
ProDom; PD003664; DMRL synthase; 1.
KW Riboflavin biosynthesis; Transferase; Complete proteome.
SQ SEQUENCE 133 AA; 13719 MW; B9724DC24660D6CD CRC64;

Query Match 95.0%; Score 19; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
8 VAEF 11

RESULT 19
YBGC_ECOLI STANDARD; PRT; 134 AA.
ID_YBGC_ECOLI
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein ybGC.
GN YBGC OR B0736 OR C0815 OR Z0904 OR ECS0771 OR SF0561 OR S0574.
OS Escherichia coli.
OS Escherichia coli O6.
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=E.coli;
RC MEDLINE=8722192; PubMed=3294803;
RX "Nucleotide sequence of a gene cluster involved in entry of E colicins
and single-stranded DNA of infecting filamentous bacteriophages into
Escherichia coli.";
RT J. Bacteriol. 169:2667-2674(1987).
RL [2]
RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
A Mau B., Shao Y.;
"The complete genome sequence of *Escherichia coli* K-12.";
Science 277:1453-1474(1997).
[3]
P SEQUENCE FROM N.A.
C SPECIES=E.coli; STRAIN=K12;
X MEDLINE=97061202; PubMed=8905232;
A Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
A Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
A Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
A Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
A Yano M., Horiuchi T.;
T "A 718-Kb DNA sequence of the *Escherichia coli* K-12 genome
I corresponding to the 12.7-28.0 min region on the linkage map.";
L DNA Res. 3:137-155(1996).
[4]
P SEQUENCE FROM N.A.
C SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
X MEDLINE=22388234; PubMed=12471157;
A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
T "Extensive mosaic structure revealed by the complete genome sequence
I of uropathogenic *Escherichia coli* K1";
L Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
[5]
P SEQUENCE FROM N.A.
C SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
X MEDLINE=21074935; PubMed=11206551;
A Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
A Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
A Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
A Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
A Welch R.A., Blattner F.R.;
T "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";
L Nature 409:529-533(2001).
[6]
P SEQUENCE FROM N.A.
C SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
X MEDLINE=21156231; PubMed=11258796;
A Hayaishi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
A Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
A Kuhara S., Shiba T., Hattori M., Shinagawa H.;
T "Complete genome sequence of enterohemorrhagic *Escherichia coli*
I O157:H7 and genomic comparison with a laboratory strain K-12.";
L DNA Res. 8:11-22(2001).
[7]
P SEQUENCE OF 1-20 FROM N.A.
C SPECIES=E.coli; STRAIN=K12 / MGL1655;
X Kim K., Allen E., Araujo R., Aparicio A.M., Botstein D.,
A Cherry M., Chung E., Dietrich F., Duncan M., Federspiel N.,
A Kaiman S., Komp C., Lashkari D., Lew H., Lin D., Namath A.,
A Osiner P., Davis R.;
L Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[8]
P SEQUENCE FROM N.A.
C SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
X MEDLINE=22272406; PubMed=12384590;
A Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
A Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
A Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Hou S.,
A Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Chen Y.,
A Yu J.;
T "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
I through comparison with genomes of *Escherichia coli* K12 and O157";
L Nucleic Acids Res. 30:4432-4441(2002).
[9]
P SEQUENCE FROM N.A.
C SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
X MEDLINE=22590274; PubMed=12704152; Venkatesan M.M., Deng W.,
A Wei J., Goldberg M.B., Burland V., Plunkett G. III, Rose D.J., Darling A.,
A Fournier G., Mayhew G.F., Flannick G., Plunkett G. III, Rose D.J., Darling A.,
A Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
A Schwartz D.C., Blattner F.R.;
T "Complete genome sequence and comparative genomics of *Shigella*
I flexneri serotype 2a strain 2457T";
L Infect. Immun. 71:2775-2786(2003).
[10]
P IDENTIFICATION BY MASS SPECTROMETRY.
C SPECIES=E.coli;
X MEDLINE=99420866; PubMed=10493123;
A Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
T "Enrichment of low abundance proteins of *Escherichia coli* by
I hydroxyapatite chromatography";
L Electrophoresis 20:2181-2195(1999).
CC -!- SIMILARITY: BELONGS TO THE 4-HYDROXYBENZOVYL-COA THIOESTERASE
FAMILY. STRONG, TO H.INFLUENZAE HI0386.
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CC -----
DR EMBL: M16489; AAA83918.1; -
DR EMBL: AE000177; AAC73830.1; -
DR EMBL: D90713; BAA35402.1; -
DR EMBL: AE016757; AAN79288.1; -
DR EMBL: AE005252; AAG55072.1; -
DR EMBL: AP002553; BAB34194.1; -
DR EMBL: U30934; AAA74398.1; -
DR EMBL: AE015086; AAN42205.1; -
DR EMBL: AE015979; AAP16078.1; -
DR PIR: A35980; WMEC15.
DR PIR: C90725; C90725.
DR PIR: D85576; D85576.
DR EcoGene: EG11110; ybgC.
DR InterPro: IPR008272; 4HBcoA_thioest_AS.
DR InterPro: IPR006684; 4HBcoA_thioestise.
DR InterPro: IPR006683; Thioestr_supf.
DR Pfam: PF03061; 4HET; 1
DR TIGRFAMs: TIGR00051; TIGR00051; 1
DR PROSITE: PS01328; 4HBcoA_THIOESTERASE; 1.
KW Hydrolase; Complete proteome.
FT ACT SITE 18 18 BY SIMILARITY.
SQ SEQUENCE 134 AA; 15562 MW; C44582B6EC3BE989 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 134;
Best Local Similarity 100.0%; Pred.No. 2.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;
QY 2 VAEF 5
DB 129 VAEF 132
RESULT 20
RIBB METTH STANDARD; PRT; 139 AA.
AC 027453;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6,7-dimethyl-8-ribitylumazine synthase (EC 2.5.1.9) (DMRL synthase)
DE (lumazine synthase) (Riboflavin synthase beta chain).
GN RIBB OR MTH1390.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.

NCBI_TaxID=187420;

[1]
SEQUENCE FROM N.A.
STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang I., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shmer G., Goyal A., Pietrowski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
*Complete genome sequence of Methanobacterium thermocautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).

-I- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
ribityl-amino-2,4-(1H,3H)-pyrimidinedione and L-3,4-dihydroxy-2-
butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-amino-
2,4-(1H,3H)-pyrimidinedione with L-3,4-dihydroxy-2-butanone-4-
phosphate yielding 6,7-dimethyl-8-lumazine (By similarity).

-I- CATALYTIC ACTIVITY: 2,6,7-dimethyl-8-(1-D-ribityl)lumazine =
riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

-I- PATHWAY: Riboflavin biosynthesis; last step.

-I- SIMILARITY: Belongs to the DMRL synthase family.

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EMBL; A5000902; AB85867.1; -;
PIR; A69052; A69052.
HSP; P11998; IRV.
HAMAP; MF_00178; -; 1.
InterPro; IPR002180; DMRL synthase.
Pfam; PF00885; DMRL synthase; 1.
ProDom; PD003664; DMRL synthase; 1.
TIGRfam; TIGR00114; ribH; 1.
Riboflavin biosynthesis; Transference; Complete proteome.
SEQUENCE 139 AA; 15464 MW; B640D8D12EE2A962 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
10 VAEF 13

SULT 21
86 ARCFCU STANDARD; PRT; 140 AA.
Q29669;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF0586.
AF0586.
Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
[1]

SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,


```

CC -!- SIMILARITY: Contains 3 EF-hand calcium-binding domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB036744; BAA95412.1; -.
CC DR EMBL; AK009956; BAB26608.1; -.
CC DR EMBL; AK009664; BAB26425.1; -.
CC DR EMBL; AK003648; BAB22914.1; -.
CC DR HSSP; P02593; 1CDM.
CC DR MGD; MGI:1931464; Calm4
CC DR InterPro; IPR002048; EF-hand.
CC DR InterPro; IPR001125; Recoverin.
CC DR Pfam; PF00036; ehand; 4.
CC DR PRINTS; PRO0450; RECOVERIN.
CC DR ProDom; PD000012; EF-hand; 2.
CC DR SMART; SM00054; EFh; 4.
CC DR PROSITE; PS00018; EF-hand; 3.
CC KW Calcium-binding; Repeat.
CC FT CA_BIND 21 32 EF-HAND 1 (POTENTIAL).
CC FT CA_BIND 57 68 EF-HAND 2 (POTENTIAL).
CC FT CA_BIND 93 104 EF-HAND 3 (POTENTIAL).
CC FT CONFLICT 9 9 E -> V (IN REF. 2; BAB22914).
CC FT CONFLICT 124 124 M -> V (IN REF. 2; BAB22914).
CC FT CONFLICT 146 148 VEN -> I (IN REF. 1).
CC SQ SEQUENCE 148 AA; 16767 MW; 2AE22BC738AD2F9D CRC64;
CC
CC Query Match 95.0%; Score 19; DB 1; Length 148;
CC Best Local Similarity 100.0%; Pred. No. 2.6e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 VAEF 5
CC DB 10 VAEF 13
CC
CC RESULT 25
CC VORX_PYRO STANDARD; PRT; 148 AA.
CC AC P02598;
CC JT 01-FEB-1991 (Rel. 17, Created)
CC JT 01-FEB-1991 (Rel. 17, Last sequence update)
CC JT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical protein in GAPDH 3'region (ORF X) (Fragment).
CC VS Pyrococcus woesei.
CC JC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC XN NCBI_TaxID=2262;
CC XN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=DSM 3773;
CC XX MEDLINE=90330536; PubMed=2165475;
CC XX Zwickl P., Fabry S., Bogaedain C., Haas A., Hensel R.;
CC XT "Glyceroldehyde-3-phosphate dehydrogenase from the hyperthermophilic
CC XT archaeobacterium Pyrococcus woesei: characterization of the enzyme,
CC XT cloning and sequencing of the gene, and expression in Escherichia
CC XT coli.";
CC XL J. Bacteriol. 172:4329-4338(1990).
CC DR PIR; S10655; S10655.
CC KW Hypothetical protein.
CC FT NON_TER 1
CC SQ SEQUENCE 148 AA; 15256 MW; 8C7E51A072DF5D50 CRC64;
CC
CC Query Match 95.0%; Score 19; DB 1; Length 148;
CC Best Local Similarity 100.0%; Pred. No. 2.6e+02;
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC YJ 2 VAEF 5

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DB 115 VAEF 118
DB [1]
DB RESULT 26
DB RISE_PYRAE STANDARD; PRT; 150 AA.
DB AC Q82TE3;
DB DT 10-OCT-2003 (Rel. 42, Created)
DB DT 10-OCT-2003 (Rel. 42, Last sequence update)
DB DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB DE 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)
DB DE (Lumazine synthase) (Riboflavin synthase beta chain).
DB GN RIBH OR PAE3296.
DB OS Pyrobaculum aerophilum.
DB OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
DB OC Thermoproteaceae; Pyrobaculum.
DB OX NCBI_TaxID=13773;
DB RN [1]
DB RP SEQUENCE FROM N.A.
DB RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
DB RX MEDLINE=21664397; PubMed=11792869;
DB RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
DB RA Miller J.H.;
DB RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
DB RT aerophilum.";
DB RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DB CC -!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex
DB CC catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-
DB CC ribityl-amino-2,4(1H,3H)-pyrimidinone and L-3,4-dihydroxy-2-
DB CC butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit
DB CC catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-
DB CC amino-2,4(1H,3H)-pyrimidinone with L-3,4-dihydroxy-2-
DB CC butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By
DB CC similarity)
DB CC -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =
DB CC riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
DB CC -!- PATHWAY: Riboflavin biosynthesis; last step.
DB CC -!- SIMILARITY: Belongs to the DMRL synthase family.
DB CC
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DB CC or send an email to license@isb-sib.ch).
DB CC -----
DB CC EMBL; AE009923; AAL64819.1; -.
DB DR HAVAP; MF 00178; -.
DB DR InterPro; IPR002180; DMRL_synthase.
DB DR Pfam; PF00885; DMRL_synthase; 1.
DB DR ProDom; PD003664; DMRL_synthase; 1.
DB DR TIGRFAMs; TIGR00114; RibH; 1.
DB KW Riboflavin biosynthesis; Transferase; Complete proteome.
DB SQ SEQUENCE 150 AA; 16474 MW; 73751C1363A8AD8D CRC64;
DB
DB Query Match 95.0%; Score 19; DB 1; Length 150;
DB Best Local Similarity 100.0%; Pred. No. 2.6e+02;
DB Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB
DB QY 2 VAEF 5
DB DB 8 VAEF 11
DB [1]
DB DB RESULT 27
DB SODC_PRIGL STANDARD; PRT; 152 AA.
DB ID SODC_PRIGL
DB AC P11418;
DB DT 01-OCT-1989 (Rel. 12, Created)
DB DT 01-OCT-1989 (Rel. 12, Last sequence update)
DB DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1).

OS Prionace glauca (Blue shark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;

OC Carcharhinidae; Prionace.

OX NCBI_TaxID=7815;

RN [1]

RP SEQUENCE.

RX MEDLINE=89290032; PubMed=2500367;

RA Calabrese L., Politelli F., O'Neill P., Gallieri A., Barra D.,

RA Schinina M.E., Bossa F.;

RT "Substitution of arginine for lysine 134 alters electrostatic

RT parameters of the active site in shark Cu,Zn superoxide dismutase.";

RL FEBS Lett. 250:49-52(1989).

CC -!- FUNCTION: Destroys radicals which are normally produced within the

CC cells and which are toxic to biological systems.

CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

DR PIR; S04623; S04623.

DR HSSP; P00442; 1CEJ.

DR InterPro; IPR001424; SOD_CU_ZN.

DR Pfam; PF00080; sdcu; 1.

DR PRINTS; PR00068; CUZNDISMTASE.

DR ProDom; PD000469; SOD_CU_ZN_1.

DR PROSITE; PS00087; SOD_CU_ZN_1; 1.

DR PROSITE; PS00332; SOD_CU_ZN_2; 1.

KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc.

FT METAL 44 44

FT METAL 46 46 COPPER.

FT METAL 61 61 COPPER AND ZINC.

FT METAL 69 69 ZINC.

FT METAL 78 78 ZINC.

FT METAL 81 81 ZINC.

FT METAL 118 118 COPPER.

FT DISULFID 55 144 BY SIMILARITY.

SQ SEQUENCE 152 AA; 15840 MW; 6617642A4F23C5AE CRC64;

Query Match 95.0%; Score 19; DB 1; Length 152;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

Db 92 VAEF 95

RESULT 28

RISB_SULSO

ID RISB_SULSO STANDARD; PRT; 154 AA.

AC Q990B5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)

DE (lumazine synthase) (Riboflavin synthase beta chain).

GN RIBH OR SSO0400.

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=2287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35092 / DSM 1617 / B2;

RX MEDLINE=21332296; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Aways M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,

RA De Moors A., Traus G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

CC -!- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex

CC catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-

CC ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydroxy-2-

CC butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit

CC catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-

CC amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydroxy-2-

CC butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By

CC similarity).

CC -!- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1'-D-ribityl)lumazine =

CC riboflavin + 4-(1'-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

CC -!- PATHWAY: Riboflavin biosynthesis; last step.

CC -!- SIMILARITY: Belongs to the DMRL synthase family.

CC -!- SIMILARITY: Belongs to the DMRL synthase family.

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CC -----

DR EMBL; AE006673; AAK40729.1; -.

DR PIR; B90184; B90184.

DR HAMAP; MF 00178; -; 1.

DR InterPro; IPR002180; DMRL synthase.

DR Pfam; PF00885; DMRL synthase; 1.

DR ProDom; PD003664; DMRL synthase; 1.

DR TIGRfams; TIGR00114; r1bH; 1.

KW Riboflavin biosynthesis; Transferase; Complete proteome.

SQ SEQUENCE 154 AA; 17247 MW; ADPA9B6A2C723210 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

Db 12 VAEF 15

RESULT 29

PCP_HABIN

ID PCP_HABIN STANDARD; PRT; 155 AA.

AC P10325;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL

DE cross-reacting lipoprotein).

GN PCP OR LPP OR H1579.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OX NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=88115138; PubMed=2828309;

RX Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;

RT "Cloning of genes encoding a 15,000-dalton peptidoglycan-associated

RT outer membrane lipoprotein and an antigenically related 15,000-dalton

RT protein from *Haemophilus influenzae*.";

RL J. Bacteriol. 170:489-498(1988).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 Science 269:496-512(1995).
 -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
 anchor.

-1- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLVB AND TO
 Y. ENTEROCOLITICA PCP.

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EMBL; M18877; AAA24938.1; --
 EMBL; U32832; AAC23228.1; --
 PIR; I64130; I64130.

TIGR; H11579; --
 InterPro; IPR000437; Prok lipoprot. S.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Signal; Complete proteome; Palmitate.

SIGNAL 1 18

CHAIN 19 155 OUTER MEMBRANE LIPOPROTEIN PCP.

LIPID 19 19 N-palmitoyl cysteine.

LIPID 19 19 S-diacylglycerol cysteine.

CONFLICT 135 143 CSIVAEFVF -> VAGKRVRI (IN REF. 1).

SEQUENCE 155 AA; 15425 MW; D7880327FCFC0985 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 155;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5

||||

138 VAEF 141

SULT 30

P_TAROF STANDARD; PRT; 157 AA.

O49065;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Root allergen protein (RAP).

Taraxacum officinale (Common dandelion).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;

Taraxacum.

NCBI_TaxID=50225;

[1]

SEQUENCE FROM N.A.

TISUS=Root;

Xu X.-Y., Bewley J.D., Greenwood J.S.;

Submitted (DRC-1997) to the EMBL/GenBank/DBJ databases.

-1- ALLERGEN: Causes an allergic reaction in human.

-1- SIMILARITY: Belongs to the BetVI family.

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CC EMBL; AF036931; AAB92255.1; --
 DR HSP; O24248; IE09.
 DR InterPro; IPR000916; Bet v.I.
 DR Pfam; PF00407; Bet v.I; 1
 DR PRINTS; PR00634; BETALLERGEN.
 DR PROSITE; PS00451; PATHOGENESIS-RELATED PROTEIN.
 KW Allergen; Plant defense; Pathogenesis-related protein.
 SQ SEQUENCE 157 AA; 17040 MW; 5892AB8593A8A7E0 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 157;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5

||||

Db 3 VAEF 6

RESULT 31

RISB SULTO

ID RISB SULTO STANDARD; PRT; 157 AA.

AC Q975N5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9) (DMRL synthase)

DE (lumazine synthase) (Riboflavin synthase beta chain).

GN RIBH OR ST0394.

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Sulfolobus.

OX NCBI_TaxID=111955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RC MEDLINE=21456156; PubMed=11572479;

RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

RA Oshima T., Kikuchi H.;

RT "Complete genome sequence of an aerobic thermophilic

RT Crenarchaeon, Sulfolobus tokodaii strain7.";

RL DNA Res. 8:123-140(2001).

CC -1- FUNCTION: Riboflavin synthase is a bifunctional enzyme complex

CC catalyzing the formation of riboflavin from 5-amino-6-(1'-D)-

CC ribityl-amino-2,4(1H,3H)-pyrimidinedione and L-3,4-dihydroxy-2-

CC butanone-4-phosphate via 6,7-dimethyl-8-lumazine. The beta subunit

CC catalyzes the condensation of 5-amino-6-(1'-D)-ribityl-

CC amino-2,4(1H,3H)-pyrimidinedione with L-3,4-dihydroxy-2-

CC butanone-4-phosphate yielding 6,7-dimethyl-8-lumazine (By

CC similarity).

CC -1- CATALYTIC ACTIVITY: 2 6,7-dimethyl-8-(1-D-ribityl)lumazine =

CC riboflavin + 4-(1-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.

CC -1- PATHWAY: Riboflavin biosynthesis; last step.

CC -1- SIMILARITY: Belongs to the DMRL synthase family.

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CC EMBL; AP000982; BAB65375.1; --

DR HAMAP; MF_00178; 1

DR InterPro; IPR002180; DMRL synthase.

DR Pfam; PF00885; DMRL synthase; 1.

DR ProDom; PD003664; DMRL synthase; 1.

DR TIGRFAMs; TIGR00114; ribH; 1.

W Riboflavin biosynthesis; Transferase; Complete proteome.
 2 SEQUENCE 157 AA; 17501 MW; 529558077E164A18 CRC64;
 Query Match 95.0%; Score 19; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 b 14 VAEF 17
 RESULT 32
 D SG55 DROME STANDARD; PRT; 163 AA.
 C P07701; Q9VE1S;
 T 01-APR-1988 (Rel. 07, Created)
 T 01-APR-1988 (Rel. 07, Last sequence update)
 T 10-OCT-2003 (Rel. 42, Last annotation update)
 E Salivary glue protein sgs-5 precursor.
 N SG55 OR CG7596.
 S Drosophila melanogaster (Fruit fly).
 C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 C Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 C Ephydroidea; Drosophilidae; Drosophila.
 X NCBI_TaxID=7227;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=Oregon-R;
 C MEDLINE=87086754; PubMed=3098981;
 A Shore E.M., Guild G.M.;
 T "Larval salivary gland secretion proteins in Drosophila structural
 analysis of the sgs-5 gene."
 J. Mol. Biol. 190:149-158(1986).
 N [2]
 P SEQUENCE FROM N.A.
 C STRAIN=Beckley;
 A Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 A Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 A Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 A Wan K.H., Doyle E.G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 A Beeson K.Y., Betos P.V., Berland B.P., Bhandari D., Bolshakov S.,
 A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 A Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 A Foaier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 A Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 A Harris N.B., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 A Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 A Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 A Mount S.M., Moy M., Murphy B., Murphy L., Murthy D.M., Nelson D.B.,
 A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 A Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 A Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 A Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 A Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 A Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
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 CC -----
 DR ENBL; X04269; CA227820.1; -;
 DR EMBL; AE003718; RAP55436.1; -;
 DR PIR; A24504; A24504.
 DR FlyBase; FBgn0003375; Sgs5.
 KW Signal.
 FT SIGNAL. 1 18 POTENTIAL.
 PT CHAIN 19 163 SALIVARY GLUE PROTEIN SGS-5.
 SQ SEQUENCE 163 AA; 18821 MW; 3A476F1D3B06D864 CRC64;
 Query Match 95.0%; Score 19; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 DB 114 VAEF 117
 RESULT 33
 ID UTRS YEAST STANDARD; PRT; 166 AA.
 AC P32630;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE UTRS protein (unknown transcript 5 protein).
 GN UTRS OR YEL035C OR SGP-ORF27.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B-6441;
 RX MEDLINE=94016558; PubMed=8411151;
 RA Melnick L., Sherman F.;
 RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
 RL of Saccharomyces cerevisiae share a common ancestry."
 J. Mol. Biol. 233:372-388(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313264; PubMed=9169868;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunkeler-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."
 RL Nature 387:78-81(1997).
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EMBL; L22173; AAA34936.1; -
EMBL; S65964; AAD13970.1; -
EMBL; S66120; AAB28442.1; -
EMBL; U18779; AAB65007.1; -
PIR; S50509; S50509.
GermOnline; 139039; -
SGD; S0000761; UTR5.
CONFLICT 1 20 MRYGKLVHYIIVHDDOR -> MRDSNVKISVFPICALYN
RGNTIN (IN REF. 1).
SEQUENCE 166 AA; 19335 MW; A58E89DFA6D3DEA CRC64;
Query Match 95.0%; Score 19; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
92 VAEF 95
SULT 34
B_RHOBA
SSB_RHOBA STANDARD; PRT; 169 AA.
P59932; Q7UKV3;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Single-strand binding protein (SSB) (Helix-destabilizing protein).
SSB OR R89917.
Rhodospirillum rubrum.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
[1]
SEQUENCE FROM N.A.
STRAIN=1;
MEDLINE=2735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1".
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
-!- FUNCTION: This protein is essential for replication of the
chromosome. It is also involved in DNA recombination and repair
(By similarity).
-!- SIMILARITY: Contains 1 SSB domain.

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EMBL; BX294150; CAD76529.1; -
PROSITE; PS50935; SSB; 1.
DNA-binding; DNA repair; DNA replication; Complete proteome.
DOMAIN 4 107
DOMAIN 113 121 POLY-GLY.
SEQUENCE 169 AA; 18108 MW; AA8F93E0FA51F287 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
28 VAEF 31
RESULT 35

BFL1 MOUSE
ID BFL1 MOUSE STANDARD; PRT; 172 AA.
AC Q07450;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bcl-2-related protein A1 (BFL-1 protein) (Hemopoietic-specific early
response protein) (A1-A).
GN BCL2A1 OR BCL2A1A OR BFL1 OR A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/J; TISSUE=Bone marrow;
RX MEDLINE=93346743; PubMed=8345191;
RA Lin E.Y., Orloffsky A., Berger M.S., Pryatowsky M.B.;
RT "Characterization of A1, a novel hemopoietic-specific early-response
gene with sequence similarity to bcl-2.";
RL J. Immunol. 151:1979-1988(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv; TISSUE=Liver;
RX MEDLINE=98307518; PubMed=9645611;
RA Hatakeyama S., Hamasaki A., Negishi I., Loh D.Y., Sando F.,
RA Nakayama K., Nakayama K.-I.;
RT "Multiple gene duplication and expression of mouse bcl-2-related
genes, A1.";
RL Int. Immunol. 10:631-637(1998).
CC -!- FUNCTION: Retards apoptosis induced by IL-3 deprivation. May
function in the response of hemopoietic cells to external signals
and in maintaining endothelial survival during infection.
CC -!- SUBCELLULAR LOCATION: Intracellular.
CC -!- TISSUE SPECIFICITY: Expressed in hemopoietic tissues, including
bone marrow, spleen and thymus.
CC -!- INDUCTION: By granulocyte-macrophage colony-stimulating factor
and LPS in macrophages.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Belongs to the Bcl-2 family.

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EMBL; L16462; AAA16886.1; -
EMBL; U23774; AAB97953.1; -
EMBL; U23773; AAB97953.1; JOINED.
PIR; I49449; I49449.
HSP; Q07817; IMAZ.
MGD; MGI:102687; Bcl2ala.
DR InterPro; IPR000712; Bcl2 BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SMC0337; BCL; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
KW Apoptosis.
FT DOMAIN 24 33 ALA/PRO-RICH.
FT DOMAIN 77 97 BH1.
FT DOMAIN 132 147 BH2.
SQ SEQUENCE 172 AA; 19914 MW; 37AD35818E756488 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

the first processed in amphibia.":
 J. Biol. Chem. 262:7901-7907(1987).
 [2] X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 MEDLINE=99167924; PubMed=10439069;
 Ha Y., Shi D., Small G.W., Threl E.C., Allewel N.M.;
 "Crystal structure of bullfrog M ferritin at 2.8 A resolution:
 analysis of subunit interactions and the binuclear metal center.";
 J. Biol. Inorg. Chem. 4:243-256(1999).
 -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
 in a soluble, nontoxic, readily available form. The functional
 molecule, which is composed of 24 chains, is roughly spherical and
 contains a central cavity into which the polymeric ferric iron
 core is deposited.
 -!- MISCELLANEOUS: THERE ARE THREE TYPES OF FERRITIN SUBUNITS: L, M
 AND H CHAINS IN AMPHIBIA.
 -!- SIMILARITY: Belongs to the ferritin family.
 -!- SIMILARITY: Contains 1 ferritin-like diiron domain.

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 EMBL; J02724; AAA49525.1; -;
 PIR; C27805; C27805.
 R PDB; 1MFR; 22-JUN-99.
 R InterPro; IPR001519; Ferritin.
 R InterPro; IPR008331; Ferritin Dps.
 R InterPro; IPR009040; Ferritin_Like.
 R Pfam; PF00210; ferritin; 1.
 R ProDom; PD000971; Ferritin; 1.
 R PROSITE; PS00540; FERRITIN 1; 1.
 R PROSITE; PS00204; FERRITIN 2; 1.
 R PROSITE; PS09095; FERRITIN LIKE; 1.
 W Iron storage; Iron; Metal-binding; 3D-structure.
 T DOMAIN 7 156 FERRITIN-LIKE DIIRON.
 T METAL 24 24 IRON (BY SIMILARITY).
 T METAL 58 58 IRON (BY SIMILARITY).
 T METAL 59 59 IRON (BY SIMILARITY).
 T METAL 62 62 IRON (BY SIMILARITY).
 T METAL 104 104 IRON (BY SIMILARITY).
 T METAL 138 138 IRON (BY SIMILARITY).
 T HELIX 11 39
 T TURN 41 43
 T HELIX 46 73
 T TURN 74 74
 T STRAND 82 82
 T HELIX 93 120
 T TURN 121 122
 T HELIX 124 133
 T TURN 134 134
 T HELIX 135 154
 T TURN 155 159
 T HELIX 161 170
 T TURN 171 171
 Q SEQUENCE 176 AA; 20592 MW; A9F0F5EB8584D46 CRC64;

 Query Match 95.0%; Score 19; DB 1; Length 176;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 2 VAEF 5
 48 VAEF 51

 RESULT 38
 RL10_THETN STANDARD; PRT; 177 AA.
 ID _RL10_THETN

Q8R7U4;
 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L10.
 GN REPLJ OR TTE2304.
 OS Thermotoga bacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermotogabacteriales;
 OC Thermotogabacteriaceae; Thermotogabacter.
 OX NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 110007;
 RX MEDLINE=21392816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 Tan H., Chen R., Wang J., Yu J., Yang H.;
 "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 CC -!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
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 EMBL; AB013173; AAM25445.1; -;
 DR HAMAP; MF 00362; -; 1.
 DR InterPro; IPR001790; Ribosomal_L10.
 DR InterPro; IPR002363; Ribosomal_L10eub.
 DR Pfam; PF00466; Ribosomal_L10; 1.
 DR PROSITE; PS01109; RIBOSOMAL_L10; FALSE NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 177 AA; 19591 MW; 50DDCF896F6F4E8 CRC64;

 Query Match 95.0%; Score 19; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 12 VAEF 15

 RESULT 39
 DSBB_PASMU STANDARD; PRT; 178 AA.
 ID DSBB_PASMU
 AC Q9L6B3; P57804;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Disulfide bond formation protein B (Disulfide oxidoreductase).
 GN DSBB OR PM0046.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 "Complete genomic sequence of Pasteurella multocida Pm70.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

CC -|- FUNCTION: Required for disulfide bond formation in some
 CC periplasmic proteins. Acts by oxidizing the dsba protein (By
 CC similarity).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -|- SIMILARITY: Belongs to the dsbB family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch.
 CC
 CC EMBL; AF237925; AAF68411.1; -;
 CC EMBL; AE006038; AAK02130.1; -;
 CC HAMAP; MF_00286; -; 1.
 CC InterPro; IPR003752; DsbB.
 CC Pfam; PF02600; DsbB; 1.
 CC
 CC Oxidoreductase; Redox-active center; Transport; Electron transport;
 CC Chaperone; Transmembrane; Inner membrane; Complete proteome.
 CC
 CC DOMAIN 1 14
 CC CYTOPLASMIC (POTENTIAL).
 CC POTENTIAL.
 CC TRANSMEM 15 31
 CC PERIPLASMIC (POTENTIAL).
 CC DOMAIN 32 49
 CC POTENTIAL.
 CC TRANSMEM 50 65
 CC POTENTIAL.
 CC DOMAIN 66 72
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 73 90
 CC POTENTIAL.
 CC DOMAIN 91 145
 CC PERIPLASMIC (POTENTIAL).
 CC TRANSMEM 146 164
 CC POTENTIAL.
 CC DOMAIN 165 177
 CC REDOX-ACTIVE (BY SIMILARITY).
 CC DISULFID 41 44
 CC REDOX-ACTIVE (BY SIMILARITY).
 CC DISULFID 105 131
 CC REDOX-ACTIVE (BY SIMILARITY).
 CC SEQUENCE 178 AA; 20036 MW; D2C45BB73B31F0BC CRC64;

Query Match 95.0%; Score 19; DB 1; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 |||||
 Db 108 VAEF 111

RESULT 40
 ESM5 DROME STANDARD; PRT; 178 AA.
 AC P13096; Q9YBI8;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enhancer of split m5 protein [E(spl)m5].
 GN HLHWS OR C66096.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89231619; PubMed=2540957;
 RA Klamet C., Knust E., Tietze K., Campos-Ortega J.A.;
 RT "Closely related transcripts encoded by the neurogenic gene complex
 RT enhancer of split of Drosophila melanogaster.";
 RL ENBO J. 8:203-210(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.P., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Bertram D.P., Bhandari D., Bolshakov S.,
 Borikova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Jimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McIsaac M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195(2000).
 [3]
 RN WRPW MOTIF.
 RX MEDLINE=95094252; PubMed=8001118;
 RA Parouh Z., Finley R.L. Jr., Kidd T., Wainwright S.M., Ingham P.W.,
 Brent R., Ish-Horowitz D.;
 RT "Groucho is required for Drosophila neurogenesis, segmentation, and
 RT sex determination and interacts directly with hairy-related bHLH
 RT proteins.";
 RL Cell 79:805-815(1994).
 CC -|- FUNCTION: Participates in the control of cell fate choice by
 CC repressor. Binds DNA on N-box motifs: 5'-CACNAG-3'.
 CC -|- SUBUNIT: Transcription repression requires formation of a complex
 CC with a co-repressor protein (Groucho). Forms homodimers.
 CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -|- DEVELOPMENTAL STAGE: Expressed at the time when separation of
 CC neural and epidermal precursors cells occurs. Mesectodermal
 CC expression appears shortly before the onset of gastrulation.
 CC -|- DOMAIN: The orange domain and the basic helix-loop-helix motif
 CC mediate repression of specific transcriptional activators, such
 CC as basic helix-loop-helix protein dimers.
 CC -|- DOMAIN: The C-terminal WRPW motif is a transcriptional repression
 CC domain necessary for the interaction with Groucho, a
 CC transcriptional co-repressor recruited to specific target DNA by
 CC Hairy-related proteins.
 CC -|- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
 CC -|- SIMILARITY: Contains 1 orange domain.
 CC
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 CC
 CC EMBL; X16552; CAA34552.1; -;
 CC EMBL; AE003754; AAF56552.1; -;
 CC PIR; S03629; S03629.

```
TRANSFAC; T01644; -.
FlyBase; FBgn0002631; HLM5.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003677; P:DNA binding; IDA.
InterPro; IPR001092; P:DNA binding; IDA.
InterPro; IPR003650; Orange.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
SMART; SM00511; ORANGE; 1.
PROSITE; PS00888; HLH; 1.
Transcription regulation; Repressor.
DNA_BIND 19 33 BASIC DOMAIN.
DOMAIN 34 74 HELIX-LOOP-HELIX MOTIF.
DOMAIN 88 129 ORANGE.
DOMAIN 175 178 WRPW MOTIF.
SEQUENCE 178 AA; 19923 MW; 19363D0F6043C84F CRC64;

Query Match 95.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
11111
45 VAEF 48

18 ARCFCU STANDARD; PRT; 178 AA.
O29147;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF1118 precursor.
AF1118.
Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
[1]
-----
SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.P., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.N., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Venter J.C.;
"The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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-----
EMBL; AE001027; AAB90141.1; -.
PIR; E69389; E69389.
TIGR; AF1118; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL 1 20 POTENTIAL.
CHAIN 21 178 HYPOTHETICAL PROTEIN AF1118.

SQ SEQUENCE 178 AA; 19319 MW; 378A4F200240D924 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
11111
155 VAEF 158

APT_HAEDU STANDARD; PRT; 179 AA.
AC QVVKQ4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).
GN APT OR HD1818.
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Johnson L.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Munson R.S., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Catalyzes a salvage reaction resulting in the formation
CC of AMP, that is energetically less costly than de novo synthesis.
CC -!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
CC D-ribose 1-diphosphate.
CC -!- PATHWAY: Purine salvage.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the purine/pyrimidine
CC phosphoribosyltransferase family.
CC
-----
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-----
EMBL; A3017156; AAP96568.1; -.
DR HAMAP; MF_00004; -.
DR InterPro; IPR005764; Ade phspho trans.
DR InterPro; IPR002375; Pr/PY rp transf.
DR InterPro; IPR000836; PRTransferase.
DR Pfam; PF00156; Pribosyltran; 1.
DR TIGRFAMs; TIGR01090; apt; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR TRANSFAC; T000103; PUR_PYR_PR_TRANSFER; 1.
SQ SEQUENCE 179 AA; 19315 MW; 13A1DAFDC13560DF CRC64;
Query Match 95.0%; Score 19; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
11111
45 VAEF 48

RESULT 43
RETB_BOVIN
ID RETB_BOVIN STANDARD; PRT; 183 AA.
AC P18902;
```

01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma retinol-binding protein (PRBP) (RBP).
RBP4.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE.
MEDLINE=91006139; PubMed=2209607;
Berni R., Stoppani M., Zapponi M.C., Meloni M.L., Monaco H.L.,
Zanotti G.;
"The bovine plasma retinol-binding protein. Amino acid sequence,
interaction with transthyretin, crystallization and preliminary X-ray
data.";
Eur. J. Biochem. 192:507-513 (1990).
[2]
SEQUENCE OF 52-183 FROM N.A.
MEDLINE=93385352; PubMed=8373966;
Liu K.H., Dore J.J. Jr., Roberts M.P., Krishnan R., Hopkins F.M.,
Godkin J.D.;
"Expression and cellular localization of retinol-binding protein
messenger ribonucleic acid in bovine blastocysts and extraembryonic
membranes.";
Biol. Reprod. 49:393-400 (1993).
[3]
X-RAY CRYSTALLOGRAPHY.
MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
similarity.";
Biopolymers 32:457-465 (1992).
[4]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=93265508; PubMed=8496140;
Zanotti G., Berni R., Monaco H.L.;
"Crystal structure of liganded and unliganded forms of bovine plasma
retinol-binding protein.";
J. Biol. Chem. 268:10728-10738 (1993).
-!- FUNCTION: Delivers retinol from the liver stores to the peripheral
tissues. In plasma, the RBP-retinol complex interacts with
transthyretin, this prevents its loss by filtration through the
kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.

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EMBL; S65585; AAB28336.1; --
PIR; I46955; I46955.
PIR; S13186; S13186.
PDB; 1ERB; 31-JAN-94.
PDB; 1HBP; 31-JAN-94.
PDB; 1HEQ; 31-JAN-94.
PDB; 1FEL; 01-NOV-94.
PDB; 1PEM; 01-NOV-94.
PDB; 1PEN; 01-NOV-94.
InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocalin_cytFABP.
Pfam; PF00661; Lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;

3D-structure. 4 160 BY SIMILARITY.
FT DISULFID 70 174 BY SIMILARITY.
FT DISULFID 120 129 BY SIMILARITY.
FT HELIX 6 8
FT TURN 13 14
FT TURN 17 20
FT STRAND 22 30
FT TURN 33 34
FT STRAND 39 47
FT TURN 49 50
FT STRAND 53 62
FT TURN 64 65
FT STRAND 68 79
FT TURN 83 84
FT STRAND 85 92
FT TURN 95 96
FT STRAND 100 109
FT STRAND 114 123
FT TURN 125 126
FT STRAND 129 138
FT TURN 141 142
FT HELIX 146 158
FT TURN 159 160
FT TURN 162 163
FT STRAND 166 167
FT TURN 173 175
SQ SEQUENCE 183 AA; 21068 MW; D6BA064CB9E67C09 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 42 VAEF 45
RESULT 44
DNAA_WOLSP
ID DNAA_WOLSP STANDARD; PRT; 186 AA.
AC P35907;
DT 01-JUN-1994 (Rel..29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chromosomal replication initiator protein dnaa (Fragment).
GN DNAA.
OS Wolbachia sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_TaxID=956;
RN [1]
RA MEDLINE=95202115; PubMed=7894745;
RX Bourzis K., Nirgianaki A., Onyango P., Savakis C.;
RT "A prokaryotic dnaa sequence in Drosophila melanogaster: Wolbachia
infection and cytoplasmic incompatibility among laboratory strains.";
RL Insect Mol. Biol. 3:131-142 (1994).
CC -!- FUNCTION: Plays an important role in the initiation and regulation
of chromosomal replication. Binds to the origin of replication; it
binds specifically double-stranded DNA at a 9 bp consensus (dnaa
box): 5'-TTATC(C/A)A(C/A)A-3'. Dnaa binds to ATP and to acidic
phospholipids (By similarity).
CC -!- SIMILARITY: Belongs to the dnaa family.

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DR EMBL; Z28981; CAA82285.1; -.
DR PIR; S39317; S39317.
DR HAMAP; MF_00377; -.
DR InterPro; IPR001957; Bac DnaA.
DR Pfam; PF00308; bac_dnaA; 1.
DR PRINTS; PR00051; DNaA.
DR PROSITE; PS01008; DNaA; PARTIAL.
KW DNA replication; DNA-binding; ATP-binding.
FT NON_TER 1
FT TER 186
SQ SEQUENCE 186 AA; 21283 MW; C423C06CEFFB0459 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 134 VAEF 137

RESULT 45
UCRI_PARDE STANDARD; PRT; 190 AA.
AC P05417;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2)
DE (Rieske iron-sulfur protein) (RISP).
DE PETA.
OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=266;
RN [1]
RS SEQUENCE FROM N.A.
RP MEDLINE=8007612; PubMed=2820981;
RA Kurowski B., Ludwig B.;
RT "The genes of the Paracoccus denitrificans bc1 complex. Nucleotide
RT sequence and homologies between bacterial and mitochondrial
RT subunits.";
RL J. Biol. Chem. 262:13805-13811(1987).
CC -!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis.
CC -!- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2
CC ferrocycytochrome c.
CC -!- COFACTOR: Binds 1 2Fe-2S iron sulfur cluster per subunit (By
CC similarity).
CC -!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- MISCELLANEOUS: The Rieske protein is a high potential 2Fe-2S
CC protein.
CC -!- SIMILARITY: Belongs to the Rieske family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17522; AAA25571.1; -.
CC PIR; A29413; A29413.
CC HSSP; P13272; IRI5.
CC InterPro; IPR005805; Rieske.
CC InterPro; IPR005806; Rieske dom.
CC InterPro; IPR006317; Rieske_proteo.

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DR InterPro; IPR006311; Tat.
DR Pfam; PF00355; Rieske; 1.
DR PRINTS; PRO162; RIESKE.
DR TIGRFAMs; TIGR01416; Rieske_proteo; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
DR PROSITE; PS00199; RIESKE_1; 1.
DR PROSITE; PS00200; RIESKE_2; 1.
KW Electron transport; Inner membrane; Transmembrane; Metal-binding;
KW Iron-sulfur; Iron; 2Fe-2S; Oxidoreductase.
FT TRANSMEM 18
FT METAL 132
FT METAL 134
FT METAL 152
FT METAL 153
FT METAL 154
FT DISULFID 137
SQ SEQUENCE 190 AA; 20299 MW; F83F5D9A9C1FBEE4 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 178 VAEF 181

RESULT 46
NTPA_METJA STANDARD; PRT; 193 AA.
AC Q57679;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nucleoside-triphosphatase (EC 3.6.1.15) (Nucleoside triphosphate
DE phosphohydrolase) (NTPase).
DE M0226.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RS SEQUENCE FROM N.A.
RP STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
RA Utterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=99332061; PubMed=1040428;
RA Hwang K.Y., Chung J.H., Kim S.-H., Han Y.S., Cho Y.;
RT "Structure-based identification of a novel NTPase from Methanococcus
RT jannaschii.";
RL Nat. Struct. Biol. 6:691-696(1999).
CC -!- FUNCTION: CAN EFFICIENTLY HYDROLYZE NONSTANDARD NUCLEOTIDES SUCH
CC AS XTP TO XMP OR ITP TO IMP, BUT NOT THE STANDARD NUCLEOTIDES. XTP
CC IS THE BEST SUBSTRATE.
CC -!- CATALYTIC ACTIVITY: NTP + H(2)O = NDP + phosphate.
CC -!- COFACTOR: Magnesium or manganese.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the HAM1 NTPase family.
CC
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EMBL; U67478; BAB98211.1; -
 PIR; C64328; C64328;
 PDB; 1B78; 28-JAN-00;
 PDB; 2MCP; 28-JAN-00;
 TIGR; MJ0226; -
 HAMAP; MF_01405; atypical; 1;
 InterPro; IPR002637; Hammp_like.
 Pfam; PF01725; Hammp_like; 1;
 TIGRFAMs; TIGR000042; TIGR000042; 1;
 Hydrolase; Manganese; Magnesium; 3D-structure; Complete proteome.
 STRAND 11 14
 HELIX 18 27
 TURN 28 30
 TURN 32 33
 STRAND 36 39
 STRAND 46 46
 HELIX 50 65
 STRAND 69 78
 HELIX 79 81
 TURN 82 83
 STRAND 85 86
 TURN 87 88
 HELIX 89 95
 TURN 96 96
 TURN 97 105
 STRAND 106 107
 STRAND 112 123
 TURN 124 125
 STRAND 126 138
 HELIX 150 153
 STRAND 155 157
 TURN 158 159
 HELIX 164 166
 TURN 169 172
 TURN 173 175
 HELIX 177 190
 TURN 191 191
 SEQUENCE 193 AA; 22202 MW; 3570565E007D3DAC CRC64;

Query Match 95.0%; Score 19; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 53 VAEF 56

RESULT 47

HAM2_BACHD
 ID HAM2_BACHD STANDARD; PRT; 194 AA.
 AC Q9K8D9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE HAM1 protein homolog 2.
 GN BH3067.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;

"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";
 Nucleic Acids Res. 28:4317-4331(2000)
 -!- SIMILARITY: Belongs to the HAM1 NTPase family.
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EMBL; AF001517; BAB06786.1; -
 PIR; C84033; C84033;
 HSSP; Q57679; 1B78.
 HAMAP; MF_01405; -; 1.
 InterPro; IPR002637; Hammp_like.
 Pfam; PF01725; Hammp_like; 1.
 ProDom; PD004952; Hammp_like; 1.
 TIGRFAMs; TIGR00042; TIGR00042; 1.
 KW Hydrolase; Complete proteome.
 SEQUENCE 194 AA; 21868 MW; BCSA0C4F19A04B3 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 194;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
 Db 14 VAEF 17

RESULT 48

TNR0_ECOLI
 ID TNR0_ECOLI STANDARD; PRT; 194 AA.
 AC P05823;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transposon Tn2501 resolvase.
 GN TNPR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87109049; PubMed=3027041;
 RA Michiels T., Cornelis G., Ellis K., Grinstead J.;
 RT "Tn2501, a component of the lactose transposon Tn951, is an example of a new category of class II transposable elements.";
 RL J. Bacteriol. 169:624-631(1987).
 CC -!- FUNCTION: RESOLVASE CATALYZES THE RESOLUTION (A SITE-SPECIFIC RECOMBINATION) OF THE COINTEGRATED REPICON TO YIELD THE FINAL TRANSPOSITION PRODUCTS.
 CC -!- MISCELLANEOUS: Tn2501 IS A CRYPTIC CLASS II TRANSPOSON FOUND AS PART OF THE LACTOSE TRANSPOSON Tn951.
 CC -!- SIMILARITY: Belongs to the site-specific recombinase resolvase family.

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EMBL; M15197; AAA27426.1; -
 PIR; B27758; RPECRS.
 HSSP; P03012; 2RSL.
 InterPro; IPR006120; HTH_7.

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R InterPro; IPR006118; Recombinase.
R InterPro; IPR006119; resolvase_N.
R Pfam; PF02796; HTH 7; 1.
R Pfam; PF02796; resolvase_N.
R PROSITE; PS00397; RECOMBINASES_1; 1.
R PROSITE; PS00398; RECOMBINASES_2; 1.
W DNA recombination; DNA integration; Transposable element.
T ACT_SITE 11 11 TRANSIENT COVALENT LINKAGE TO DNA DURING
T ACT_SITE 11 11 STRAND CLEAVAGE AND REJOINING
T ACT_SITE 11 11 (BY SIMILARITY).
T DNA BIND 170 189 H-T-H MOTIF (PROBABLE).
T SEQUENCE 194 AA; 21420 MW; DEDFC0BA6406EAD1 CRC64;
Q SEQUENCE 196 AA; 21852 MW; 7CF47F6D88DBD497 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 194;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 120 VAEF 123

RESULT 49
PINF_ECOLI
ID PINF_ECOLI STANDARD; PRT; 196 AA.
AC P77170;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative DNA-invertase from lambdoid prophage Qin.
GN PINF OR B1545.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12."
RA Science 277:1453-1474(1997).
[2]
SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RA corresponding to the 28.0-40.1 min region on the linkage map."
RA DNA Res. 3:363-377(1996).
[3]
SIMILARITY: Belongs to the site-specific recombinase resolvase
family.
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EMBL; AE000252; AAC74618.1; -.
EMBL; D90798; BAA15249.1; -.
PIR; D64909; D64909.
HSSP; P03012; 2RSL.

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DR EcoGene; EG13824; pinQ.
DR InterPro; IPR006120; HTH 7.
DR InterPro; IPR006118; Recombinase.
DR InterPro; IPR006119; resolvase_N.
DR Pfam; PF02796; HTH 7; 1.
DR Pfam; PF02796; resolvase_N.
DR PROSITE; PS00397; RECOMBINASES_1; FALSE_NEG.
DR PROSITE; PS00398; RECOMBINASES_2; 1.
KW Hypothetical protein; DNA recombination; DNA integration; DNA-binding;
KW DNA invertase; Complete proteome.
FT ACT_SITE 11 11 TRANSIENT COVALENT LINKAGE TO DNA DURING
FT ACT_SITE 11 11 STRAND CLEAVAGE AND REJOINING
FT ACT_SITE 11 11 (BY SIMILARITY).
SQ SEQUENCE 196 AA; 21852 MW; 7CF47F6D88DBD497 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 120 VAEF 123

RESULT 50
PINF_ECOLI
ID PINF_ECOLI STANDARD; PRT; 196 AA.
AC P77574;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative DNA-invertase from lambdoid prophage Rac.
GN PINF OR B1374 OR C3146.
OS Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562; 217992;
[1]
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12."
RA Science 277:1453-1474(1997).
[2]
SEQUENCE FROM N.A.
STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RA corresponding to the 28.0-40.1 min region on the linkage map."
RA DNA Res. 3:363-377(1996).
[3]
SEQUENCE FROM N.A.
STRAIN=O6:HL / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RA "Extensive mosaic structure revealed by the complete genome sequence
RA of uropathogenic Escherichia coli."
RA Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- SIMILARITY: Belongs to the site-specific recombinase resolvase

```

MEDLINE=93315143; PubMed=7696892;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the *Escherichia coli*
genome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
[4]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22398234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic *Escherichia coli*";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
[5]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postfick E., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Großbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";
Nature 409:529-533(2001).
[6]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11206551;
Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yaeunaga T.,
Kubara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic *Escherichia coli*
O157:H7 and genomic comparison with a laboratory strain K-12";
DNA Res. 8:11-22(2001).
[7]
SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
"Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
through comparison with genomes of *Escherichia coli* K12 and O157";
Nucleic Acids Res. 30:4432-4441(2002).
[8]
SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=32590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of *Shigella*
flexneri serotype 2a strain 2457T";
Infect. Immun. 71:2775-2786(2003).
-!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPF
TRANSCRIPTION
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- PTM: PHOSPHORYLATED BY UHPF (PROBABLE).
-!- SIMILARITY: Contains 1 response regulatory domain.
-!- SIMILARITY: BELONGS TO THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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EMBL; M17102; AAA24720.1; -.
EMBL; M83475; AAA24724.1; -.
EMBL; L10328; AAA62021.1; -.
EMBL; AE000444; AAC76692.1; -.
EMBL; AE016769; AAN83027.1; -.
EMBL; AE005598; AAG58868.1; -.
EMBL; AP002566; BAB38029.1; -.
EMBL; AE015386; AAN45232.1; ALT_INIT.
EMBL; AE016391; AAP18964.1; -.
PIR; A26325; BVECAU.
PIR; F91204; F91204.
PIR; H86050; H86050.
HSSP; P10957; IRLN.
ECO2DBASE; G020.9; 6TH EDITION.
EcoGene; EG11051; uhpa.
InterPro; IPI000792; HTH LuxR.
InterPro; IPR001785; Response_reg.
Pfam; PF00198; GcrE; 1.
Pfam; PF00072; response_reg; 1.
PRINTS; PR00038; HTHLUXR.
ProDom; PD000307; HTH LuxR; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00421; HTH LUXR; 1.
SMART; SM00448; REC1.
PROSITE; PS00622; HTH LUXR FAMILY; 1.
PROSITE; PS00110; RESPONSE_REGULATORY; 1.
Sensory transduction; Phosphorylation; Transcription regulation;
DNA-binding; Activator; Sugar transport; Complete proteome.
DOMAIN 1 116 RESPONSE REGULATORY.
MOD RES 54 54 PHOSPHORYLATION (BY SIMILARITY).
DNA_BIND 155 174 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 196 AA; 20689 MW; 8F409F8ADE08276 CRC64;

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Query Match          95.0%; Score 19; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      |||||
      30 VAEF 33

RESULT 52
HPA_SALTY          STANDARD;          PRT;          196 AA.
1  27667;
2  01-AUG-1992 (Rel. 23, Created)
3  01-AUG-1992 (Rel. 23, Last sequence update)
4  28-FEB-2003 (Rel. 41, Last annotation update)
5  Transcriptional regulatory protein uhpA.
6  UHPA OR STM3790.
7  Salmonella typhimurium.
8  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
9  Enterobacteriaceae; Salmonella.
10 NCBI_FaxID=602;
11 [1]
12 SEQUENCE FROM N.A.
13 STRAIN=LT2;
14 MEDLINE=92234930; PubMed=1569007;
15 Island M.D., Wei B.-Y., Kadner R.J.;
16 "Structure and function of the uhp genes for the sugar phosphate
17 transport system in Escherichia coli and Salmonella typhimurium.";
18 J. Bacteriol. 174:2754-2762(1992).
19 [2]
20 SEQUENCE FROM N.A.
21 STRAIN=LT2 / SGSC1412 / ATCC 700720;
22 MEDLINE=21534948; PubMed=11677609;
23 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

```

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Florica L., Miller W., Stoneking T., Nhan M.,
 Watson K., Wilson R.K.;
 "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 Nature 413:852-856(2001).
 CC -!- FUNCTION: APPEARS TO BE THE POSITIVE ACTIVATOR OF UHPT
 CC -!- TRANSCRIPTION.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- PTM: PHOSPHORYLATED BY UHPB (PROBABLE).
 CC -!- SIMILARITY: Contains 1 response regulatory domain.
 CC -!- SIMILARITY: BELONGS TO THE LUXS/UHPA FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC
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 or send an email to license@isb-sib.ch).
 CC

DR	EMBL: M89480; AAA27243.1; -.
DR	EMBL: AE008876; NAL22648.1; -.
DR	FIR; A41853; A41853.
DR	HSSP; P10957; LRNL.
DR	StyGene; SG10406; uhpA.
DR	InterPro; IPX007792; HTH LuxR.
DR	InterPro; IPX001789; Response_reg.
DR	Pfam; PF00196; GerE; 1.
DR	Pfam; PF00072; response_reg; 1.
DR	PRINTS; PR00038; HTHLUXR.
DR	ProDom; PR000307; HTH LuxR; 1.
DR	ProDom; PD000039; Response_reg; 1.
DR	SMART; SM00421; HTH LUXR; 1.
DR	SMART; SM00448; REC; 1.
DR	PROSITE; PS00622; HTH LUXR FAMILY; 1.
DR	PROSITE; PS00110; RESPONSE REGULATION; 1.
DR	Sensory transduction; Phosphorylation; Transcription regulation;
KW	DNA-binding; Activator; Sugar transport; Complete proteome.
FT	DOMAIN 1 116 RESPONSE REGULATION.
FT	MOD RES 54 54 PHOSPHORYLATION (BY SIMILARITY).
FT	MOD RES 155 174 H-T-T MOTIF (BY SIMILARITY).
FT	DNA_BIND 196 AA: 207990 MW: 4C80FF931C69078F CRC64;
SO	SEQUENCE

RESULT 53	ACID_MOUSE	ACID_MOUSE	STANDARD;	PRT;	198 AA.
ID	ACID_MOUSE				
AC	Q9WE0;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Activation-induced cytidine deaminase (EC 3.5.4.5)	(Cytidine			
DE	aminohydrolase).				
GN	AICDA OR AID.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OC	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99303612; PubMed=10373455;				
RA	Muranatsu M., Sankaranand V.S., Anant S., Sugai M., Kinoshita K.,				

Davidson N.O., Honjo T.;
 "Specific expression of activation-induced cytidine deaminase (AID), a novel member of the RNA-editing deaminase family in germinal center B cells.";
 J. Biol. Chem. 274:18470-18476(1999).
 C -1- FUNCTION: RNA-editing deaminase involved in somatic hypermutation, gene conversion, and class-switch recombination. Required for several crucial steps of B-cell terminal differentiation necessary for efficient antibody responses.
 C -1- CATALYTIC ACTIVITY: Cytidine + H(2)O = uridine + NH(3).
 C -1- COFACTOR: Zinc (By similarity).
 C -1- SIMILARITY: Belongs to the cytidine and deoxycytidylate deaminases family.
 C
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 C
 C EMBL; AF132979; A041793.1; -.
 C MGD; MG1342279; Aicda.
 C GO; GO:0004126; F:cytidine deaminase activity; IDA.
 C InterPro; IPR007904; APOBEC_C.
 C Pfam; PF05240; APOBEC_C; 1.
 C PROSITE; PS00903; CYT-DCMP_DEAMINASES; 1.
 C METAL 56 56 ZINC (BY SIMILARITY).
 C METAL 87 87 ZINC (BY SIMILARITY).
 C METAL 90 90 ZINC (BY SIMILARITY).
 C SEQUENCE 198 AA; 24030 MW; 18A3BA10CA54BBE2 CRC64;
 C
 C Query Match 95.0%; Score 19; DB 1; Length 198;
 C Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 C Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C
 C 2 VAEF 5
 C 94 VAEF 97
 C
 C RESULT 54
 C HIS5_SULSO
 C ID HIS5_SULSO STANDARD; PRT; 199 AA.
 C AC O33777;
 C DT 15-DEC-1998 (Rel. 37, Created)
 C DT 28-FEB-2003 (Rel. 41, Last sequence update)
 C DE Imidazole glycerol phosphate synthase subunit high (EC 2.4.2.-) (IGP synthase subunit high) (ImGP synthase subunit high) (IGPS subunit high).
 C DE HIS5 (ImGP synthase subunit high) (IGPS subunit high).
 C EN HIS5 OR SSC0600 OR C08.050.
 C OS Sulfolobus solfataricus.
 C CC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 C CC Sulfolobus.
 C CX NCBI_taxid=2287;
 C [1]
 C SEQUENCE FROM N.A.
 C RP STRAIN=ATCC 35092 / DSM 1617 / P2;
 C RX MEDLINE=97352708; PubMed=9209067;
 C RA Charlebois R.L., Senses C.W., Doolittle W.F., Brown J.R.;
 C RT "Evolutionary analysis of the hisCABdFDEHI gene cluster from the archaeon Sulfolobus solfataricus P2.";
 C RL J. Bacteriol. 179:4429-4432(1997).
 C [2]
 C SEQUENCE FROM N.A.
 C RP STRAIN=ATCC 35092 / DSM 1617 / P2;
 C RX MEDLINE=20165948; PubMed=10701121;
 C RA Charlebois R.L., Singh R.K., Chan-Weher C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Erauso M., Duguet M., Faguy D.,

Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F., Ragan M.A., Senses C.W.;
 "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
 Genome 43:116-136(2000).
 [3]
 C SEQUENCE FROM N.A.
 C RP STRAIN=ATCC 35092 / DSM 1617 / P2;
 C RX MEDLINE=21332296; PubMed=11427726;
 C RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Aways M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A., De Moers A., Erauso G., Fletcher C., Gordon P.M.K., Medina N., Peng X., Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T., Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 C -1- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to IGP, AICAR and glutamate. The his5 subunit provides the ammonia necessary to amidotransferase activity that produces the ammonia necessary to hisf for the synthesis of IGP and AICAR (By similarity).
 C -1- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulose-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazole-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
 C -1- PATHWAY: Histidine biosynthesis; fifth step.
 C -1- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
 C -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 C -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
 C
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 C
 C EMBL; U82227; AAB63025.1; -.
 C EMBL; Y18930; CAB57700.1; -.
 C EMBL; AE006689; AAK40911.1; -.
 C PIR; H90206; H90206.
 C HAMAP; MF 00278; -. 1.
 C InterPro; IPR000991; GATase_1.
 C Pfam; PF00117; GATase_1.
 C PROSITE; PS00442; GATASE_TYPE_I; FALSE NEG.
 C KW Histidine biosynthesis; Transferase; Glutamine amidotransferase; Complete proteome.
 C FT ACT_SITE 76 76 BY SIMILARITY.
 C FT ACT_SITE 178 178 BY SIMILARITY.
 C FT ACT_SITE 180 180 BY SIMILARITY.
 C SQ SEQUENCE 199 AA; 22533 MW; 17DB1A86724C095 CRC64;
 C
 C Query Match 95.0%; Score 19; DB 1; Length 199;
 C Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 C Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C
 C 2 VAEF 5
 C 51 VAEF 54
 C
 C RESULT 55
 C RETB_HORSE
 C ID RETB_HORSE STANDARD; PRT; 201 AA.
 C AC Q28369;
 C DT 28-FEB-2003 (Rel. 41, Created)
 C DT 28-FEB-2003 (Rel. 41, Last sequence update)
 C DT 28-FEB-2003 (Rel. 41, Last annotation update)
 C DE Plasma retinol-binding protein precursor (PRBP) (RBP).

RP4.
Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
[1]
SEQUENCE FROM N.A.
TISSUE=Endometrium;
MEDLINE=95226610; PubMed=7536053;
McDowell K.J., Adams M.H., Franklin K.M., Baker C.B.;
"Changes in equine endometrial retinol-binding protein RNA during the
estrous cycle and early pregnancy and with exogenous steroids.";
Biol. Reprod. 52:438-443(1995).
-1- FUNCTION: Delivers retinol from the liver stores to the peripheral
tissues. In plasma, the RBP-retinol complex interacts with
transferrin, this prevents its loss by filtration through the
kidney glomeruli.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the lipocalin family.
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EMBL: U21208; AAC48461.1; -
PIR: I45257; I46257.
HSP: P27485; I4QB.
InterPro: IPR002345; Lipocalin.
InterPro: IPR000566; Lipocalin_cytfabp.
Pfam: PF00061; lipocalin; 1.
PRINTS: PR00179; LIPOCALIN.
PROSITE: PS00213; LIPOCALIN; 1.
Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal;
Lipocalin.
SIGNAL: 1 18 POTENTIAL.
CHAIN 19 201 PLASMA RETINOL-BINDING PROTEIN.
DISULFID 22 178 BY SIMILARITY.
DISULFID 88 192 BY SIMILARITY.
DISULFID 138 147 BY SIMILARITY.
SEQUENCE 201 AA; 23022 MW; 12CF80834E4262DC CRC64;
Query Match 95.0%; Score 19; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
|||
60 VAEF 63
SULT 56
TB HUMAN
RETE HUMAN STANDARD; PRT; 201 AA.
P02753; O43478; O43479; Q8W3A3; Q9P178;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Plasma retinol-binding protein precursor (PRBP) (RBP) (PRO22222).
RP4.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=84069802; PubMed=6316270;
Colantuoni V., Romano V., Seusi G., Santoro C., Costanzo F.,
Raugel G., Cortese R.;
"Cloning and sequencing of a full length cDNA coding for human

retinol-binding protein.";
Nucleic Acids Res. 11:7769-7776(1983).
[2]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
SEQUENCE OF 1-189 FROM N.A.
MEDLINE=86055755; PubMed=2998779;
D'Onofrio C., Colantuoni V., Cortese R.;
"Structure and cell-specific expression of a cloned human retinol
binding protein gene: the 5'-flanking region contains hepatoma
specific transcriptional signals.";
EMBO J. 4:1981-1989(1985).
[4]
SEQUENCE OF 19-201, AND DISULFIDE BONDS.
MEDLINE=88019004; PubMed=2444024;
Rask L., Anundi H., Fohlman J., Peterson P.A.;
"The complete amino acid sequence of human serum retinol-binding
protein.";
Ups. J. Med. Sci. 92:115-146(1987).
[5]
SEQUENCE OF 19-201.
MEDLINE=81254137; PubMed=6942701;
Rask L., Anundi H., Boehme J., Eriksson U., Ronne H., Sege K.,
Peterson P.A.;
"Structural and functional studies of vitamin A-binding proteins.";
Ann. N.Y. Acad. Sci. 359:79-90(1981).
[6]
SEQUENCE OF 19-183.
MEDLINE=80004132; PubMed=573217;
Rask L., Anundi H., Peterson P.A.;
"The primary structure of the human retinol-binding protein.";
FEBS Lett. 104:55-58(1979).
[7]
SEQUENCE OF 18-201 FROM N.A.
TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
He F.;
"Functional prediction of the coding sequences of 79 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[8]
PARTIAL SEQUENCE.
MEDLINE=95395382; PubMed=7666002;
Jaconi S., Rose K., Hughes G.J., Saurat J.-H., Siegenthaler G.;
"Characterization of two post-translationally processed forms of
human serum retinol-binding protein: altered ratios in chronic renal
failure.";
J. Lipid Res. 36:1247-1253(1995).
[9]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=91017498; PubMed=2217163;

Cowan S.W., Newcomer M.E., Jones T.A.;
"Crystallographic refinement of human serum retinol binding protein
at 2-A resolution.";
Proteins 8:44-61(1990).
[10]
X-RAY CRYSTALLOGRAPHY.
MEDLINE=92322903; PubMed=1623143;
Monaco H.L., Zanotti G.;
"Three-dimensional structure and active site of three hydrophobic
molecule-binding proteins with significant amino acid sequence
similarity.";
Biopolymers 32:457-465(1992).
[11]
X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH TTR.
MEDLINE=92322903; PubMed=1623143;
Naylor H.M., Newcomer M.E.;
"The structure of human retinol-binding protein (RBP) with its
carrier protein transthyretin reveals an interaction with the carboxy
terminus of RBP.";
Biochemistry 38:2647-2653(1999).
[12]
VARIANTS RBP DEFICIENCY ASN-59 AND ASP-93.
MEDLINE=99103495; PubMed=9888420;
Seeliger M.W., Biesalski H.K., Wissinger B., Gollnick H., Gielen S.,
Frank J., Beck S., Zrenner E.;
"Phenotype in retinol deficiency due to a hereditary defect in retinol
binding protein synthesis.";
Invest. Ophthalmol. Vis. Sci. 40:3-11(1999).
[13]
CHARACTERIZATION OF VARIANTS ASN-59 AND ASP-93.
MEDLINE=99247593; PubMed=10232633;
Biesalski H.K., Frank J., Beck S.C., Heinrich F., Illek B., Reifen R.,
Gollnick H., Seeliger M.W., Wissinger B., Zrenner E.;
"Biochemical but not clinical vitamin A deficiency results from
mutations in the gene for retinol binding protein.";
Am. J. Clin. Nutr. 69:931-936(1999).
-!- FUNCTION: Delivers retinol from the liver stores to the peripheral
tissues. In plasma, the RBP-retinol complex interacts with
transthyretin, this prevents its loss by filtration through the
kidney glomeruli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=21063.46; MW_ERR=1.88; METHOD=Electrospray;
RANGE=17-199.
-!- DISEASE: Defects in RBP4 are a cause of retinol-binding protein
deficiency [MIM:180250]. This condition causes night vision
problems. It produces a typical "fundus xerophthalmicus."
-!- DISEASE: A deficiency of vitamin A blocks secretion of the binding
protein posttranslationally and results in defective delivery and
supply of vitamin to the epidermal cells (a condition associated
with a dermatosis).
-!- SIMILARITY: Belongs to the lipocalin family.
-!- DATABASE: NAME=Mutations of the RBP4 gene;
NOTE=Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/rbp4mut.htm".

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or send an email to license@sib-sib.ch).

EMBL; X00129; CAA24959.1; --
EMBL; BC020633; AAH20633.1; --
EMBL; X02775; CAA25553.1; --
EMBL; X02824; CAB46489.1; --
EMBL; AF119868; AAF69622.1; ALT_INIT.
EMBL; AF025334; AAC02945.1; --
EMBL; AF025335; AAC02946.1; --
PIR; A93494; VAHU.
PDB; 1BRP; 15-JUL-91.

PDB; 1BRP; 31-JAN-94.
PDB; 1BRQ; 31-JAN-94.
PDB; 1QAB; 09-APR-99.
DR SWISS-2DPAGE; P02753; HUMAN.
DR Siena-2DPAGE; P02753; --
DR Genew; HGNC:9922; RBP4.
DR MIM; 180250; --
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005501; F:retinoid binding; TAS.
DR InterPro; IPR002345; Lipocalin.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal;
KW Lipocalin; Disease mutation; Vision; 3D-structure.
FT SIGNAL 1 18 PLASMA RETINOL-BINDING PROTEIN.
FT CHAIN 19 201
FT DISULFID 22 178
FT DISULFID 88 192
FT DISULFID 138 147
FT VARIANT 59 59
FT VARIANT 93 93
FT CONFLICT 8 8 I -> N (in RBP deficiency).
FT CONFLICT 13 17 /FTID=VAR_009276.
FT STRAND 23 23 G -> D (in RBP deficiency).
FT HELIX 24 26 /FTID=VAR_009277.
FT TURN 31 32 F -> L (IN REF. 1 AND 3).
FT HELIX 35 38 LGSOR -> WAA (IN REF. 1 AND 3).
FT STRAND 40 48
FT STRAND 60 66
FT TURN 67 69
FT TURN 70 80
FT STRAND 82 83
FT STRAND 86 96
Query Match 95.0%; Score 19; DB 1; Length 201;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 60 VAEF 63
RESULT 57
RETB_PIG ID RETB_PIG STANDARD; PRT; 201 AA.
AC P27485; DT 01-AUG-1992 (Rel. 23; Created)
DT 15-JUL-1998 (Rel. 36; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Plasma retinol-binding protein precursor (PRBP) (RBP).
GN RBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92331004; PubMed=1723146;
RA Trout W.E., McDonnell J.J., Kramer K.K., Baumbach G.A., Roberts R.M.;
RT "The retinol-binding protein of the expanding pig blastocyst:
disc.";
RT Mol. Endocrinol. 5:1533-1540(1991).
RL [2]
RN X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS), AND REVISIONS TO 134 AND 185.
RX MEDLINE=98437649; PubMed=9757135;
RA Zanotti G., Panzavolta M., Marcato A., Malpeli G., Folli C., Berni R.;
RT "Structure of pig plasma retinol-binding protein at 1.65-A

resolution.";
 Acta Crystallogr. D 54:1049-1052(1998).
 -I- FUNCTION: Delivers retinol from the liver stores to the peripheral tissues. In plasma, the RBP-retinol complex interacts with transthyretin, this prevents its loss by filtration through the kidney glomeruli.
 -I- SUBCELLULAR LOCATION: Secreted.
 -I- SIMILARITY: Belongs to the lipocalin family.

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 EMBL; M68860; AAA31113.1; --
 PIR; A39486; A39486.
 PDB; 1AQB; 28-JAN-98.
 InterPro; IPR002345; Lipocalin.
 InterPro; IPR000566; Lipocalin_cytFABP.
 Pfam; PF00061; Lipocalin.1.
 PRINTS; PR00179; LIPOCALIN.
 PROSITE; PS00213; LIPOCALIN; 1.
 Plasma; Vitamin A; Retinol-binding; Transport; Liver; Signal;
 Lipocalin; 3D-structure.

 CHAIN 1 18 POTENTIAL.
 STRAND 19 201 PLASMA RETINOL-BINDING PROTEIN.
 DISULFID 22 178
 DISULFID 88 192
 DISULFID 138 147
 CONFLICT 134 134 V -> A (IN REF. 1).
 CONFLICT 185 185 I -> L (IN REF. 1).
 STRAND 23 23
 HELIX 24 26
 TURN 31 32
 TURN 35 38
 HELIX 40 48
 STRAND 55 65
 TURN 67 68
 STRAND 71 80
 TURN 82 83
 STRAND 86 97
 TURN 101 102
 STRAND 103 110
 TURN 113 114
 STRAND 118 127
 STRAND 132 141
 TURN 143 144
 STRAND 145 156
 TURN 159 160
 HELIX 164 176
 TURN 177 178
 STRAND 180 181
 TURN 184 185
 TURN 191 192
 SEQUENCE 201 AA; 23067 MW; A20E39D3C9471DC8 CRC64;

 Query Match 95.0%; Score 19; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 VAEF 5
 ||||
 60 VAEF 63

 SULT 58
 TB_RABIT
 P06912;
 01-JAN-1988 (Rel. 06, Created)

 RESULT 59
 YIGZ_ECOLI
 ID YIGZ_ECOLI STANDARD; PRT; 204 AA.
 AC P27862;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yigZ.
 GN YIGZ OR B3848.

01-OCT-1996 (Rel. 34, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasma retinol-binding protein precursor (PRBP) (RBP).
 GN RBP4
 OS Oryctolagus cuniculus (Rabbit)
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93011736; PubMed=1339354;
 RA Lee S.Y., Uebels J.L., Soprano D.R.;
 RT "The lacrimal gland synthesizes retinol-binding protein.";
 RL Exp. Eye Res. 55:163-171(1992).
 RN [2]
 RP SEQUENCE OF 19-201.
 RX MEDLINE=85207643; PubMed=3838985;
 RA Sundelin J., Laurent B.C., Anundi H., Traegaardh L., Larhammar D.,
 RA Bjorck L., Eriksson U., Akerstrom B., Jones A., Newcomer M.,
 RA Peterson P.A., Rask L.;
 RT "Amino acid sequence homologies between rabbit, rat, and human serum
 retinol-binding proteins.";
 RL J. Biol. Chem. 260:6472-6480(1985).
 CC -I- FUNCTION: Delivers retinol from the liver stores to the peripheral
 tissues. In plasma, the RBP-retinol complex interacts with
 transthyretin, this prevents its loss by filtration through the
 kidney glomeruli.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the lipocalin family.

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 EMBL; S45958; AAB23582.1; --
 PIR; A49178; VABP.
 HSP; P18902; LFEN.
 InterPro; IPR002345; Lipocalin.
 InterPro; IPR000566; Lipocalin_cytFABP.
 Pfam; PF00061; Lipocalin.1.
 PRINTS; PR00179; LIPOCALIN.
 PROSITE; PS00213; LIPOCALIN; 1.
 Plasma; Vitamin A; Retinol-binding; Transport; Liver; Lipocalin;
 Signal.
 KW SIGNAL.
 FT CHAIN 1 18
 FT CHAIN 19 201 PLASMA RETINOL-BINDING PROTEIN.
 FT DISULFID 22 178 BY SIMILARITY.
 FT DISULFID 88 192 BY SIMILARITY.
 FT DISULFID 138 147 BY SIMILARITY.
 SQ SEQUENCE 201 AA; 23102 MW; 4153FCF050184136 CRC64;

 Query Match 95.0%; Score 19; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 VAEF 5
 ||||
 60 VAEF 63

 RESULT 59
 YIGZ_ECOLI
 ID YIGZ_ECOLI STANDARD; PRT; 204 AA.
 AC P27862;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yigZ.
 GN YIGZ OR B3848.


```

CC -1- SUBUNIT: INTERACTS WITH CDC20 AND WITH ADAM17 (TACE).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC -1- SIMILARITY: Contains 1 HORMA domain.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/MAD2L1ID304.html".
CC -----
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CC -----
DR ENBL; U85410; AAC50781.1; --
DR ENBL; U31278; AAC52060.1; --
DR ENBL; AJ000186; CAA03943.1; --
DR ENBL; AB056160; BAB63410.1; --
DR ENBL; BC000356; AAH00356.1; --
DR ENBL; BC005945; AAH05945.1; --
DR PIR; G01942; G01942.
DR PDB; 1DUJ; 08-MAR-00.
DR Genew; HGNC:6763; MAD2L1.
DR GK; Q13257; --
DR MIM; 601467; --
DR GO; GO:0005699; C:kinetochore; TAS.
DR GO; GO:0007067; P:mitosis; TAS.
DR GO; GO:0007093; P:mitotic checkpoint; TAS.
DR InterPro; IPR003511; DNABind_HORMA.
DR Pfam; PF02301; HORMA; 1.
DR PROSITE; PS50815; HORMA; 1.
KW Cell cycle; Mitosis; Nuclear protein; 3D-structure.
FT DOMAIN 14 197
FT STRAND 11 12
FT STRAND 15 15
FT HELIX 17 34
FT TURN 35 35
FT TURN 41 42
FT STRAND 44 48
FT TURN 49 50
FT STRAND 51 55
FT HELIX 59 73
FT STRAND 83 90
FT TURN 91 94
FT STRAND 95 103
FT STRAND 106 106
FT TURN 112 113
FT HELIX 122 141
FT STRAND 149 158
FT TURN 165 166
FT STRAND 173 175
FT TURN 179 181
FT STRAND 185 193
SQ SEQUENCE 205 AA; 23510 MW; B8DCBF0043836764 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 20 VAEF 23
RESULT 61
MD21_MOUSE
ID MD21_MOUSE STANDARD; PRT; 205 AA.
AC Q921B5; Q9J153;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1).

```

```

GN MAD2L1 OR MAD2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Jin D.-Y.; Jeang K.-T.;
RT "Identification of a novel component of the spindle assembly
RT checkpoint in mammalian cells.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20348739; PubMed=10892650;
RA Dobles M.; Liberal V.; Scott M.L.; Beneser R.; Sorger P.K.;
RT "Chromosome missegregation and apoptosis in mice lacking the mitotic
RT checkpoint protein Mad2.";
RL Cell 101:635-645(2000).
CC -1- FUNCTION: REQUIRED FOR THE EXECUTION OF THE MITOTIC CHECKPOINT
CC WHICH MONITORS THE PROCESS OF KINETOCORE-SPINDLE ATTACHMENT AND
CC DELAYS THE ONSET OF ANAPHASE WHEN THIS PROCESS IS NOT COMPLETE. IT
CC INHIBITS THE ACTIVITY OF THE ANAPHASE PROMOTING COMPLEX BY
CC SEQUESTERING CDC20 UNTIL ALL CHROMOSOMES ARE ALIGNED AT THE
CC METAPHASE PLATE (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH CDC20.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MAD2 FAMILY.
CC -1- SIMILARITY: Contains 1 HORMA domain.
CC -----
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CC -----
DR ENBL; U83902; AAD09238.1; --
DR ENBL; AF261919; AAF69525.1; --
DR HSSP; Q13257; 1DUJ.
DR MGD; MGI:1860374; Mad2l1.
DR GO; GO:0000776; C:kinetochore; IDA.
DR GO; GO:0005816; C:spindle pole body; IDA.
DR GO; GO:0000707; P:mitotic chromosome segregation; IMP.
DR GO; GO:0007094; P:mitotic spindle checkpoint; IMP.
DR InterPro; IPR003511; DNABind_HORMA.
DR Pfam; PF02301; HORMA; 1.
DR PROSITE; PS50815; HORMA; 1.
KW Cell cycle; Mitosis; Nuclear protein.
FT DOMAIN 14 197
FT CONFLICT 157 157 T -> A (IN REF. 1).
FT CONFLICT 178 178 C -> S (IN REF. 1).
FT CONFLICT 201 201 T -> I (IN REF. 1).
SQ SEQUENCE 205 AA; 23598 MW; A9F3E28BC4C9738E CRC64;
Query Match 95.0%; Score 19; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 20 VAEF 23
RESULT 62
YAC1_LEGPN
ID YAC1_LEGPN STANDARD; PRT; 208 AA.
AC P37033;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

```

DE Hypothetical 23.7 kDa protein in acn 5'/region.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Philadelphia 1;
RX MEDLINE=93374864; PubMed=8366052;
RA Mengaud J.M., Horwitz M.A.;
RT "The major iron-containing protein of Legionella pneumophila is an
RT aconitase homologous with the human iron-responsive element-binding
RT protein.";
RL J. Bacteriol. 175:5666-5676(1993).
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CC -----
DR EMBL; L22081; AAA25294.1; -.
DR PIR; A48642; A48642.
KW Hypothetical protein.
SQ SEQUENCE. 208 AA; 23714 MW; 155C758G3A20C800 CRC64;

Query Match          95.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 45 VAEF 48

RESULT 63
HMUO_CORDI
ID HMUO_CORDI STANDARD; PRT; 215 AA.
AC P71119;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heme oxygenase [EC 1.14.99.3].
GN HMUO OR DP1689.
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C7;
RX MEDLINE=97159681; PubMed=9006041;
RA Schmitt M.P.;
RT "Utilization of host iron sources by Corynebacterium diphtheriae:
RT identification of a gene whose product is homologous to eukaryotic
RT heme oxygenases and is required for acquisition of iron from heme and
RT hemoglobin.";
RL J. Bacteriol. 179:838-845(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Biotype Gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910;
RA Cerdano-Taraga A.M., Efstathiou A., Dover L.G., Holden M.T.G.,
RA Pallen M., Bentley S.D., Besra G.S., Churcher C., James K.D.,
RA De Jozsa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagsis K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129."
RL Nucleic Acids Res. 31:6516-6523(2003).

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CC -----
DR EMBL; U73860; AAC44832.1; -.
DR EMBL; BX248358; CAE50198.1; -.
DR HSP; P09601; IQQ8.
DR InterPro; IPR002051; Heme_oxygenase.
DR Pfam; PF01116; Heme_oxygenase; 1.
DR PRINTS; PR00088; HAEMOXYGNASE.
DR PROSITE; PS00593; HEME_OXYGENASE; 1.
KW Heme; Oxidoreductase.
FT METAL 20 20 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT CONFLICT 34 34 E -> K (IN REF. 1).
FT CONFLICT 60 60 A -> V (IN REF. 1).
FT CONFLICT 92 93 DG -> GS (IN REF. 1).
FT CONFLICT 192 192 N -> H (IN REF. 1).
SQ SEQUENCE 215 AA; 24116 MW; 60D9E8E2ED7ED456 CRC64;

Query Match          95.0%; Score 19; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 39 VAEF 42

RESULT 64
COAT_CWIX
ID COAT_CWIX STANDARD; PRT; 218 AA.
AC Q66120;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbers mosaic virus (strain Ixora) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117114;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96005047; PubMed=7561763;
RA McCarvey P.E., Foushant M., Geleka L., Cellini F., Kaper J.M.;
RT "The complete sequence of a cucumber mosaic virus from Ixora that is
RT deficient in the replication of satellite RNAs.";
RL J. Gen. Virol. 76:2257-2270(1995).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20219; AAC54619.1; -.
DR PIR; D71392; D71392.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.

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D  RAN TETPY STANDARD; PRT; 223 AA.
C  P41514;
T  01-NOV-1995 (Rel. 32, Created)
T  01-NOV-1995 (Rel. 32, Last sequence update)
T  28-FEB-2003 (Rel. 41, Last annotation update)
S  GTP-binding nuclear protein RAN/TC4.
E  Tetrahymena pyriformis.
C  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
C  Tetrahymenina; Tetrahymena.
X  NCBI_TaxID=5908;
N  [1]
P  SEQUENCE FROM N.A.
C  STRAIN=W;
X  MEDLINE=94299154; PubMed=8026746;
X  Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
A  Nozawa Y.;
T  "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
T  low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena
T  thermophila and amiconucleated Tetrahymena pyriformis.";
C  Gene 144:123-125(1994).
C  -!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic
C  transport. Required for the import of protein into the nucleus and
C  also for RNA export. Involved in chromatin condensation and
C  control of cell cycle (By similarity).
C  -!- SUBUNIT: Monomer.
C  -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
C  -!- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.
C  -----
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C  or send an email to license@isb-sib.ch).
C  -----
C  EMBL; D21825; BAA04849.1; --
C  HSPF; P17080; I2K.
R  InterPro; IPR002041; RAN.
R  InterPro; IPR001806; Ras_trnsmfmg.
R  InterPro; IPR005225; Small_GTP.
R  Pfam; PF00071; ras; 1.
R  PRINTS; PR00627; GTPRANTC4.
R  PRINTS; PR00449; RASTRNSFRMG.
R  SMART; SM00176; RAN; 1.
R  TIGRFAMs; TIGR00233; small_GTP; 1.
R  PROSITE; PS01115; RAN; 1.
C  GTP-binding; Nuclear protein; Protein transport.
C  NP_BIND 18 25 GTP (BY SIMILARITY).
C  NP_BIND 66 70 GTP (BY SIMILARITY).
C  NP_BIND 123 126 GTP (BY SIMILARITY).
C  DOMAIN 128 143 IBB (BY SIMILARITY).
C  SEQUENCE 223 AA; 25422 MW; 5474DAD58AF0977 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2Y 2 VAEP 5
2b 9 VAEP 12
RESULT 68
VATD TETH STANDARD; PRT; 223 AA.
AC 087880;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
E  V-type ATP synthase subunit D (EC 3.6.3.14) (V-type ATPase subunit D).
C  ATPD OR VATD.
C  Thermus thermophilus.

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OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=20250964; PubMed=10789522;
RA Yoshida M.;
RA Yokoyama K., Ohkuma S., Taguchi H., Yasunaga T., Wakabayashi T.,
RT "V-type H+-ATPase/synthase from a thermophilic eubacterium, Thermus
RT thermophilus. Subunit structure and operon.";
RL J. Biol. Chem. 275:13955-13961(2000).
CC -!- FUNCTION: Produces ATP from ADP in the presence of a proton
CC gradient across the membrane.
CC -!- CATALYTIC ACTIVITY: ATP + H+(2)O + H+(+) (In) = ADP + phosphate +
CC H+(+) (Out).
CC -!- SIMILARITY: Belongs to the V-ATPase D subunit family.
CC -----
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CC -----
CC EMBL; D63799; BAA33198.2; --
CC HAMAP; MF_00271; 1.
DR InterPro; IPR002699; ATPsynth_Deub.
DR Pfam; PF01813; ATP-synt_D; 1.
DR ProDom; PD004122; ATPsynth_Deub; 1.
DR TIGRFAMs; TIGR00309; V_ATPase_subd; 1.
KW Hydrolase; ATP synthetase; Hydrogen ion transport.
SQ SEQUENCE 223 AA; 24677 MW; B666AB00DF0B08B CRC64;
Query Match 95.0%; Score 19; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEP 5
Db 36 VAEP 39
RESULT 69
RAN TETH STANDARD; PRT; 225 AA.
AC P41515;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GTP-binding nuclear protein RAN/TC4.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=B1868;
RX MEDLINE=94299154; PubMed=8026746;
RA Nagata K.-I., Takemasa T., Alam S., Hattori T., Watanabe Y.,
RA Nozawa Y.;
RT "Cloning of cDNAs encoding a cell-cycle-regulatory GTP-binding
RT low-M(r) (GBLM) protein, Ran/TC4, from micronucleated Tetrahymena
RT thermophila and amiconucleated Tetrahymena pyriformis.";
RL Gene 144:123-125(1994).
CC -!- FUNCTION: GTP-binding protein involved in nucleocytoplasmic
CC transport. Required for the import of protein into the nucleus and
CC also for RNA export. Involved in chromatin condensation and
CC control of cell cycle (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the small GTPase superfamily. Ran family.

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EMBL; D17748; BAA04600.1; -;
 HSP; P17080; LA2K.
 InterPro; IPR002041; RAN.
 InterPro; IPR001806; Ras transfrmg.
 InterPro; IPR005225; Small_GTP.
 Pfam; PF00071; ras; 1.
 PRINTS; PR00627; GTPRANTC4.
 PRINTS; PR00449; RASTRNSPRMG.
 SMART; SM00176; RAN; 1.
 TIGRFAMs; TIGR00231; small_GTP; 1.
 GTP-binding; Nuclear protein; Protein transport.
 NP BIND 18 25 GTP (BY SIMILARITY).
 NP BIND 66 70 GTP (BY SIMILARITY).
 NP BIND 123 126 GTP (BY SIMILARITY).
 DOMAIN 128 143 IBB (BY SIMILARITY).
 SEQUENCE 225 AA; 25649 MW; 69F8B8409AF703F8 CRC64;

Query Match 95.0%; Score 19; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

2 VAEF 5
 ||||
 9 VAEF 12

SULT 70

32 NPVOP STANDARD; PRT; 228 AA.
 P24080;
 01-MAR-1992 (Rel. 21, Created)
 01-MAR-1992 (Rel. 21, Last sequence update)
 01-NOV-1997 (Rel. 35, Last annotation update)
 Hypothetical 26.0 kDa protein in pP34-EXO intergenic region (ORF 4).
 Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMPNV).
 Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 Nucleopolyhedrovirus.
 NCBI_TaxID=164623;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=89293086; PubMed=2661722;
 Gombart A.F., Blisseard G.W., Rohrmann G.F.;
 "Characterization of the genetic organization of the HindIII M region of the multicapsid nuclear polyhedrosis virus of Orgyia pseudotsugata reveals major differences among baculoviruses."
 J. Gen. Virol. 70:1815-1828(1989).
 [2]

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SEQUENCE FROM N.A.
 MEDLINE=97271300; PubMed=9126251;
 Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 Rohrmann G.F.;
 "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."
 Virology 229:381-395(1997).
 -!- SIMILARITY: TO CORRESPONDING ORF IN ACMPNV.

CC -----
 DR EMBL; D13796; BAA02952.1; -;
 DR EMBL; D13929; BAA03030.1; -;
 DR EMBL; U75930; AAC59129.1; -;
 DR PIR; D30857; D30857.
 KW Hypothetical protein; Late protein.
 SQ SEQUENCE 228 AA; 25962 MW; F0766AD21F60039D CRC64;

Query Match 95.0%; Score 19; DB 1; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 ||||
 DB 84 VAEF 87

RESULT 71

NADD_PSEPK STANDARD; PRT; 230 AA.
 AC Q88DL5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable nicotinate-nucleotide adenyltransferase (EC 2.7.7.18)
 DE (Deamido-NAD(+) pyrophosphorylase) (Deamido-NAD(+) diphosphorylase)
 DE (Nicotinate mononucleotide adenyltransferase) (NAMN
 adenyltransferase).
 DE NADD OR P4810.
 GN Pseudomonas putida (strain KT2440).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
 Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoft A., Tsemmler B.,
 Fraser C.M.;
 "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."
 Environ. Microbiol. 4:799-808(2002).
 RL -!- FUNCTION: Catalyzes the reversible adenylation of nicotinate mononucleotide (NAMN) to nicotinic acid adenine dinucleotide (NAD) (by similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + nicotinate ribonucleotide = diphosphate + deamido-NAD(+).
 CC -!- PATHWAY: NAD biosynthesis.
 CC -!- SIMILARITY: Belongs to the nad family.
 CC -----
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EMBL; AE016792; AA070379.1; -;
 TIGR; PF4810; -;
 HAMAP; MF_00244; -; 1.
 InterPro; IPR004820; Cytidylyltransf.
 Pfam; PF01467; CTP transf 2; 1.
 KW Pyridine nucleotide biosynthesis; Transferase; Nucleotidyltransferase;
 KW NAD; Complete proteome.
 SQ SEQUENCE 230 AA; 25291 MW; 4CF04E8F70B48941 CRC64;

```

Query Match          95.0%; Score 19; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 42 VAEF 45

RESULT 72
R3_PORPU STANDARD; PRT; 230 AA.
D RR3_PORPU
C P51308;
T 01-OCT-1996 (Rel. 34, Created)
T 01-OCT-1996 (Rel. 34, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Chloroplast 30S ribosomal protein S3.
N RPS3.
S Porphyra purpurea.
G Chloroplast.
C Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
X NCBI_TaxID=278;
P SEQUENCE FROM N.A.
C STRAIN=Avonport;
A Reith M.E., Munnolland J.;
T "Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.";
L Plant Mol. Biol. Rep. 13:333-335(1995).
C -1- SUBUNIT: Part of the 30S ribosomal subunit.
C -1- SUBCELLULAR LOCATION: Chloroplast.
C -1- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
C -1- SIMILARITY: Contains 1 KH type-2 domain.
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C -----
C EMBL; U38804; AAC08194.1; -.
R PIR; S73229; S73229.
R HAMAP; MF_01309; 1.
R InterPro; IPR004087; KH dom.
R InterPro; IPR009019; KH_prok.
R InterPro; IPR004044; KH_TYPE_2.
R InterPro; IPR001351; Ribosomal_S3_C.
R InterPro; IPR008282; Ribosomal_S3_N.
R InterPro; IPR005704; S3_bact.
R Pfam; PF00013; KH; 1.
R Pfam; PF00189; Ribosomal_S3_C; 1.
R Pfam; PF00417; Ribosomal_S3_N; 1.
R SMART; SMO0322; KH; 1.
R TIGRFSMS; TIGR01009; rpsC_bact; 1.
R PROSITE; PS50823; KH_TYPE_2; 1.
R PROSITE; PS00548; RIBOSOMAL_S3; 1.
W Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
T DOMAIN 39 109 KH TYPE-2.
Q SEQUENCE 230 AA; 25631 MW; 5489B93704D7F0ED CRC64;

Query Match          95.0%; Score 19; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 118 VAEF 121

RESULT 73
BIE_COREF

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ID UBIE COREF STANDARD; PRT; 230 AA.
AC Q8PSB3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Menquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
GN UBIE OR C60481.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
CC -1- FUNCTION: Methyltransferase required for the conversion of
CC dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
CC S-adenosyl-L-homocysteine + menaquinol.
CC -1- PATHWAY: Menaquinone biosynthesis; last step.
CC -1- SIMILARITY: Belongs to the ubiE family.
CC -----
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CC -----
CC EMBL; AF005215; BAC17291.1; ALT_INIT.
DR HAMAP; MF_01813; 1.
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM_Bind.
DR InterPro; IPR004033; UbiE/COQ5_Metrf.
DR Pfam; PF01209; UbiE_methyltran; 1.
DR PROSITE; PS01183; UbiE_1; FALSE NEG.
DR PROSITE; PS01184; UbiE_2; FALSE NEG.
KW Menaquinone biosynthesis; Transferase; Methyltransferase;
KW Complete proteome.
KW SEQUENCE 230 AA; 25366 MW; E10DCB602A1CD886 CRC64;

Query Match          95.0%; Score 19; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 145 VAEF 148

RESULT 74
UBIE CORGL STANDARD; PRT; 230 AA.
ID UBIE CORGL
AC Q8NT39;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
GN UBIE OR CGL0471.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.

```

```
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
XC -!- FUNCTION: Methyltransferase required for the conversion of
XC dimethylmenaquinone (DMK2) to menaquinone (MK2) (By similarity).
XC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
XC S-adenosyl-L-homocysteine + menaquinol.
XC -!- PATHWAY: Menaquinone biosynthesis; last step.
XC -!- SIMILARITY: Belongs to the ubiE family.
XC -----
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XC or send an email to license@isb-sib.ch).
XC -----
XC EMBL; AP005275; BAB97864.1; -.
XC HAMAP; MF_01813; -.
XC InterPro; IPR001601; Methyltransf.
XC InterPro; IPR000051; SAM bind.
XC InterPro; IPR004033; UbiE/COQ5 Methyl.
XC Pfam; PF01209; UbiE_methyltransf; 1.
XC PROSITE; PS01183; UBI1_1; FALSE NEG.
XC PROSITE; PS01184; UBI2; FALSE NEG.
XC MenAquinone biosynthesis; Transferase; Methyltransferase;
XC Complete proteome.
XC SEQUENCE 230 AA; 25244 MW; A8548173B7901400 CRC64;
XC -----
Query Match 95.0%; Score 19; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 2 VAEF 5
DB 145 VAEF 148
|||||
RESULT 75
ID YGIB ECOLI STANDARD; PRT; 234 AA.
AC P24195.
JT 01-MAR-1992 (Rel. 21, Created)
JT 01-MAR-1992 (Rel. 21, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ygiB.
EN YGIB OR B3037 OR C3783 OR SF3077 OR S3282.
DS Escherichia coli.
DS Escherichia coli O6, and
DS Shigella flexneri.
DS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
DS Enterobacteriaceae; Escherichia.
DX NCBI_TaxID=562, 217992, 623;
[1]
RN SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=92223101; PubMed=1314093;
RA Yang T.-P., Depew R.E.;
RT "Nucleotide sequence of a region duplicated in Escherichia coli toc
RT mutants.";
RL Biochim. Biophys. Acta 1130:227-228(1992).
[2]
RN SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97428617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
```

```
RN SEQUENCE FROM N.A.
RP SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
[4]
RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
[5]
RN SEQUENCE FROM N.A.
RP SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
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EMBL; M77129; AAA71875.1; -.
EMBL; U28377; AAA69205.1; -.
EMBL; AE000385; AAC76073.1; -.
EMBL; AE016766; AAN82227.1; -.
EMBL; AE015319; AAN4555.1; ALT INIT.
EMBL; AE016988; AAF18368.1; -.
PIR; S22360; S22360.
ECogene; EG11164; YgiB.
Hypothetical protein; Complete proteome.
SQ SEQUENCE 234 AA; 24868 MW; 08D5DE931072C966 CRC64;
Query Match 95.0%; Score 19; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 100 VAEF 103
|||||
Search completed: May 24, 2004, 17:41:02
Job time : 58.5714 secs
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GenCore version 5.1.6
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protein - protein search, using sw model

n on: May 24, 2004, 17:33:08 ; Search time 35.7143 Seconds

(without alignments)
44.173 Million cell updates/sec

file: US-09-594-978A-1

quence: 20

1 XVAEF 5

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1017041 seqs, 315518202 residues

tal number of hits satisfying chosen parameters: 1017041

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

tabase :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriapi:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result NO.	Score	Query Match %	Length	ID	Description
1	19	95.0	20	6	Q9T518
2	19	95.0	22	2	Q9R5C0
3	19	95.0	30	5	P82214
4	19	95.0	33	16	O25518
5	19	95.0	35	17	Q8Z219
6	19	95.0	36	6	Q9TQR7
7	19	95.0	44	2	Q48420
8	19	95.0	45	16	Q830H9
9	19	95.0	48	16	O25478
10	19	95.0	51	16	Q7UXL5
11	19	95.0	52	2	Q44941
12	19	95.0	54	16	Q8X3Y8
13	19	95.0	54	16	Q8TF13
14	19	95.0	61	2	Q8V8B8
15	19	95.0	61	4	Q9P166
16	19	95.0	68	12	Q99GZ9

17	19	95.0	68	16	Q82X12
18	19	95.0	69	10	Q7X7L1
19	19	95.0	69	16	Q8NPA7
20	19	95.0	71	13	Q8AUQ2
21	19	95.0	71	13	Q8AUP0
22	19	95.0	72	2	P97252
23	19	95.0	74	16	Q97JU4
24	19	95.0	74	16	Q82MX0
25	19	95.0	77	6	Q862M8
26	19	95.0	77	16	Q88VS7
27	19	95.0	79	12	Q98582
28	19	95.0	80	2	Q9XI36
29	19	95.0	81	16	Q89WL6
30	19	95.0	84	16	Q9KAV4
31	19	95.0	84	16	Q821D2
32	19	95.0	84	16	Q7VPV6
33	19	95.0	85	3	Q43116
34	19	95.0	87	6	Q99149
35	19	95.0	87	9	Q7X3Y9
36	19	95.0	88	2	Q98590
37	19	95.0	88	10	Q41185
38	19	95.0	89	2	Q9ZGY2
39	19	95.0	89	16	Q9CNX1
40	19	95.0	89	16	Q9CFD1
41	19	95.0	90	4	Q81ZX3
42	19	95.0	91	13	Q98TB2
43	19	95.0	94	2	Q8Kf12
44	19	95.0	94	6	Q46425
45	19	95.0	96	16	Q8U8Q1
46	19	95.0	96	16	Q89WX7
47	19	95.0	96	17	Q8U0G9
48	19	95.0	97	12	Q86535
49	19	95.0	97	16	Q8Y476
50	19	95.0	99	16	Q9HZ38
51	19	95.0	99	16	Q885M3
52	19	95.0	100	16	Q82UR2
53	19	95.0	101	2	Q8V554
54	19	95.0	101	17	Q77YC2
55	19	95.0	102	16	Q81R27
56	19	95.0	103	4	Q722N2
57	19	95.0	103	16	Q9F368
58	19	95.0	103	16	Q89MS9
59	19	95.0	104	9	Q856B5
60	19	95.0	105	5	Q8SVK0
61	19	95.0	105	9	Q856U1
62	19	95.0	105	17	Q96Z31
63	19	95.0	106	1	P71530
64	19	95.0	106	6	Q9BGL5
65	19	95.0	106	10	Q23682
66	19	95.0	107	3	Q9C1L1
67	19	95.0	107	5	Q81HV3
68	19	95.0	107	16	Q8NRX6
69	19	95.0	109	13	Q9PU82
70	19	95.0	109	16	O53333
71	19	95.0	109	16	Q7TX28
72	19	95.0	110	12	O11343
73	19	95.0	110	16	Q88EG3
74	19	95.0	111	17	Q8U296
75	19	95.0	112	5	Q86PL2
76	19	95.0	112	13	Q98SR4
77	19	95.0	112	13	Q98SR3
78	19	95.0	112	16	Q91315
79	19	95.0	113	2	P95437
80	19	95.0	113	2	O69133
81	19	95.0	113	17	Q8TYL3
82	19	95.0	114	16	Q8U5K8
83	19	95.0	115	4	Q9Y5V1
84	19	95.0	115	17	Q9V203
85	19	95.0	116	11	Q8CD94
86	19	95.0	116	12	Q9DW67
87	19	95.0	118	4	Q8TCV1
88	19	95.0	118	10	Q7X1W4
89	19	95.0	119	2	Q9EXG6

Q82x12 nitrosomona	Q7x711 oryza sativ	Q8npa7 corynebacte	Q8aug2 salmo trutt	Q8aup0 salmo salar	P97252 escherichia	Q97JU4 clostridium	Q82mx0 streptomyce	Q862m8 bos taurus	Q88vs7 lactobacill	Q98582 paramecium	Q9ki36 agrobacteri	Q89w16 bradyrhizob	Q9kav4 bacillus ha	Q821d2 chlamydophi	Q7vpv6 chlamydia p	Q43116 colletotric	Q99149 ovis aries	Q7x3y9 bacterioph	Q98590 nitrosomona	Q41185 arabidopsis	Q98gy2 yersinia pe	Q9cnx1 pasteurella	Q9cfd1 lactococcus	Q81zx3 homo sapien	Q98tb2 ambloplites	Q8xy12 rhizobium e	Q46425 cryotolagus	Q8u8q1 agrobacteri	Q89wx7 bradyrhizob	Q8u0g9 pyrococcus	Q86535 hepatitis a	Q8y476 listeria mo	Q9hz38 pseudomonas	Q885m3 pseudomonas	Q82ur2 nitrosomona	Q8vs54 lactobacill	Q77yc2 sulfolobus	Q81r27 bacillus an	Q722n2 homo sapien	Q9f368 streptomyce	Q89ms9 bradyrhizob	Q856b5 mycobacteri	Q8svk0 encephalito	Q856u1 mycobacteri	Q96z31 sulfolobus	P71530 methanococc	Q9bgl5 ovnis aries	Q23682 arabidopsis	Q9c1l1 neurospora	Q81hv3 plasmodium	Q8nrx6 corynebacte	Q9pu82 crocodylus	O53333 mycobacteri	O7tx28 mycobacteri	O11343 molluscum c	Q8eg3 pseudomonas	Q8u296 pyrococcus	Q86pl2 caenorhabdi	Q98sr4 acipenser s	Q98sr3 acipenser s	Q9i315 pseudomonas	P95437 pseudomonas	O69133 burkholderi	Q8tyl3 methanopyru	Q8u5k8 agrobacteri	Q9y5v1 homo sapien	Q9v203 pyrococcus	Q8cd94 mus musculu	Q9dw67 rat cytomeg	Q8tcv1 homo sapien	Q7x1w4 oryza sativ	Q9exg6 listeria mo
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90	19	95.0	119	5	Q95Y64	Q95Y64 caenorhabdi	163	19	95.0	140	13	Q9JIE5	Q9JIE5 agalynchnis
91	19	95.0	119	5	Q95Y64	Q95Y64 caenorhabdi	164	19	95.0	140	16	Q9JIE5	Q9JIE5 agalynchnis
92	19	95.0	119	16	Q92R99	Q92R99 rhizobium m	165	19	95.0	140	16	Q9JIE5	Q9JIE5 agalynchnis
93	19	95.0	119	16	Q92R99	Q92R99 rhizobium m	166	19	95.0	140	16	Q9JIE5	Q9JIE5 agalynchnis
94	19	95.0	119	16	Q92R99	Q92R99 rhizobium m	167	19	95.0	140	16	Q9JIE5	Q9JIE5 agalynchnis
95	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	168	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
96	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	169	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
97	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	170	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
98	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	171	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
99	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	172	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
100	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	173	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
101	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	174	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
102	19	95.0	120	2	Q9ALH9	Q9ALH9 uncultured	175	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
103	19	95.0	121	4	Q92R99	Q92R99 rhizobium m	176	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
104	19	95.0	121	4	Q92R99	Q92R99 rhizobium m	177	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
105	19	95.0	121	4	Q92R99	Q92R99 rhizobium m	178	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
106	19	95.0	122	16	Q9PHJ7	Q9PHJ7 oryza sativ	179	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
107	19	95.0	122	16	Q9PHJ7	Q9PHJ7 oryza sativ	180	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
108	19	95.0	123	16	Q9GJ7M	Q9GJ7M pasteurilla	181	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
109	19	95.0	123	16	Q9GJ7M	Q9GJ7M pasteurilla	182	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
110	19	95.0	124	9	Q93976	Q93976 bacteriophage	183	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
111	19	95.0	124	16	Q9FQZ0	Q9FQZ0 corynebacte	184	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
112	19	95.0	125	16	Q918K2	Q918K2 bacillus ce	185	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
113	19	95.0	125	16	Q93643	Q93643 mycobacteri	186	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
114	19	95.0	125	16	Q97VZ0	Q97VZ0 mycobacteri	187	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
115	19	95.0	125	17	Q92336	Q92336 methanobact	188	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
116	19	95.0	126	2	Q939V9	Q939V9 anabaena so	189	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
117	19	95.0	126	6	Q9X5F8	Q9X5F8 bos taurus	190	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
118	19	95.0	126	12	Q94351	Q94351 simian viru	191	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
119	19	95.0	126	16	Q9PNZ4	Q9PNZ4 campylobact	192	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
120	19	95.0	126	16	Q9WFX5	Q9WFX5 bordetella	193	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
121	19	95.0	127	12	Q91BF3	Q91BF3 spodoptera	194	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
122	19	95.0	127	16	Q928V1	Q928V1 mycobacteri	195	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
123	19	95.0	127	16	Q928V1	Q928V1 mycobacteri	196	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
124	19	95.0	127	16	Q928V1	Q928V1 mycobacteri	197	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
125	19	95.0	127	16	Q928V1	Q928V1 mycobacteri	198	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
126	19	95.0	128	2	Q938X8	Q938X8 acinetobact	199	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
127	19	95.0	128	2	Q938X8	Q938X8 acinetobact	200	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
128	19	95.0	128	2	Q938X8	Q938X8 acinetobact	201	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
129	19	95.0	128	10	Q9ZSM5	Q9ZSM5 dendrobium	202	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
130	19	95.0	128	16	Q915K0	Q915K0 salmonella	203	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
131	19	95.0	129	10	Q958B1	Q958B1 arabidopsis	204	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
132	19	95.0	129	12	Q94339	Q94339 simian viru	205	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
133	19	95.0	130	9	Q9W5Y1	Q9W5Y1 bacteriophage	206	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
134	19	95.0	130	12	Q9W5Y1	Q9W5Y1 bacteriophage	207	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
135	19	95.0	131	2	Q94CY0	Q94CY0 gamma-prote	208	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
136	19	95.0	132	2	Q94307	Q94307 anabaena sp	209	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
137	19	95.0	132	9	Q9SPD0	Q9SPD0 pseudomonas	210	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
138	19	95.0	132	16	Q9G418	Q9G418 anabaena sp	211	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
139	19	95.0	133	2	Q9GH32	Q9GH32 gamma-prote	212	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
140	19	95.0	133	16	Q9RZR3	Q9RZR3 deinococcus	213	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
141	19	95.0	133	16	Q9RZR3	Q9RZR3 deinococcus	214	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
142	19	95.0	133	16	Q9RZR3	Q9RZR3 deinococcus	215	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
143	19	95.0	134	5	Q957W7	Q957W7 mycobacteri	216	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
144	19	95.0	134	5	Q957W7	Q957W7 mycobacteri	217	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
145	19	95.0	134	16	Q92OT7	Q92OT7 salmonella	218	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
146	19	95.0	134	16	Q92OT7	Q92OT7 salmonella	219	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
147	19	95.0	134	16	Q92OT7	Q92OT7 salmonella	220	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
148	19	95.0	134	17	Q96QF7	Q96QF7 methanosarc	221	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
149	19	95.0	134	17	Q96QF7	Q96QF7 methanosarc	222	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
150	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	223	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
151	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	224	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
152	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	225	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
153	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	226	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
154	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	227	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
155	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	228	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
156	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	229	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
157	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	230	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
158	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	231	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
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161	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	234	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis
162	19	95.0	135	16	Q96QF7	Q96QF7 methanosarc	235	19	95.0	142	10	Q9JIE5	Q9JIE5 agalynchnis

235	19	95.0	165	4	Q96ED1	Q96ed1 homo sapien	309	19	95.0	188	16	Q8XC46	Q8xc46 escherichia
237	19	95.0	165	5	Q8SRD1	Q8srd1 encephalito	310	19	95.0	188	17	Q8TNJ0	Q8tnj0 methanosarc
238	19	95.0	165	11	Q9D6S8	Q9d6s8 mus musculus	311	19	95.0	189	2	Q84CM0	Q84cm0 streptomyc
239	19	95.0	166	2	Q52661	Q52661 rhodobacter	312	19	95.0	189	5	Q20199	Q20199 caenorhabdi
240	19	95.0	166	10	Q8R296	Q8r296 oryza sativ	313	19	95.0	189	8	Q8WJ84	Q8wj84 eriosorus h
241	19	95.0	166	10	Q949R0	Q949r0 oryza sativ	314	19	95.0	189	10	Q07299	Q07299 zea mays (m
242	19	95.0	166	10	Q849R0	Q849r0 pyrobaculum	315	19	95.0	189	16	Q8U549	Q8u549 agrobacteri
243	19	95.0	167	17	Q8ZVJ9	Q8zvj9 pyrobaculum	316	19	95.0	189	16	Q8FC12	Q8fc12 escherichia
244	19	95.0	167	2	Q8GAC0	Q8gac0 arthrobacte	317	19	95.0	190	4	Q96F12	Q96f12 homo sapien
245	19	95.0	168	2	Q47850	Q47850 pantoea agg	318	19	95.0	190	4	Q96F12	Q96f12 homo sapien
246	19	95.0	168	16	Q8ZRFV0	Q8zrfv0 yersinia pe	319	19	95.0	190	16	Q93RS6	Q93rs6 streptomyc
247	19	95.0	169	16	Q9X8N2	Q9x8n2 streptomyc	320	19	95.0	191	2	Q93KL3	Q93kl3 uncultured
248	19	95.0	169	16	Q7UKV3	Q7ukv3 rhodopirell	321	19	95.0	191	10	Q94LF2	Q94lf2 oryza sativ
249	19	95.0	169	16	Q7USD8	Q7usd8 synechococc	322	19	95.0	191	10	Q84MW8	Q84mw8 oryza sativ
250	19	95.0	170	16	Q93JC6	Q93jc6 streptomyc	323	19	95.0	191	16	Q9KKV1	Q9kkv1 vibrio chol
251	19	95.0	170	16	Q881F4	Q881f4 pseudomonas	324	19	95.0	191	16	Q8EAK2	Q8eak2 shewanella
252	19	95.0	171	10	Q84QL9	Q84ql9 oryza sativ	325	19	95.0	192	10	Q8L647	Q8l647 deschampsia
253	19	95.0	171	12	Q8JQ15	Q8jq15 black queen	326	19	95.0	192	16	Q8UG64	Q8ug64 agrobacteri
254	19	95.0	172	11	Q9AWP5	Q9awp5 oryza sativ	327	19	95.0	192	16	Q9ADP7	Q9adp7 streptomyc
255	19	95.0	172	11	Q5K179	Q5k179 mus musculus	328	19	95.0	192	16	Q83D37	Q83d37 coxiella bu
256	19	95.0	172	11	Q8K164	Q8k164 mus musculus	329	19	95.0	193	2	F74983	F74983 yersinia en
257	19	95.0	172	11	Q55177	Q55177 mus musculus	330	19	95.0	193	16	Q9KY43	Q9ky43 streptomyc
258	19	95.0	172	17	Q9U236	Q9u236 pyrococcus	331	19	95.0	193	16	Q82B77	Q82b77 streptomyc
259	19	95.0	172	17	Q8U1U0	Q8u1u0 pyrococcus	332	19	95.0	194	2	Q9EVD1	Q9evd1 erwinia amy
260	19	95.0	173	5	Q20526	Q20526 caenorhabdi	333	19	95.0	194	2	Q8GQ2	Q8gq2 serratia ma
261	19	95.0	173	5	Q8SWX9	Q8swx9 drosophila	334	19	95.0	194	2	Q8GE12	Q8gei2 erwinia pyr
262	19	95.0	174	11	Q8CTG2	Q8ctg2 mus musculus	335	19	95.0	194	2	Q7X3V2	Q7x3v2 vibrio angu
263	19	95.0	174	16	Q8ECL6	Q8ec16 shewanella	336	19	95.0	194	16	Q9A7S1	Q9a7s1 caulobacter
264	19	95.0	174	16	Q33289	Q33289 mycobacteri	337	19	95.0	194	16	Q8UBS8	Q8ubs8 agrobacteri
265	19	95.0	174	16	Q7V6A9	Q7v6a9 prochloroco	338	19	95.0	195	10	Q9LMI9	Q9lmi9 arabidopsis
266	19	95.0	174	16	Q7TX22	Q7tx22 mycobacteri	339	19	95.0	195	16	Q89TJ4	Q89tj4 bradyrhizob
267	19	95.0	175	11	Q92SA9	Q92sa9 rattus norv	340	19	95.0	195	16	Q88SG8	Q88sg8 lactobacill
268	19	95.0	175	16	Q8A2B2	Q8a2b2 bacteroides	341	19	95.0	196	2	Q93KM6	Q93km6 uncultured
269	19	95.0	175	17	Q82DE1	Q82del1 streptomyc	342	19	95.0	196	5	Q9GNR5	Q9gnr5 stytonychia
270	19	95.0	176	17	Q7VD73	Q7vd73 prochloroco	343	19	95.0	196	5	Q93568	Q93568 caenorhabdi
271	19	95.0	176	16	Q976D7	Q976d7 sulfoblobu	344	19	95.0	196	5	Q9GNR7	Q9gnr7 stytonychia
272	19	95.0	178	5	Q8MTA3	Q8mta3 drosophila	345	19	95.0	196	11	Q9CVX4	Q9cvx4 mus musculu
273	19	95.0	178	16	Q7VJ04	Q7vj04 helicobacte	346	19	95.0	196	11	Q8FT59	Q8ft59 corynebacte
274	19	95.0	178	16	Q7UT14	Q7ut14 rhodopirell	347	19	95.0	196	16	Q8DGL7	Q8dgl7 synechococ
275	19	95.0	179	2	Q54157	Q54157 shigella fl	348	19	95.0	196	16	Q8Z2K7	Q8z2k7 salmonella
276	19	95.0	179	11	Q8R057	Q8r057 mus musculu	349	19	95.0	197	2	Q93KN1	Q93knl uncultured
277	19	95.0	179	16	Q7VXQ4	Q7vxq4 haemophilu	350	19	95.0	197	9	Q8H9Q1	Q8h9q1 vibrio harv
278	19	95.0	179	16	Q7UD52	Q7ud52 shigella fl	351	19	95.0	197	16	Q9CGV5	Q9cgv5 lactococcus
279	19	95.0	180	2	Q8KSU7	Q8ksu7 gamma-prote	352	19	95.0	197	17	Q8TZV4	Q8tzv4 pyrococcus
280	19	95.0	180	10	Q8RXU1	Q8rxu1 arabidopsis	353	19	95.0	198	2	Q8K3L5	Q8k3l5 pyrococcus
281	19	95.0	180	10	Q9M098	Q9m098 arabidopsis	354	19	95.0	198	16	Q9ANC6	Q9anc6 rhizobium 1
282	19	95.0	180	10	Q8LDX3	Q8ldx3 arabidopsis	355	19	95.0	198	16	Q50927	Q50927 nitrosomona
283	19	95.0	180	16	Q8ZPH9	Q8zph9 salmonella	356	19	95.0	199	4	Q9H3L5	Q9h3l5 homo sapien
284	19	95.0	180	16	Q8Z707	Q8z707 salmonella	357	19	95.0	199	4	Q8EX83	Q8ex83 homo sapien
285	19	95.0	180	16	Q8Z707	Q8z707 salmonella	358	19	95.0	199	11	Q8BXC6	Q8bxc6 mus musculu
286	19	95.0	180	16	Q8Z707	Q8z707 salmonella	359	19	95.0	199	11	Q8BJI3	Q8bj13 mus musculu
287	19	95.0	180	16	Q8Z707	Q8z707 salmonella	360	19	95.0	199	16	Q8XTM5	Q8xtm5 raietonia s
288	19	95.0	180	16	Q8Z707	Q8z707 salmonella	361	19	95.0	199	16	Q7U983	Q7u983 synechococ
289	19	95.0	180	16	Q8Z707	Q8z707 salmonella	362	19	95.0	200	16	Q8ZMY2	Q8zmy2 salmonella
290	19	95.0	181	5	Q8MUA9	Q8mu9 ancylostoma	363	19	95.0	200	16	Q9LOA5	Q9loa5 streptomyc
291	19	95.0	181	16	Q8YBS5	Q8ybs5 anabaena sp	364	19	95.0	200	16	Q8ZQA6	Q8zqa6 salmonella
292	19	95.0	182	16	Q7V2G9	Q7v2g9 prochloroco	365	19	95.0	200	16	Q8Z7W8	Q8z7w8 salmonella
293	19	95.0	182	17	Q8TWZ2	Q8twz2 methanopyru	366	19	95.0	201	2	Q9X407	Q9x407 methylosulf
294	19	95.0	183	4	Q8TCQ9	Q8tcq9 homo sapien	367	19	95.0	201	2	Q9X407	Q9x407 methylosulf
295	19	95.0	184	16	Q8X5C1	Q8x5c1 escherichia	368	19	95.0	201	10	Q48848	Q48848 arabidopsis
296	19	95.0	184	16	Q9ZLY9	Q9zly9 helicobacte	369	19	95.0	202	16	Q98127	Q98127 rhizobium 1
297	19	95.0	184	16	Q8LYT2	Q8lyt2 pseudomonas	370	19	95.0	202	2	Q8RNS6	Q8rns6 lactobacill
298	19	95.0	184	16	Q7VC97	Q7vc97 prochloroco	371	19	95.0	202	16	Q8YBY2	Q8yby2 listeria mo
299	19	95.0	184	16	Q8UH5	Q8uh5 agrobacteri	372	19	95.0	202	16	Q69982	Q69982 streptomyc
300	19	95.0	185	16	Q9RZH9	Q9rzh9 deinococcus	373	19	95.0	202	16	P73372	P73372 synechocyst
301	19	95.0	186	2	Q56745	Q56745 wolbachia s	374	19	95.0	203	2	Q9RBB8	Q9rbb8 arthrobacte
302	19	95.0	186	2	P72209	P72209 proteus mir	375	19	95.0	203	10	Q49A97	Q49a97 oryza sativ
303	19	95.0	187	2	Q93T67	Q93t67 riemerella	376	19	95.0	203	16	Q8BP95	Q8bp95 xanthomonas
304	19	95.0	187	16	Q98FP5	Q98fd5 rhizobium 1	377	19	95.0	203	16	Q89Y8	Q89y8 xanthomonas
305	19	95.0	187	16	Q92W30	Q92wb0 rhizobium m	378	19	95.0	203	16	Q88DQ5	Q88dq5 pseudomonas
306	19	95.0	188	5	Q8T317	Q8t317 drosophila	379	19	95.0	204	2	Q9RBE6	Q9rbe6 xanthomonas
307	19	95.0	188	16	Q83722	Q83722 treponema p	380	19	95.0	204	4	Q9NZ83	Q9nzs3 homo sapien
308	19	95.0	188	16	Q8ZH37	Q8zh37 yersinia pe	381	19	95.0	204	4	Q7Z2N7	Q7z2n7 homo sapien

382	19	95.0	204	16	Q92P26	Q92fz6 rickettsia	455	19	95.0	224	16	Q8NRP2	Q8nrp2 corynebacte
383	19	95.0	204	16	Q8PQC4	Q8pqc4 xanthomonas	456	19	95.0	225	16	Q886L5	Q886l5 rhizobium 1
384	19	95.0	204	16	Q93J78	Q93j78 streptomyce	457	19	95.0	225	16	Q825R9	Q825r9 streptomyce
385	19	95.0	204	16	Q7UB59	Q7ub59 shigella fl	458	19	95.0	226	2	Q93AD7	Q93ad7 arthrobacte
386	19	95.0	205	16	Q8X310	Q8x310 escherichia	459	19	95.0	226	2	Q848B9	Q848b9 streptomyce
387	19	95.0	205	16	Q8GSL8	Q8gsl8 bifidobacte	460	19	95.0	226	5	Q8WPD3	Q8wpd3 paracentrot
388	19	95.0	205	16	Q8FBI0	Q8fbi0 escherichia	461	19	95.0	226	11	Q8CSE1	Q8cse1 mus musculu
389	19	95.0	205	16	Q8DVM4	Q8dvm4 streptococc	462	19	95.0	226	16	Q8YDM2	Q8ydm2 brucella me
390	19	95.0	205	16	Q83IV9	Q83iv9 shigella fl	463	19	95.0	226	16	Q8FUS4	Q8fus4 brucella su
391	19	95.0	206	2	Q9KWD3	Q9kwd3 agrobacteri	464	19	95.0	227	2	Q9KJZ2	Q9kjj2 pseudomonas
392	19	95.0	206	11	Q8COY5	Q8coy5 mus musculu	465	19	95.0	227	10	Q8GRV7	Q8grv7 oryza sativ
393	19	95.0	206	16	Q8EC34	Q8ec34 shewanella	466	19	95.0	227	17	Q8ZVD4	Q8zvd4 pyrobaculum
394	19	95.0	207	10	Q8H4R2	Q8h4r2 oryza sativ	467	19	95.0	228	16	Q8Z6Q3	Q8z6q3 salmonella
395	19	95.0	208	16	Q8PD60	Q8pd60 xanthomonas	468	19	95.0	228	16	Q9RS24	Q9rs24 deinococcus
396	19	95.0	208	16	Q82AM2	Q82am2 streptomyce	469	19	95.0	228	16	Q8Z1S3	Q8z1s3 yersinia pe
397	19	95.0	209	2	Q9RBB6	Q9rb66 arthrobacte	470	19	95.0	228	16	Q8FSE2	Q8fse2 corynebacte
398	19	95.0	209	4	Q9BYW9	Q9byw9 homo sapien	471	19	95.0	228	16	Q894X0	Q894x0 clostridium
399	19	95.0	209	16	Q8UP55	Q8ufes agrobacteri	472	19	95.0	228	16	Q83T36	Q83t36 salmonella
400	19	95.0	210	16	Q8ZPD7	Q8zpd7 salmonella	473	19	95.0	229	10	Q9CASS	Q9cas5 arabidopsis
401	19	95.0	210	16	Q8G4Z4	Q8g4z4 bifidobacte	474	19	95.0	229	16	Q667S3	Q667s3 aquifex aeo
402	19	95.0	210	16	Q83L90	Q83l90 shigella fl	475	19	95.0	229	16	Q8CSD8	Q8csd8 staphylococ
403	19	95.0	211	10	Q7XA92	Q7xa92 fragaria an	476	19	95.0	229	16	Q832X6	Q832x6 enterococcu
404	19	95.0	211	16	Q92R80	Q92r80 rhizobium m	477	19	95.0	230	2	Q9RBB0	Q9rbbo arthrobacte
405	19	95.0	211	16	Q8P940	Q8p940 xanthomonas	478	19	95.0	230	5	O76405	O76405 caenorhabdi
406	19	95.0	212	2	Q3RBB7	Q3rb77 arthrobacte	479	19	95.0	230	10	Q84RH7	Q84rh7 lycopersico
407	19	95.0	212	10	Q8RUH2	Q8ruh2 oryza sativ	480	19	95.0	230	16	Q8UHL0	Q8uhl0 agrobacteri
408	19	95.0	212	16	Q914X9	Q914x9 pseudomonas	481	19	95.0	230	16	Q8D0F9	Q8dof9 yersinia pe
409	19	95.0	213	10	Q8H3F6	Q8h3f6 oryza sativ	482	19	95.0	230	16	Q7WQY2	Q7wqy2 bordetella
410	19	95.0	213	16	Q9KPF59	Q9kpf59 vibrio chol	483	19	95.0	230	16	Q7W204	Q7w204 bordetella
411	19	95.0	213	16	Q8YXB0	Q8yxb0 anabaena sp	484	19	95.0	230	16	Q7VUL1	Q7vul1 bordetella
412	19	95.0	213	16	Q8NTZ8	Q8ntz8 corynebacte	485	19	95.0	231	5	Q8MXA3	Q8mxa3 trypanosoma
413	19	95.0	213	16	Q87VGB	Q87vgb pseudomonas	486	19	95.0	231	5	O81684	O81684 drosophila
414	19	95.0	213	17	Q9HR09	Q9hr09 halobacteri	487	19	95.0	231	16	Q9HXR1	Q9hxr1 pseudomonas
415	19	95.0	214	2	Q54380	Q54380 lactococcus	488	19	95.0	231	16	Q882T2	Q882t2 rhizobium 1
416	19	95.0	214	2	Q8KP00	Q8kp00 gamma-prote	489	19	95.0	231	16	Q82E94	Q82e94 listeria in
417	19	95.0	214	2	Q9RC84	Q9rc84 bacillus ha	490	19	95.0	231	16	Q8YXG7	Q8yxg7 brucella me
418	19	95.0	215	2	Q9Z480	Q9z480 agrobacteri	491	19	95.0	231	16	Q8Y9H1	Q8y9h1 listeria mo
419	19	95.0	215	10	O22136	O22136 arabidopsis	492	19	95.0	231	16	Q8XUT7	Q8xut7 ralstonia s
420	19	95.0	215	16	Q98DH0	Q98dh0 rhizobium 1	493	19	95.0	231	16	Q8PQL3	Q8pql3 corynebacte
421	19	95.0	215	16	Q8EP35	Q8ep35 xanthomonas	494	19	95.0	232	2	Q9RBD1	Q9rbdi arthrobacte
422	19	95.0	216	2	Q9RBD2	Q9rbd2 arthrobacte	495	19	95.0	232	16	Q9A6A4	Q9a6a4 caulobacter
423	19	95.0	216	14	P97979	P97979 unidentified	496	19	95.0	232	16	P96241	P96241 mycobacteri
424	19	95.0	216	16	Q92QS1	Q92qs1 rhizobium m	497	19	95.0	232	16	Q7TVJ7	Q7tvj7 mycobacteri
425	19	95.0	216	16	Q88MA0	Q88ma0 pseudomonas	498	19	95.0	232	17	Q8PVL0	Q8pvl0 methanosaar
426	19	95.0	217	16	Q88GA2	Q88ga2 pseudomonas	499	19	95.0	234	2	Q9RBC9	Q9rbcb arthrobacte
427	19	95.0	217	17	Q8UIA8	Q8uia8 pyrococcus	500	19	95.0	234	5	Q9N327	Q9n327 caenorhabdi
428	19	95.0	218	2	Q9REX4	Q9rex4 arthrobacte	501	19	95.0	234	10	Q9FQC4	Q9fqc4 zea mays (m
429	19	95.0	218	10	Q40630	Q40630 oryza sativ	502	19	95.0	234	10	Q94K12	Q94k12 arabidopsis
430	19	95.0	218	10	Q9L2I5	Q9l2y5 arabidopsis	503	19	95.0	234	10	Q8XIF8	Q8xif8 arabidopsis
431	19	95.0	218	16	Q91470	Q91470 pseudomonas	504	19	95.0	234	16	Q8YSQ0	Q8ysq0 anabaena sp
432	19	95.0	218	16	Q8ZES1	Q8zes1 yersinia pe	505	19	95.0	234	16	Q8XBP4	Q8xbp4 escherichia
433	19	95.0	218	16	Q88NB6	Q88nb6 pseudomonas	506	19	95.0	234	16	Q81DL3	Q81dl3 bacillus ce
434	19	95.0	219	16	Q92B71	Q92e71 listeria in	507	19	95.0	235	2	Q9AKL9	Q9akl9 rickettsia
435	19	95.0	219	16	Q69984	Q69984 streptomyce	508	19	95.0	235	2	Q9AKB8	Q9akb8 rickettsia
436	19	95.0	219	16	Q8XKE5	Q8xkes streptomyce	509	19	95.0	235	2	Q9AKG3	Q9akg3 rickettsia
437	19	95.0	219	16	Q7UGG1	Q7ugg1 rhodospirill	510	19	95.0	235	2	Q849C9	Q849c9 streptomyce
438	19	95.0	220	17	Q26842	Q26842 methanobact	511	19	95.0	235	16	Q8W6X8	Q8w6x8 cyanophaga
439	19	95.0	220	17	Q9HQA1	Q9hqa1 halobacteri	512	19	95.0	235	16	Q2XBL1	Q2xb1 rhizobium m
440	19	95.0	221	4	Q96GF5	Q96gf5 homo sapien	513	19	95.0	235	16	Q82IJ4	Q82ij4 rickettsia
441	19	95.0	221	16	Q9KAB1	Q9kab1 bacillus ha	514	19	95.0	235	16	Q8XYZ8	Q8xyz8 ralstonia s
442	19	95.0	221	16	Q93J34	Q93j34 streptomyce	515	19	95.0	236	2	Q9JPA0	Q9jpa0 rhodocyclu
443	19	95.0	221	16	Q82CX2	Q82cx2 streptomyce	516	19	95.0	236	10	Q9LVA8	Q9lva8 arabidopsis
444	19	95.0	222	2	Q9RBD9	Q9rbd9 arthrobacte	517	19	95.0	236	10	Q8SK05	Q8sk05 arabidopsis
445	19	95.0	222	16	Q8F9P8	Q8f9p8 leptospira	518	19	95.0	236	16	Q8UBG5	Q8ubg5 agrobacteri
446	19	95.0	223	5	Q8SUL0	Q8sul0 encephalito	519	19	95.0	237	2	Q9RBC0	Q9rbco arthrobacte
447	19	95.0	223	10	Q94B57	Q94b57 arabidopsis	520	19	95.0	237	2	Q84B84	Q84b84 vibrio fisc
448	19	95.0	223	16	Q92BP8	Q92bp8 streptomyce	521	19	95.0	237	16	Q9KFS9	Q9kfs9 bacillus ha
449	19	95.0	223	16	Q883K9	Q883k9 pseudomonas	522	19	95.0	237	16	Q8N57	Q8n57 rhizobium 1
450	19	95.0	223	16	Q8XGZ1	Q8xgz1 salmonella	523	19	95.0	237	16	Q97IV4	Q97iv4 clostridium
451	19	95.0	224	3	Q03362	Q03362 saccharomyc	524	19	95.0	237	16	Q8ELK7	Q8elk7 oceanobacil
452	19	95.0	224	4	Q92799	Q92799 homo sapien	525	19	95.0	237	17	Q9TMA2	Q9tma2 methanosaar
453	19	95.0	224	11	Q99NG0	Q99ng0 rattus norv	526	19	95.0	238	2	Q9RBP4	Q9rbp4 rhodococcus
454	19	95.0	224	16	Q8Y8J7	Q8y8j7 listeria mo	527	19	95.0	238	16	Q9CIV5	Q9civ5 lactococcus

528	19	95.0	238	16	Q9L246	Q9L246 streptomyce	601	19	95.0	253	16	Q8X4N5	Q8X4N5 escherichia
529	19	95.0	239	3	Q9UVW7	Q9UVW7 candida alb	602	19	95.0	253	16	Q9AK07	Q9AK07 streptomyce
530	19	95.0	239	16	Q836K1	Q836K1 enterococcu	603	19	95.0	253	16	Q8FE98	Q8FE98 escherichia
531	19	95.0	239	16	Q82UL5	Q82UL5 nitrosomona	604	19	95.0	253	16	Q83QB3	Q83QB3 shigella fl
532	19	95.0	239	17	Q82UI3	Q82UI3 pyrococcus	605	19	95.0	253	17	Q9Y895	Q9Y895 aeropyrum p
533	19	95.0	240	17	Q30144	Q30144 archaeoglob	606	19	95.0	254	2	Q9REX0	Q9REX0 athrobacte
534	19	95.0	241	2	Q7WTF7	Q7WTF7 streptomyce	607	19	95.0	254	2	Q825Q1	Q825Q1 clostridium
535	19	95.0	241	10	Q9SVW3	Q9SVW3 arabidopsis	608	19	95.0	254	8	Q98RW7	Q98RW7 guillardia
536	19	95.0	241	10	Q7XR82	Q7XR82 oryza sativ	609	19	95.0	254	10	Q94A55	Q94A55 arabidopsis
537	19	95.0	241	16	Q7WJN5	Q7WJN5 bordetella	610	19	95.0	254	10	Q22536	Q22536 oryza sativ
538	19	95.0	241	16	Q7WJN5	Q7WJN5 bordetella	611	19	95.0	254	10	Q9ATW0	Q9ATW0 zea mays (m
539	19	95.0	241	16	Q7WJN5	Q7WJN5 bordetella	612	19	95.0	254	16	Q8ZGH5	Q8ZGH5 yersinia pe
540	19	95.0	242	5	Q81683	Q81683 drosophila	613	19	95.0	255	2	Q9BE0	Q9BE0 athrobacte
541	19	95.0	242	5	Q81682	Q81682 drosophila	614	19	95.0	255	8	Q95OV2	Q95OV2 tetrahymena
542	19	95.0	242	16	Q8DH96	Q8DH96 synchococ	615	19	95.0	255	16	Q89JK6	Q89JK6 bradyrhizob
543	19	95.0	242	16	Q8CYH8	Q8CYH8 streptococ	616	19	95.0	256	2	Q9RBD5	Q9RBD5 athrobacte
544	19	95.0	242	3	Q9AN57	Q9AN57 bradyrhizob	617	19	95.0	256	8	Q9T7M4	Q9T7M4 tetrahymena
545	19	95.0	243	16	Q8G0Y5	Q8G0Y5 bruceella su	618	19	95.0	256	10	Q94HB4	Q94HB4 oryza sativ
546	19	95.0	244	6	Q8HXL4	Q8HXL4 sus scrofa	619	19	95.0	256	10	Q65325	Q65325 arabidopsis
547	19	95.0	244	16	Q8DSN5	Q8DSN5 streptococ	620	19	95.0	256	10	Q7XF17	Q7XF17 oryza sativ
548	19	95.0	244	16	Q7UQX9	Q7UQX9 rhodopirell	621	19	95.0	256	10	Q9W21	Q9W21 frangipani
549	19	95.0	245	10	Q940J5	Q940J5 arabidopsis	622	19	95.0	257	10	Q8GUK5	Q8GUK5 arabidopsis
550	19	95.0	245	10	Q7XK61	Q7XK61 oryza sativ	623	19	95.0	257	11	Q9CP85	Q9CP85 mus musculu
551	19	95.0	246	6	Q28535	Q28535 mustela vis	624	19	95.0	257	11	Q99JB5	Q99JB5 rhizobium m
552	19	95.0	246	16	Q8P151	Q8P151 xanthomonas	625	19	95.0	257	16	Q92L02	Q92L02 corynebacte
553	19	95.0	246	16	Q8P6V1	Q8P6V1 xanthomonas	626	19	95.0	257	16	Q8NLT7	Q8NLT7 corynebacte
554	19	95.0	246	16	Q8RDB0	Q8RDB0 streptomyce	627	19	95.0	257	16	Q9X7Q4	Q9X7Q4 athrobacte
555	19	95.0	246	16	Q8FM47	Q8FM47 corynebacte	628	19	95.0	258	2	Q9RBB1	Q9RBB1 xenopus lae
556	19	95.0	246	16	Q89MY3	Q89MY3 bradyrhizob	629	19	95.0	258	13	Q7S288	Q7S288 pseudomonas
557	19	95.0	246	16	Q82AC3	Q82AC3 streptomyce	630	19	95.0	258	16	Q9X8L2	Q9X8L2 streptomyce
558	19	95.0	247	2	Q48830	Q48830 lactobacill	631	19	95.0	258	16	Q7WCV7	Q7WCV7 bordetella
559	19	95.0	247	16	Q88ZC3	Q88ZC3 lactobacill	632	19	95.0	258	16	Q7W5C3	Q7W5C3 bordetella
560	19	95.0	248	5	Q97008	Q97008 leishmania	633	19	95.0	258	16	Q7VZN8	Q7VZN8 bordetella
561	19	95.0	248	10	Q949B9	Q949B9 oryza sativ	634	19	95.0	258	16	Q7VZN8	Q7VZN8 thermoplasm
562	19	95.0	248	10	Q93935	Q93935 helianthus	635	19	95.0	258	17	Q9HLA1	Q9HLA1 eubacterium
563	19	95.0	248	10	Q81216	Q81216 zea mays (m	636	19	95.0	259	2	Q9JSP2	Q9JSP2 pseudomonas
564	19	95.0	248	10	Q84RL6	Q84RL6 zea mays (m	637	19	95.0	259	2	Q8VMN6	Q8VMN6 pseudomonas
565	19	95.0	248	10	Q7XA61	Q7XA61 oryza sativ	638	19	95.0	259	13	Q7ZT19	Q7ZT19 xenopus lae
566	19	95.0	248	16	Q8ZG59	Q8ZG59 yersinia pe	639	19	95.0	259	16	P74082	P74082 synchocyst
567	19	95.0	248	16	Q8A971	Q8A971 bacteroides	640	19	95.0	259	16	Q9PJ15	Q9PJ15 campylobact
568	19	95.0	248	17	Q9YCF6	Q9YCF6 aeropyrum p	641	19	95.0	259	16	Q98K61	Q98K61 rhizobium l
569	19	95.0	249	5	Q62042	Q62042 caenorhabdi	642	19	95.0	259	16	Q7U9R3	Q7U9R3 synchococc
570	19	95.0	249	10	Q9LXK3	Q9LXK3 hordeum vul	643	19	95.0	259	17	Q8ZT71	Q8ZT71 Pyrobaculum
571	19	95.0	249	10	Q7ATL9	Q7ATL9 zea mays (m	644	19	95.0	260	2	Q9RBA7	Q9RBA7 athrobacte
572	19	95.0	249	10	Q7XU33	Q7XU33 oryza sativ	645	19	95.0	260	2	Q8G976	Q8G976 pseudomonas
573	19	95.0	249	12	Q919L4	Q919L4 culex nigri	646	19	95.0	260	2	Q849Q8	Q849Q8 pseudomonas
574	19	95.0	249	16	Q8PKD5	Q8PKD5 chlamydia m	647	19	95.0	260	16	Q9YVJ0	Q9YVJ0 anabaena sp
575	19	95.0	249	16	Q8PG49	Q8PG49 xanthomonas	648	19	95.0	260	16	Q8F545	Q8F545 corynebacte
576	19	95.0	249	16	Q8FIP0	Q8FIP0 leptospira	649	19	95.0	260	16	Q81EA0	Q81EA0 bacillus ce
577	19	95.0	249	16	Q83N41	Q83N41 coxiella bu	650	19	95.0	260	16	Q7W0U7	Q7W0U7 bordetella
578	19	95.0	249	16	Q82M75	Q82M75 streptomyce	651	19	95.0	260	16	Q7W0U7	Q7W0U7 bordetella
579	19	95.0	249	17	Q29512	Q29512 archaeoglob	652	19	95.0	260	16	Q7WV38	Q7WV38 bordetella
580	19	95.0	250	10	Q9ATL8	Q9ATL8 zea mays (m	653	19	95.0	261	2	Q66247	Q66247 actinobacil
581	19	95.0	250	11	Q84JF6	Q84JF6 mus musculu	654	19	95.0	261	2	Q9XDR0	Q9XDR0 actinobacil
582	19	95.0	250	11	Q8C4H6	Q8C4H6 mus musculu	655	19	95.0	261	3	Q9P8F1	Q9P8F1 glomus moss
583	19	95.0	250	16	Q25228	Q25228 helicobacte	656	19	95.0	261	3	Q9P8E9	Q9P8E9 glomus moss
584	19	95.0	251	2	Q93A69	Q93A69 gamma-prote	657	19	95.0	261	6	Q95LN6	Q95LN6 macaca fasc
585	19	95.0	251	5	Q8SVK8	Q8SVK8 encephalito	658	19	95.0	261	11	Q8K2L3	Q8K2L3 mus musculu
586	19	95.0	251	11	Q9D4Z4	Q9D4Z4 mus musculu	659	19	95.0	261	11	Q9DCE1	Q9DCE1 mus musculu
587	19	95.0	251	17	Q28320	Q28320 archaeoglob	660	19	95.0	261	11	Q9JMJ6	Q9JMJ6 mus musculu
588	19	95.0	252	2	Q03540	Q03540 escherichia	661	19	95.0	261	11	Q9BMJ6	Q9BMJ6 mus musculu
589	19	95.0	252	9	Q8HA20	Q8HA20 bacterioph	662	19	95.0	261	11	Q9BH40	Q9BH40 mus musculu
590	19	95.0	252	10	Q94CS9	Q94CS9 oryza sativ	663	19	95.0	261	16	Q9K8W5	Q9K8W5 bacillus ha
591	19	95.0	252	10	Q7XA62	Q7XA62 oryza sativ	664	19	95.0	261	16	Q987X7	Q987X7 rhizobium l
592	19	95.0	252	16	Q9A534	Q9A534 caulobacter	665	19	95.0	261	16	Q8U993	Q8U993 agrobacteri
593	19	95.0	252	16	Q8AU66	Q8AU66 lactobacill	666	19	95.0	261	16	Q87YH4	Q87YH4 pseudomonas
594	19	95.0	252	16	Q7UT61	Q7UT61 rhodopirell	667	19	95.0	261	16	Q7WPP1	Q7WPP1 bordetella
595	19	95.0	252	17	Q97VV6	Q97VV6 sulfolobus	668	19	95.0	261	16	Q7WBP9	Q7WBP9 bordetella
596	19	95.0	253	2	Q97VV6	Q97VV6 peptobacter	669	19	95.0	262	3	Q8RSJ2	Q8RSJ2 gamma-prote
597	19	95.0	253	5	Q8KH15	Q8KH15 drosophila	670	19	95.0	262	3	Q9P8E8	Q9P8E8 glomus moss
598	19	95.0	253	5	Q95U55	Q95U55 streptococ	671	19	95.0	262	16	Q9WZP2	Q9WZP2 thermotoga
599	19	95.0	253	10	Q8W371	Q8W371 oryza sativ	672	19	95.0	262	16	Q8EDY1	Q8EDY1 shewanella
600	19	95.0	253	16	Q8ZFH9	Q8ZFH9 yersinia pe	673	19	95.0	262	17	Q8U0A9	Q8U0A9 pyrococcus

674	19	95.0	263	16	Q8D064	Q8d064 yersinia pe	747	19	95.0	276	16	Q8Z016	Q8z016 anabaena sp
675	19	95.0	263	16	Q8A0Q5	Q8a0q5 bacteroides	748	19	95.0	276	16	Q8P223	Q8p223 xanthomonas
676	19	95.0	263	16	Q7W22	Q7w22 bordetella	749	19	95.0	276	16	Q881P0	Q881p0 pseudomonas
677	19	95.0	263	16	Q7WbJ9	Q7wbj9 bordetella	750	19	95.0	277	2	O85287	O85287 sphingomona
678	19	95.0	264	4	Q8TDN7	Q8tdn7 homo sapien	751	19	95.0	277	2	P72544	P72544 synechococc
679	19	95.0	264	10	Q940D9	Q940d9 pinus taeda	752	19	95.0	277	16	Q8P8X6	Q8p8x6 xanthomonas
680	19	95.0	265	4	Q8TDC1	Q8tdc1 homo sapien	753	19	95.0	278	16	Q9JXZ5	Q9jxz5 neisseria m
681	19	95.0	265	5	O15953	O15953 drosophila	754	19	95.0	278	16	Q9JVK5	Q9jvk5 neisseria m
682	19	95.0	265	10	Q8G3R6	Q8g3r6 cryza sativ	755	19	95.0	278	16	Q83694	Q83694 treponema p
683	19	95.0	265	11	Q91ZX8	Q91zx8 rattus norv	756	19	95.0	278	16	Q8E5D6	Q8e5d6 streptococc
684	19	95.0	265	17	Q978W2	Q978w2 thermoplas	757	19	95.0	279	16	Q8E3D1	Q8e3d1 rhizobium l
685	19	95.0	267	17	Q978W2	Q978w2 actinobacil	758	19	95.0	279	16	Q7W3Y6	Q7w3y6 bordetella
686	19	95.0	267	2	O05364	O05364 gamma-prote	759	19	95.0	279	16	Q7V7G9	Q7v7g9 bordetella
687	19	95.0	267	2	Q83Y72	Q83y72 gamma-prote	760	19	95.0	279	17	Q7V7G9	Q7v7g9 halobacteri
688	19	95.0	267	10	Q8GZD2	Q8gzd2 zea mays (m	761	19	95.0	280	2	P71101	P71101 curtopbacter
689	19	95.0	267	11	Q8B2W5	Q8b2w5 mus musculu	762	19	95.0	280	2	Q8GFG7	Q8gfg7 rhodococcus
690	19	95.0	267	16	Q8A8V3	Q8a8v3 caulobacter	763	19	95.0	280	10	Q9LGD0	Q9lgd0 cryza sativ
691	19	95.0	267	16	Q8U757	Q8u757 agrobacteri	764	19	95.0	280	10	Q92LF6	Q92lf6 rhizobium m
692	19	95.0	267	16	Q88H22	Q88h22 pseudomonas	765	19	95.0	280	16	Q81CH3	Q81ch3 brucella me
693	19	95.0	267	17	Q8ZXK1	Q8zxk1 pyrobaculum	766	19	95.0	280	16	Q8NRY7	Q8nry7 corynebacte
694	19	95.0	268	5	Q8T4T4	Q8t4t4 aedes aegyp	767	19	95.0	280	17	Q8TU99	Q8tu99 methanosarc
695	19	95.0	268	5	Q8N0R8	Q8n0r8 aedes aegyp	768	19	95.0	281	2	Q9ADV7	Q9adv7 ehrlichia c
696	19	95.0	268	5	Q9R1G0	Q9r1g0 aedes aegyp	769	19	95.0	281	10	Q9Z0L7	Q9z0l7 arabidopsis
697	19	95.0	268	5	Q8T4T5	Q8t4t5 aedes aegyp	770	19	95.0	281	10	O04035	O04035 arabidopsis
698	19	95.0	268	5	Q16900	Q16900 aedes aegyp	771	19	95.0	281	12	Q040W8	Q040w8 squash leaf
699	19	95.0	268	10	Q8W189	Q8w189 cryza sativ	772	19	95.0	281	16	Q82M07	Q82m07 streptomyc
700	19	95.0	268	16	Q8D0N4	Q8d0n4 yersinia pe	773	19	95.0	281	16	Q7UC85	Q7uc85 rhodospirell
701	19	95.0	269	4	Q8TBI5	Q8tbis homo sapien	774	19	95.0	281	17	Q962Y6	Q962y6 sulfobolus
702	19	95.0	269	11	Q91V8	Q91v8 mus musculu	775	19	95.0	282	2	Q9KH99	Q9kha9 pseudomonas
703	19	95.0	269	11	Q7TN36	Q7tn36 rattus norv	776	19	95.0	282	2	O68913	O68913 streptomyc
704	19	95.0	269	16	Q8FS10	Q8fs10 corynebacte	777	19	95.0	282	16	Q9KGP1	Q9kgp1 bacillus ha
705	19	95.0	269	16	Q7WF26	Q7wf26 bordetella	778	19	95.0	282	16	Q98KW3	Q98kw3 rhizobium l
706	19	95.0	269	16	Q7W3P9	Q7w3p9 bordetella	779	19	95.0	282	16	Q9Z688	Q9z688 clostridium
707	19	95.0	269	16	Q7V8T6	Q7v8t6 bordetella	780	19	95.0	282	16	Q8DN8	Q8dn8 streptococc
708	19	95.0	269	17	Q57836	Q57836 pyrococcus	781	19	95.0	282	16	Q89176	Q89176 bradyrhizob
709	19	95.0	270	16	Q8NTB3	Q8ntb3 corynebacte	782	19	95.0	282	16	Q82DZ5	Q82dz5 streptomyc
710	19	95.0	271	2	Q86443	Q86443 pseudomonas	783	19	95.0	283	2	O85983	O85983 sphingomona
711	19	95.0	271	2	Q9N2J4	Q9n2j4 canis famil	784	19	95.0	283	2	Q31VK3	Q31vk3 sphingomona
712	19	95.0	271	8	O21312	O21312 tetrahymena	785	19	95.0	284	3	O13848	O13848 schizosacch
713	19	95.0	271	16	Q7UNX6	Q7unx6 rhodospirell	786	19	95.0	284	4	Q9HAB8	Q9hab8 homo sapien
714	19	95.0	271	16	Q7UMF0	Q7umf0 rhodospirell	787	19	95.0	284	16	Q8DTC4	Q8dct4 streptococc
715	19	95.0	272	2	Q8G3V5	Q8ggv5 lactobacill	788	19	95.0	284	16	O8A5T6	O8ast6 bacteroides
716	19	95.0	272	2	Q8GFH0	Q8gfh0 rhodococcus	789	19	95.0	285	10	Q9SHW9	Q9shw9 arabidopsis
717	19	95.0	272	5	Q17131	Q17131 babesia equ	790	19	95.0	285	12	Q9PVX4	Q9pvx4 xestia c-ni
718	19	95.0	272	5	Q9TYB0	Q9tyb0 babesia equ	791	19	95.0	285	15	O87X11	O87x11 pseudomonas
719	19	95.0	272	5	Q9TYB1	Q9tyb1 babesia equ	792	19	95.0	286	2	O05327	O05327 sphingomona
720	19	95.0	272	5	Q9TYA7	Q9tya7 babesia equ	793	19	95.0	286	3	Q7ZVV6	Q7zvv6 brachydania
721	19	95.0	272	5	Q9TYB2	Q9tyb2 babesia equ	794	19	95.0	286	16	Q8ZPM8	Q8zpm8 salmonella
722	19	95.0	272	5	Q9TYA9	Q9tya9 babesia equ	795	19	95.0	286	16	O8ZE21	O8ze21 yersinia pe
723	19	95.0	272	5	Q9TYA8	Q9tya8 babesia equ	796	19	95.0	286	16	Q8DWF0	Q8dwf0 streptococc
724	19	95.0	272	5	O46365	O46365 babesia equ	797	19	95.0	286	16	Q883F1	Q883f1 pseudomonas
725	19	95.0	272	5	Q9TYB3	Q9tyb3 babesia equ	798	19	95.0	287	5	Q81410	Q81410 caenorhabdi
726	19	95.0	272	5	O45145	O45145 caenorhabdi	799	19	95.0	287	16	O8X649	O8x649 escherichia
727	19	95.0	273	2	Q9F5J1	Q9f5j1 streptomyc	800	19	95.0	287	16	O86719	O86719 streptomyc
728	19	95.0	273	5	Q20243	Q20243 caenorhabdi	801	19	95.0	287	16	O8F189	O8f189 escherichia
729	19	95.0	273	11	Q8R4X1	Q8r4x1 mus musculu	802	19	95.0	287	16	O8F189	O8f189 escherichia
730	19	95.0	273	16	Q9PCH8	Q9pch8 streptomyc	803	19	95.0	287	16	O88M34	O88m34 pseudomonas
731	19	95.0	273	17	Q8TUV2	Q8tuv2 pyrobaculum	804	19	95.0	287	16	O83KY1	O83ky1 shigella fl
732	19	95.0	273	17	Q8TXU3	Q8txu3 methanopyru	805	19	95.0	287	16	O8H0U7	O8hou7 arabidopsis
733	19	95.0	274	5	Q20303	Q20303 caenorhabdi	806	19	95.0	288	16	O8YGG8	O8ygg8 brucella me
734	19	95.0	274	11	Q8CDS2	Q8cds2 mus musculu	807	19	95.0	288	16	O8YGG8	O8ygg8 bacillus an
735	19	95.0	274	16	Q9KFK4	Q9kfk4 bacillus ha	808	19	95.0	288	16	O81A22	O81a22 bacillus ce
736	19	95.0	274	16	Q9A112	Q9a112 streptococc	809	19	95.0	289	11	Q8BMV2	Q8bm2 mus musculu
737	19	95.0	274	16	Q97DB2	Q97db2 clostridium	810	19	95.0	289	11	Q8BKP5	Q8bkp5 mus musculu
738	19	95.0	274	16	Q8P2P0	Q8p2p0 streptococc	811	19	95.0	289	16	Q92MY8	Q92my8 rhizobium m
739	19	95.0	274	16	Q8FTL7	Q8ftl7 corynebacte	812	19	95.0	289	16	O87IC4	O87ic4 vibrio para
740	19	95.0	274	16	Q8F5I3	Q8f5i3 leptospira	813	19	95.0	290	2	Q44HE4	Q44he4 vibrio vuln
741	19	95.0	274	16	Q8F5I3	Q8f5i3 leptospira	814	19	95.0	290	4	Q8TAB2	Q8tab2 homo sapien
742	19	95.0	274	16	Q8F5I3	Q8f5i3 leptospira	815	19	95.0	290	11	Q9CYZ7	Q9cyz7 mus musculu
743	19	95.0	275	16	Q9VST1	Q9vst1 bordetella	816	19	95.0	290	11	Q8AVB1	Q8avb1 brachydania
744	19	95.0	275	16	Q98H12	Q98h12 rhizobium l	817	19	95.0	290	16	O8UCU3	O8uc3 agrobacteri
745	19	95.0	275	16	Q87E28	Q87f28 clostridium	818	19	95.0	291	2	Q8ZN71	Q8zn71 streptomyc
746	19	95.0	276	5	Q18536	Q18536 caenorhabdi	819	19	95.0	291	12	Q7TLM0	Q7t1m0 choristoneu

820	19	95.0	291	16	Q97LH6	Q97Lb6 clostridium	893	13	Q7ZX07	Q7zx07 xenopus lae
821	19	95.0	291	16	Q84533	Q84633 chlamydia t	894	16	Q8U746	Q8u746 agrobacteri
822	19	95.0	292	5	Q33766	Q33766 spingomonas	895	16	Q8PGN2	Q8pgn2 xanthomonas
823	19	95.0	292	5	Q16616	Q16616 caenorhabdi	896	17	Q8Z2C4	Q8z2c4 pyrobaculum
824	19	95.0	292	5	Q7Y2C5	Q7Y2c5 bacterioph	897	5	Q18327	Q18327 caenorhabdi
825	19	95.0	293	5	Q9GNY9	Q9gny9 leishmania	898	5	Q8STV9	Q8stv9 encephalito
826	19	95.0	293	16	Q83315	Q83315 treponema p	899	10	Q8LNR7	Q8lnr7 arabidopsis
827	19	95.0	293	16	Q88LZ3	Q88Lz3 pseudomonas	900	10	Q8VGH1	Q8vgh1 mus musculu
828	19	95.0	293	16	Q828J6	Q828j6 streptomyce	901	16	Q82PD4	Q82pd4 streptomyce
829	19	95.0	294	4	Q9RGK4	Q9rgk4 bacteroides	902	16	Q8VEG8	Q8veg8 mus musculu
830	19	95.0	294	4	Q9NRW3	Q9nrw3 homo sapien	903	16	Q9CH02	Q9ch02 lactococcus
831	19	95.0	294	10	Q8G1P1	Q8g1p1 oryza sativ	904	16	Q8NLL4	Q8nll4 corynebacte
832	19	95.0	295	2	Q9DXK6	Q9dxk6 bacteroides	905	16	Q7V947	Q7v947 pyrobaculo
833	19	95.0	295	9	Q854V0	Q854v0 mycobacteri	906	309	Q8T000	Q8t000 arabidopsi
834	19	95.0	295	9	Q94DE7	Q94de7 oryza sativ	907	309	Q8VGU8	Q8vgu8 mus musculu
835	19	95.0	295	16	Q9EPG2	Q9epg2 xylella fas	908	309	Q7TRC3	Q7trc3 mus musculu
836	19	95.0	295	16	Q9KV64	Q9kv64 vibrio chol	909	16	Q8ARE1	Q8are1 mycoplasma
837	19	95.0	295	163	Q8K9N8	Q8k9n8 streptococ	910	310	Q8Y6E6	Q8y6e6 homo sapien
838	19	95.0	295	163	Q8A8K1	Q8a8k1 bacteroides	911	310	Q9SPD6	Q9spd6 arabidopsi
839	19	95.0	295	16	Q8AET9	Q8aet9 xylella fas	912	310	Q84Z99	Q84z99 oryza sativ
840	19	95.0	296	2	Q9LC87	Q9lc87 nocardioide	913	310	Q8K2C6	Q8k2c6 mus musculu
841	19	95.0	296	17	Q8TU61	Q8tu61 methanosarc	914	310	Q8K2C6	Q8k2c6 mus musculu
842	19	95.0	296	17	Q8PWS7	Q8pws7 methanosarc	915	310	Q8EMQ9	Q8emq9 anasacta mo
843	19	95.0	297	2	Q93LQ8	Q93lq8 klebsiella	916	310	Q8CK67	Q8ck67 pasteurella
844	19	95.0	297	10	Q82163	Q82163 arabidopsi	917	310	Q8BE77	Q8be77 pseudomonas
845	19	95.0	297	16	Q8YV53	Q8yv53 anabaena sp	918	310	Q8YF62	Q8yfr1 cryza sativ
846	19	95.0	297	16	Q8XG56	Q8xg56 anabaena sp	919	311	Q8VFE2	Q8vfe2 mus musculu
847	19	95.0	297	16	Q8XFB0	Q8xfb0 anabaena sp	920	311	Q8FN28	Q8fn28 rhizobium l
848	19	95.0	297	16	Q8R977	Q8r977 thermocanaer	921	311	Q8FN28	Q8fn28 corynebacte
849	19	95.0	298	13	Q7ZV21	Q7zv21 brachydanic	922	311	Q8FU71	Q8fu71 corynebacte
850	19	95.0	298	16	Q8U7A1	Q8u7a1 agrobacteri	923	311	Q8HWP5	Q8hwp5 lactobacilli
851	19	95.0	298	16	Q8ELP1	Q8elp1 oceanobacil	924	311	Q8HMX6	Q8hmx6 halobacteri
852	19	95.0	298	16	Q89IM9	Q89im9 clostridium	925	311	Q97ZS5	Q97zs5 sulfolobus
853	19	95.0	299	2	Q9ADV6	Q9adv6 ehrlichia c	926	311	Q8ZTIS	Q8zti5 pyrobaculum
854	19	95.0	299	2	Q83H57	Q83h57 bradyrhizob	927	311	Q8ZTIS	Q8zti5 pyrobaculum
855	19	95.0	299	2	Q8GF66	Q8gf66 rhodococcus	928	311	Q8ZTIS	Q8zti5 pyrobaculum
856	19	95.0	299	4	Q9NXA8	Q9nxa8 homo sapien	929	312	Q8GFG9	Q8gfg9 rhodococcus
857	19	95.0	299	4	Q9NV14	Q9nv14 homo sapien	930	312	Q12125	Q12125 saccharomyc
858	19	95.0	299	4	Q9NQ56	Q9nq56 homo sapien	931	312	Q7XYT9	Q7xyt9 oryza sativ
859	19	95.0	299	4	Q8TC61	Q8tc61 homo sapien	932	312	Q8NQR2	Q8nqr2 corynebacte
860	19	95.0	299	4	Q9NQ48	Q9nq48 homo sapien	933	313	Q25791	Q25791 plasmodium
861	19	95.0	299	11	Q9JHQ5	Q9jhg5 mus musculu	934	313	Q8VGE0	Q8vge0 mus musculu
862	19	95.0	299	11	Q8CDG8	Q8cdg8 mus musculu	935	313	Q8VGE0	Q8vge0 mus musculu
863	19	95.0	299	11	Q8BRX8	Q8brx8 mus musculu	936	313	Q92AX6	Q92ax6 listeria in
864	19	95.0	299	16	Q9KKW8	Q9kkw8 vibrio chol	937	313	Q8Y6K0	Q8y6k0 listeria mo
865	19	95.0	299	16	Q8EIG6	Q8eig6 shewanella	938	313	Q7U8G9	Q7u8g9 synechococc
866	19	95.0	299	16	Q8EIG6	Q8eig6 shewanella	939	314	Q8WQX2	Q8wqx2 leishmania
867	19	95.0	299	16	Q8DSV7	Q8dsv7 vibrio para	940	314	Q8VFD7	Q8vfd7 mus musculu
868	19	95.0	299	16	Q8ZWF0	Q8zwf0 pyrobaculum	941	314	Q7TRY2	Q7try2 mus musculu
869	19	95.0	299	17	Q8ZWF0	Q8zwf0 pyrobaculum	942	314	Q7TRY2	Q7try2 mus musculu
870	19	95.0	300	2	Q8GFG8	Q8gfg8 rhodococcus	943	314	Q7TRY2	Q7try2 mus musculu
871	19	95.0	300	16	Q8EJ78	Q8ejt8 streptococ	944	314	Q7TRY2	Q7try2 mus musculu
872	19	95.0	300	16	Q8D772	Q8dy72 streptococ	945	314	Q7TRY2	Q7try2 mus musculu
873	19	95.0	300	16	Q7W5F1	Q7w5f1 bordetella	946	314	Q7TRY2	Q7try2 mus musculu
874	19	95.0	301	5	Q3IHK7	Q3ihk7 babesia div	947	314	Q7TRY2	Q7try2 mus musculu
875	19	95.0	301	16	Q93X14	Q93x14 oryza sativ	948	314	Q7TRY2	Q7try2 mus musculu
876	19	95.0	301	16	Q7V7A7	Q7vv77 bordetella	949	314	Q7TRY2	Q7try2 mus musculu
877	19	95.0	301	17	Q8ZAP5	Q8zxp5 pyrobaculum	950	314	Q7TRY2	Q7try2 mus musculu
878	19	95.0	302	8	Q95GH8	Q95gh8 arabidopsi	951	314	Q7TRY2	Q7try2 mus musculu
879	19	95.0	302	10	Q9SGS4	Q9sgs4 arabidopsi	952	314	Q7TRY2	Q7try2 mus musculu
880	19	95.0	302	10	Q8LDJ9	Q8ldj9 arabidopsi	953	314	Q7TRY2	Q7try2 mus musculu
881	19	95.0	302	16	Q8KAL5	Q8kal5 chlorobium	954	314	Q7TRY2	Q7try2 mus musculu
882	19	95.0	303	5	Q8M275	Q8m275 drosophila	955	314	Q7TRY2	Q7try2 mus musculu
883	19	95.0	303	5	Q8IPV4	Q8ipv4 drosophila	956	314	Q7TRY2	Q7try2 mus musculu
884	19	95.0	303	16	Q8NTU5	Q8ntu5 corynebacte	957	314	Q7TRY2	Q7try2 mus musculu
885	19	95.0	303	16	Q7WHF7	Q7whf7 bordetella	958	314	Q7TRY2	Q7try2 mus musculu
886	19	95.0	303	16	Q7W9B0	Q7w9b0 bordetella	959	314	Q7TRY2	Q7try2 mus musculu
887	19	95.0	303	16	Q7VVR7	Q7vvr7 bordetella	960	314	Q7TRY2	Q7try2 mus musculu
888	19	95.0	304	2	Q3IAC8	Q3iac8 pseudomonas	961	314	Q7TRY2	Q7try2 mus musculu
889	19	95.0	304	10	Q8LBSH	Q8lbs8 arabidopsi	962	314	Q7TRY2	Q7try2 mus musculu
890	19	95.0	304	11	Q8BN03	Q8bn03 mus musculu	963	314	Q7TRY2	Q7try2 mus musculu
891	19	95.0	304	11	Q8BN03	Q8bn03 mus musculu	964	314	Q7TRY2	Q7try2 mus musculu
892	19	95.0	305	2	Q84EL1	Q84ell campylobact	965	314	Q7TRY2	Q7try2 mus musculu
						Q84ell stigmatella				

966 19 95.0 317 9 Q854X2 mycobacteri
967 19 95.0 317 10 Q81AG7 arabidopsis
968 19 95.0 317 11 P97827 rattus norv
969 19 95.0 317 11 Q322J2 cricetus
970 19 95.0 317 16 Q812Y4 bacillus ce
971 19 95.0 317 17 Q30168 archaeglob
972 19 95.0 318 2 Q9X5F7 zymomonas m
973 19 95.0 318 2 Q83UD0 neisseria g
974 19 95.0 318 2 Q7WZ93 nomomuraea
975 19 95.0 318 3 Q9C135 mortierella
976 19 95.0 318 10 Q8LCB9 arabidopsis
977 19 95.0 318 10 Q7XE27 oryza sativ
978 19 95.0 318 11 Q9CZ21 mus musculu
979 19 95.0 318 11 Q8VGA9 corynebacte
980 19 95.0 318 16 Q8FECC escherichia fl
981 19 95.0 318 16 Q83LQ1 shigella fl
982 19 95.0 318 17 Q8TT71 methanosarc
983 19 95.0 318 17 Q8TQ14 methanosarc
984 19 95.0 319 3 Q9C0Z8 schizosacch
985 19 95.0 319 5 Q9STC9 drosophila
986 19 95.0 319 10 Q9SW32 arabidopsis
987 19 95.0 319 16 Q8FTS9 corynebacte
988 19 95.0 319 16 Q83E34 coxiella bu
989 19 95.0 319 17 Q9HK71 thermoplasm
990 19 95.0 319 17 Q8TR50 methanosarc
991 19 95.0 320 10 Q8LD47 arabidopsis
992 19 95.0 320 10 Q8LFT4 arabidopsis
993 19 95.0 320 10 Q8LKN3 arabidopsis
994 19 95.0 320 10 Q9LUF3 arabidopsis
995 19 95.0 320 10 Q9C972 arabidopsis
996 19 95.0 320 10 Q84WV9 arabidopsis
997 19 95.0 320 10 Q9CAH5 arabidopsis
998 19 95.0 321 2 Q7X1G1 leptospiril
999 19 95.0 321 4 Q8N6A0 homo sapien
1000 19 95.0 322 2 Q7WX56 homo sapien

ALIGNMENTS

RESULT 1
9TS18
ID Q9TS18 PRELIMINARY; PRT; 20 AA.
AC Q9TS18; PRT; 20 AA.

DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Cytotoxin-binding protein (Fragment).
XS Cryptolagus cuniculus (Rabbit).
XC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
XC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
XX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94039134; PubMed=7693466;
RA Lutz F., Mohr M., Grimmig M., Leidolf R., Linder D.;
RT "Pseudomonas aeruginosa cytoxin-binding protein in rabbit
erythrocyte membranes. An oligomer of 28 kDa with similarity to
transmembrane channel proteins".
RL Eur. J. Biochem. 217:1123-1128(1993).
DR PIR; S39049; S39049.
DR HSP; P47865; 1U4N.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000425; MTP.
DR Pfam; PF00230; MTP; 1
SQ SEQUENCE 20 AA; 2414 MW; 40B82D7DB5283D2D CRC64;

Query Match 95.0%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 14 VAEF 17
RESULT 2
Q9R5CO PRELIMINARY; PRT; 22 AA.
ID Q9R5CO
AC Q9R5CO;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE Cytochrome P-460 (Fragment).
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE.
RX MEDLINE=93224468; PubMed=8385668;
RA McTavish H., Hooper A.B.; Arciero D., Logan M., Mundfrom G.,
RA Fuchs J.A., Hooper A.B.;
RT "Multiple copies of genes coding for electron transport proteins in
the bacterium Nitrosomonas europaea".
RL J. Bacteriol. 175:2445-2447(1993).
SQ SEQUENCE 22 AA; 2549 MW; C22664F5EEICE75F CRC64;

Query Match 95.0%; Score 19; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 3 VAEF 6

RESULT 3
P82214
ID P82214 PRELIMINARY; PRT; 30 AA.

AC P82214;
DT 01-OCT-2001 (TREMELrel. 18, Created)
DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin regulatory light chain 2 (MLC-2) (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RX STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
silkworm".
RL I Chuan Hsueh Pao 28:217-224(2001).
CC -1- SUBUNIT: MYOSIN IS AN HEXAMER OF 2 HEAVY CHAINS & 4 LIGHT CHAINS
(BY SIMILARITY).
CC -1- MISCELLANEOUS: THIS CHAIN BINDS CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR GO; GO:0016459; C:myosin; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007517; P:muscle development; IEA.
DR InterPro; IPR02048; EF-hand.
DR PROSITE; PS00018; EF HAND; PARTIAL.
KW Myosin; Calcium-binding; Muscle protein.
FT CA BIND 25 >30 BY SIMILARITY.
FT NON TER 30
SQ SEQUENCE 30 AA; 3369 MW; 5B5287CE9EF538F3 CRC64;

Query Match 95.0%; Score 19; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
13 VAEF 16

SUITS 4

5518

O25518 PRELIMINARY; PRT; 33 AA.

O25518; 1998 (TrEMBLrel. 05, Created)

01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Hypothetical protein HP0847.

HP0847.

Helicobacter pylori (Campylobacter pylori).

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

Helicobacteraceae; Helicobacter.

NCBI_TaxID=210;

[1]

SEQUENCE FROM N.A.

STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-P., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Corton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

Venter J.C.;

"The complete genome sequence of the gastric pathogen Helicobacter

pylori."

Nature 388:539-547(1997).

EMBL; AE000596; AAD07920.1; --

PIR; G64625; G64625.

TIGR; HP0847; --

Hypothetical protein; Complete proteome.

SEQUENCE 33 AA; 3704 MW; FA3F52631C0DB943 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 33;

Best Local Similarity 100.0%; Pred. No. 5.1e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5

15 VAEF 18

SUITS 5

ZZ19

O82Z19 PRELIMINARY; PRT; 35 AA.

O82Z19; 1998 (TrEMBLrel. 20, Created)

01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Hypothetical protein PAE0485.

PAE0485.

Pyrobaculum aerophilum.

Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;

Thermoproteaceae; Pyrobaculum.

NCBI_TaxID=13773;

[1]

SEQUENCE FROM N.A.

STRAIN=IM2 / ATCC 51768 / DSM 7523;

MEDLINE=21664397; PubMed=11792869;

Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

Miller J.H.;

"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum

aerophilum."

Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

DR EMBL; AE009770; AAL62822.1; --

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 35 AA; 3934 MW; A324B4F94F6A14BB CRC64;

Query Match 95.0%; Score 19; DB 17; Length 35;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

18 VAEF 21

RESULT 6

Q9TQR7

ID Q9TQR7 PRELIMINARY; PRT; 36 AA.

AC Q9TQR7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Transferrin (Fragment).

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OC NCBI_TaxID=9795;

RN [1]

SEQUENCE FROM N.A.

RP Giffard J.M., Brandon R.B., Bell T.K.;

RA "Further identification of single nucleotide polymorphisms in the

equine transferrin gene."

RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF185729; AAF05508.1; --

DR EMBL; AF185722; AAF05501.1; --

DR EMBL; AF185723; AAF05502.1; --

DR EMBL; AF185724; AAF05503.1; --

DR EMBL; AF185725; AAF05504.1; --

DR EMBL; AF185726; AAF05505.1; --

DR EMBL; AF185727; AAF05506.1; --

DR EMBL; AF185728; AAF05507.1; --

DR HSP; P19134; ITFD.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008199; F:ferric iron binding; IEA.

DR GO; GO:0006879; P:iron ion homeostasis; IEA.

DR GO; GO:0006826; P:iron ion transport; IEA.

DR InterPro; IPR001156; Transferrin.

DR Pfam; PF00405; transferrin; 1.

FT NON_TER 1

FT NON_TER 36

SQ SEQUENCE 36 AA; 3802 MW; E2DDDI22186D5FA8 CRC64;

Query Match 95.0%; Score 19; DB 6; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

28 VAEF 31

RESULT 7

Q48420

ID Q48420 PRELIMINARY; PRT; 44 AA.

AC Q48420;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

OS Klebsiella pneumoniae

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.

OC NCBI_TaxID=573;

RN [1]

SEQUENCE FROM N.A.

C STRAIN=ATCC 25955;
 A Willard B.L.;
 T "Investigation of the Klebsiella pneumoniae 1,3-propanediol pathway:
 T Characterization and expression of glycerol dehydratase and 1,3-
 T propanediol oxidoreductase."
 L Thesis (1994), Chemical Engineering, University of Wisconsin-Madison.
 N [2]
 P SEQUENCE FROM N.A.
 C STRAIN=ATCC 25955;
 A Skraly F.A., Willard B.L., Cameron D.C.;
 T "The dha regulation of Klebsiella pneumoniae."
 L Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
 C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 C -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
 R EMBL; U30903; AAA74254.1; -;
 R HSPB; P11244; 1FX8
 R GO; GO:0016021; C:integral to membrane; IEA.
 R GO; GO:0005215; F:transporter activity; IEA.
 R GO; GO:0006810; P:transport; IEA.
 R InterPro; IPR000425; MIP.
 R Pfam; PF00230; MIP; 1.
 R ProDom; PD000295; MIP family; 1.
 M Hypothetical protein; Transmembrane; Transport.
 T NON_TER 44 44
 C SEQUENCE 44 AA; 4537 MW; 39851658FF88E734 CRC64;
 Query Match 95.0%; Score 19; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 / 2 VAEF 5
 12 VAEF 15
 RESULT 8
 330H9
 Q830H9 PRELIMINARY; PRT; 45 AA.
 Q830H9; 01-JUN-2003 (TREMBlrel. 24, Created)
 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 E Hypothetical protein.
 Y EF2805.
 E Enterococcus faecalis (Streptococcus faecalis).
 C Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 C NCBI_TaxID=1351;
 C [1]
 C SEQUENCE FROM N.A.
 C STRAIN=V583 / ATCC 700802;
 C MEDLINE=22550857; PubMed=12663927;
 A Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 A Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 A Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
 A Daugherty S., DeBoy R.T., Durkin S., Kolony J., Madupu R., Nelson W.,
 A Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 A Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 C "Role of mobile DNA in the evolution of vancomycin-resistant
 C Enterococcus faecalis."
 C Science 299:2071-2074 (2003).
 C EMBL; AE016955; AA082500.1; -;
 C TIGR; BF2805; -;
 C SEQUENCE 45 AA; 5278 MW; 89CB55F5CB4C014A CRC64;
 Query Match 95.0%; Score 19; DB 16; Length 45;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 / 2 VAEF 5
 21 VAEF 24

RESULT 9
 025478 PRELIMINARY; PRT; 48 AA.
 AC 025478;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein HP0789.
 GN HP0789.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OC NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RC MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori."
 RL Nature 388:539-547 (1997).
 DR EMBL; AE000591; AAO07847.1; -;
 DR PIR; B64618; E64618.
 DR TIGR; HP0789; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 48 AA; 5492 MW; ED5911D96F57BFEB CRC64;
 Query Match 95.0%; Score 19; DB 16; Length 48;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 15 VAEF 18
 RESULT 10
 Q70XL5 PRELIMINARY; PRT; 51 AA.
 AC Q70XL5;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN RB1255.
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OC NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RC MEDLINE=22735913; PubMed=12835416;
 RA Glöckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlepper H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294135; CAD71991.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 51 AA; 5951 MW; 60F62389C0FDA6A7 CRC64;
 Query Match 95.0%; Score 19; DB 16; Length 51;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
31 VAEF 34

SULT 11
4941

Q44941 PRELIMINARY; PRT; 52 AA.
Q44941; 1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Short ORF.
LON.
Bacillus brevis (Brevibacillus brevis).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.
NCBI_TaxID=1393;
[1]
SEQUENCE FROM N.A.
STRAIN=HPD31;
Ito K., Ueda S., Yamagata H.;
"Cloning, characterization, and inactivation of the Bacillus brevis
lon gene";
J. Bacteriol. 174:2281-2287(1982).
EMBL; D00863; BAA00736.1; -.
PIR; A42375; A42375.
SEQUENCE 52 AA; 5558 MW; 5D689099F84F9AAF CRC64;
Query Match 95.0%; Score 19; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
47 VAEF 50

SULT 12
X3Y8

Q8X3Y8 PRELIMINARY; PRT; 54 AA.
Q8X3Y8;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein 22382.
22382.
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
[1]
SEQUENCE FROM N.A.
STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Poramousis K.,
Apodaca J., Anantharaman I.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
Nature 409:529-533(2001).
EMBL; AE005369; AAC56425.1; -.
PIR; E85745; E85745.
Hypothetical protein; Complete proteome.
SEQUENCE 54 AA; 6507 MW; 8B5FACD985E6140CE CRC64;
Query Match 95.0%; Score 19; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||||
Db 32 VAEF 35

RESULT 13
Q8FIF3 PRELIMINARY; PRT; 54 AA.
AC Q8FIF3;
01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN C1469.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016759; AAN79938.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 54 AA; 5322 MW; 6B3C3D0F21ED4376 CRC64;
Query Match 95.0%; Score 19; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||||
Db 4 VAEF 7

RESULT 14
Q8VSE8 PRELIMINARY; PRT; 61 AA.
AC Q8VSE8;
01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN CP0186.
OS Shigella flexneri 2a.
OC Plasmid pCP301.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=42897;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301;
Jin O., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
Zhu B., Xu B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
Hou Y.D.;
"Complete DNA sequence and analysis of the large virulence plasmid
pCP301 of Shigella flexneri";
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF386526; AAL72547.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 61 AA; 6858 MW; F1CC17B10B28CBFC CRC64;

Query Match 95.0%; Score 19; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 54 VAEF 57

RESULT 15
 D Q9P166 PRELIMINARY; PRT; 61 AA.
 C Q9P166;
 I 01-OCT-2000 (TREMELrel. 15, Created)
 T 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 T 01-OCT-2000 (TREMELrel. 15, Last annotation update)
 S PRO2435
 E Homo sapiens (Human)
 C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 X NCBI_TaxID=9606;
 N [1]
 P SEQUENCE FROM N.A.
 C TISSUE=Liver;
 A Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
 A He F.;
 I "Functional prediction of the coding sequences of 79 new genes deduced
 T by analysis of cDNA clones from human fetal liver."
 L Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 R EMBL: AF119881; AAF69635.1; -
 Q SEQUENCE 61 AA; 7467 MW; 6433950D4657C1D4 CRC64;

Query Match 95.0%; Score 19; DB 4; Length 61;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 30 VAEF 33

RESULT 16
 D Q9GZ9 PRELIMINARY; PRT; 68 AA.
 C Q9GZ9;
 T 01-JUN-2001 (TREMELrel. 17, Created)
 T 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 T 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 E ORF49 (Hypothetical protein) (Unknown)
 S Helicoverpa zea single nucleocapsid nucleopolyhedrovirus,
 S Helicoverpa armigera nucleopolyhedrovirus G4, and
 S Helicoverpa armigera nuclear polyhedrosis virus.
 C Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 C Nucleopolyhedrovirus.
 X NCBI_TaxID=10468, 148363, 51313;
 N [1]
 P SEQUENCE FROM N.A.
 C SPECIES=Helicoverpa zea single nucleocapsid nucleopolyhedrovirus;
 A Chen X., Zhang W.-J., Wong J., Chun G., Lu A., McCutchen B.P.,
 A Presnail J.K., Herrmann R., Dolan M., Tingey S., Hu Z.-H., Vlask J.M.;
 T "Genome sequence analysis of Helicoverpa zea single nucleocapsid
 T nucleopolyhedrovirus."
 T Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 L [2]
 P SEQUENCE FROM N.A.
 C SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 A Deng F., Chen X., Vlask J.M., Arif B.M., Hu Z.;
 T "Sequence analysis of the gp37 gene of Heliothis armigera single-
 T nucleocapsid nucleopolyhedrovirus."
 L Zhongguo Bingdaxue 15:35-42(2000).
 N [3]
 P SEQUENCE FROM N.A.
 C SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;

RA Wang H., Hu Z., Sun X., Vlask J.M., Chen X.;
 RT "Sequence analysis of the iap3 gene of Heliothis armigera single-
 RT nucleocapsid nucleopolyhedrovirus."
 RL Zhongguo Bingdaxue 15:43-49(2000).
 RV [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RX MEDLINE=21078302; PubMed=11210934;
 RA Wang H., Chen X., Wang H., Arif B.M., Vlask J.M., Hu Z.;
 RT "Nucleotide sequence and transcriptional analysis of a putative basic
 RT DNA-binding protein of Helicoverpa armigera polyhedrovirus."
 RL Virus Genes 22:113-120(2001).
 RV [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RX MEDLINE=21064569; PubMed=1125177;
 RA Chen X., Ijkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
 RA Peters S., Zuidema D., Lankhorst R.K., Vlask J.M., Hu Z.;
 RT "The sequence of the Helicoverpa armigera single-nucleocapsid
 RT nucleopolyhedrovirus genome."
 RL J. Gen. Virol. 82:241-257(2001).
 RV [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;
 RA Chen X., Ijkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,
 RA Peters S., Zuidema D., Lankhorst R.K., Vlask J.M., Hu Z.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RV [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
 RX PubMed=12050807;
 RA Zhang C.X., Wu J.C.;
 RT "Genome structure and the p10 gene of the Helicoverpa armigera
 RT nucleopolyhedrovirus."
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Li Hsueh Pao 33:179-184(2001).
 RV [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=CI;
 RA Zhang C.X., Jin W.R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RV [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Helicoverpa armigera nuclear polyhedrosis virus;
 RA Fang M., Hu Z., Chen X., Vlask J.M.;
 RT "Genetic organization of the HindIII-L region of Helicoverpa armigera
 RT single-nucleocapsid nucleopolyhedrovirus."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF334030; AAL56194.1; -
 DR EMBL: AF271059; AAG53791.1; -
 DR EMBL: AF303045; AAK96298.1; -
 DR EMBL: AF266694; AAK64316.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 68 AA; 7962 MW; 61B7718BFBB195FF CRC64;

Query Match 95.0%; Score 19; DB 12; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
 Db 29 VAEF 32

RESULT 17
 Q82X12 PRELIMINARY; PRT; 68 AA.
 ID Q82X12
 AC Q82X12;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Helix-turn-helix protein, CopG family.
 GN NE0289.
 OS Nitrosomonas europaea.

Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Nitrosomonadaceae; Nitrosomonas.
 NCBI_TaxID=915;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=ATCC 19718 / IF0 14298;
 MEDLINE=22586410; PubMed=12700255;
 Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
 Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,
 Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.D.;
 "Complete genome sequence of the ammonia-oxidizing bacterium and
 obligate chemolithoautotroph Nitrosomonas europaea.";
 J. Bacteriol. 185:2759-2773(2003).
 EMBL; BX321857; CAD84200.1; -
 Complete proteome.
 SEQUENCE 68 AA; 7800 MW; 8A839B537524DD6 CRC64;
 Query Match 95.0%; Score 19; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 VAEF 5
 31 VAEF 34

SULT 18
 (71)
 QX711 PRELIMINARY; PRT; 69 AA.
 01-OCT-2003 (TrEMBLrel. 25, Created)
 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 OSJNBa004M1.9-22 protein (OSJNBa0053B21.1 protein).
 OSJNBa004M1.9-22 OR OSJNBa0053B21.1.
 Oryza sativa (Rice)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.
 NCBI_TaxID=4530;
 [1]
 SEQUENCE FROM N.A.
 Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
 Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
 Lu Y.Q., Yu S.H., Liu X.H., Liu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
 Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
 Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
 Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
 Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
 Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
 Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
 Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AL731601; CAE05035.1; -
 EMBL; AL731599; CAE05527.1; -
 SEQUENCE 69 AA; 7267 MW; 7783933BC873F0BE CRC64;
 Query Match 95.0%; Score 19; DB 10; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 VAEF 5
 31 VAEF 34

SULT 19
 NPA7
 QGNPA7 PRELIMINARY; PRT; 69 AA.
 01-OCT-2002 (TrEMBLrel. 22, Created)
 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 Hypothetical protein Cg11907.

CGL1907.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005280; BAB99300.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 69 AA; 7815 MW; C0E2A072C2295DD2 CRC64;
 Query Match 95.0%; Score 19; DB 16; Length 69;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VAEF 5
 DB 23 VAEF 26

RESULT 20
 Q8AUQ2 PRELIMINARY; PRT; 71 AA.
 ID Q8AUQ2;
 AC Q8AUQ2;
 DT 01-VAR-2003 (TrEMBLrel. 23, Created)
 DT 01-VAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Transferrin (Fragment).
 OS Salmo trutta (Brown trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8032;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Str-1, Str-2, Str-3, Str-4, Str-9, Str-10, and Str-11;
 RX MEDLINE=22135992; PubMed=12140239;
 RA Antunes A., Templeton A.R., Guyonard R., Alexandrino P.;
 RT "The role of nuclear genes in intraspecific evolutionary inference:
 genealogy of the transferrin gene in the brown trout.";
 Mol. Biol. Evol. 19:1272-1287(2002).
 DR EMBL; AF488650; ANI17027.1; -
 DR EMBL; AF488849; ANI17032.1; -
 DR EMBL; AF488858; ANI17032.1; -
 DR EMBL; AF488857; ANI17032.1; JOINED.
 DR EMBL; AF488866; ANI17037.1; -
 DR EMBL; AF488865; ANI17037.1; JOINED.
 DR EMBL; AF488874; ANI17042.1; -
 DR EMBL; AF488873; ANI17042.1; JOINED.
 DR EMBL; AF488914; ANI17068.1; -
 DR EMBL; AF488913; ANI17068.1; JOINED.
 DR EMBL; AF488922; ANI17073.1; -
 DR EMBL; AF488930; ANI17078.1; -
 DR EMBL; AF488929; ANI17078.1; JOINED.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:iron ion binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Transferrin.
 DR Pfam; PF00405; transferrin; 1.
 DR PRINTS; PR00422; TRANSFERRIN.
 FT NON_TER 1 1
 FT NON_TER 71 71
 SQ SEQUENCE 71 AA; 7546 MW; 892E38F2DD2AC4D CRC64;
 Query Match 95.0%; Score 19; DB 13; Length 71;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Y      2 VAEF 5
b      33 VAEF 36

RESULT 21
BAUPO PRELIMINARY; PRT; 71 AA.
C Q8AUP0;
I 01-MAR-2003 (TREMBLrel. 23, Created)
I 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
I 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
E Transferrin (Fragment).
S Salmo salar (Atlantic salmon).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Actinopterygii; Neopterygii; Teleostei; Euteleostei;
C Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
C NCBI_TaxID=8030;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=Ssa-1, and Ssa-2;
C MEDLINE=22135932; PubMed=12140239;
A Antunes A., Templeton A.R., Guyomard R., Alexandrino P.;
I "The role of nuclear genes in intraspecific evolutionary inference:
I Genealogy of the transferrin gene in the brown trout.";
I Mol. Biol. Evol. 19:1272-1287(2002).
R EMBL; AF488834; AAN17017.1; -.
R EMBL; AF488833; AAN17017.1; JOINED.
R EMBL; AF488842; AAN17022.1; -.
R EMBL; AF488841; AAN17022.1; JOINED.
R GO; GO:000576; C:extracellular; IEA.
R GO; GO:0008199; P:ferrous iron binding; IEA.
R GO; GO:0006879; P:iron ion homeostasis; IEA.
R GO; GO:0006826; P:iron ion transport; IEA.
R Pfam; PF00405; Transferrin.
R PRINTS; PR00422; TRANSFERRIN.
I NON_TER 1
I NON_TER 71
I NON_TER 71
Q SEQUENCE 71 AA; 7504 MW; 9D86A61234CBACAD CRC64;

Query Match 95.0%; Score 19; DB 13; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      33 VAEF 36

RESULT 22
97252 PRELIMINARY; PRT; 72 AA.
C P97252;
T 01-MAY-1997 (TREMBLrel. 03, Created)
T 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
E Late control gene D protein (Fragment).
N D.
S Escherichia coli.
C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
C Enterobacteriaceae; Escherichia.
C NCBI_TaxID=562;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=KL2;
C MEDLINE=97251358; PubMed=9097040;
X A Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
A Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
A Mizobuchi K., Mori H., Mori K., Motomura K., Nakade S., Nakamura Y.,
A Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
A Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,

Yamamoto Y., Horiuchi T.;
"A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
DR EMBL; D90847; BAA15949.1; -.
DR EMBL; D90846; BAA15938.1; -.
FT NON_TER 1
SQ SEQUENCE 72 AA; 8099 MW; 42A63B25B00EADCB CRC64;

Query Match 95.0%; Score 19; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
Db      5 VAEF 8

RESULT 24
Q82MX0 PRELIMINARY; PRT; 74 AA.
ID Q82MX0;
AC Q82MX0;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN SAV1532.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
P SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;

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2A Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., T.,
2B Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
2C Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
2D "Genome sequence of an industrial microorganism Streptomyces
2E avermitilis: deducing the ability of producing secondary
2F metabolites.";
2G Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
2H [2]
2I SEQUENCE FROM N.A.
2J STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
2K MEDLINE=22608306; PubMed=12692562;
2L Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
2M Sakaki Y., Hattori M., Omura S.;
2N "Complete genome sequence and comparative analysis of the industrial
2O microorganism Streptomyces avermitilis.";
2P Nat. Biotechnol. 21:1526-531(2003).
2Q EMBL; AP005027; BAC69243.1; -
2R Hypothetical protein; Complete proteome.
2S SEQUENCE 74 AA; 7960 MW; D8CE71C8B0A8B01 CRC64;
2T
2U Query Match 95.0%; Score 19; DB 16; Length 74;
2V Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
2W Matches 4; Conservative 0; Mismatches 0;
2X
2Y 2 VAEF 5
2Z ||||
3A 36 VAEF 39
3B
3C RESULT 25
3D Q862M8 PRELIMINARY; PRT; 77 AA.
3E ID Q862M8,
3F AC Q862M8,
3G DT 01-JUN-2003 (TRENBLrel. 24, Created)
3H JT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
3I DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
3J DE Similar to MAD2 protein (Fragment).
3K OS Bos taurus (Bovine).
3L DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
3M Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;
3N Bovidae; Bovinae; Bos.
3O NCBI_TaxID=9913;
3P [1]
3Q SEQUENCE FROM N.A.
3R MEDLINE=22544902; PubMed=12658628;
3S Ishikawa H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
3T Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
3U Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
3V "Characterization of gene expression profiles in early bovine
3W pregnancy using a custom cDNA microarray.";
3X Mol. Reprod. Dev. 65:9-18(2003).
3Y EMBL; AB098952; BAC56442.1; -
3Z InterPro; IPR003511; DNABind_HORMA.
3A PROSITE; PS50815; HORMA; 1.
3B NON_TER 1
3C NON_TER 77
3D SEQUENCE 77 AA; 8832 MW; E2E1D625C948E571 CRC64;
3E
3F Query Match 95.0%; Score 19; DB 6; Length 77;
3G Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
3H Matches 4; Conservative 0; Mismatches 0;
3I
3J 2 VAEF 5
3K ||||
3L 6 VAEF 9
3M
3N RESULT 26
3O Q88VS7 PRELIMINARY; PRT; 77 AA.
3P ID Q88VS7,
3Q AC Q88VS7,
3R DT 01-JUN-2003 (TRENBLrel. 24, Created)
3S DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

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DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN LP 1960.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
ON [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Turchini R., Peters S.A., Sarda-brink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerckhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RA "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
RL EMBL; AL935257; CAD64344.1; -
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 77 AA; 8618 MW; C00E2BFF1D401F2F CRC64;
3T
3U Query Match 95.0%; Score 19; DB 16; Length 77;
3V Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
3W Matches 4; Conservative 0; Mismatches 0;
3X
3Y 2 VAEF 5
3Z ||||
3A 68 VAEF 71
3B
3C RESULT 27
3D Q98582 PRELIMINARY; PRT; 79 AA.
3E ID Q98582,
3F AC Q98582;
3G DT 01-FEB-1997 (TRENBLrel. 02, Created)
3H DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
3I DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
3J DE A532L protein.
3K GN A532L.
3L OS Paramesicium bursaria chlorella virus 1 (PBCV-1).
3M OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
3N NCBI_TaxID=10506;
3O [1]
3P SEQUENCE FROM N.A.
3Q MEDLINE=96400190; PubMed=8806566;
3R Kutish G.P., Li Y., Lu Z., Furuta M., Rock D.L., Van Etten J.L.;
3S "Analysis of 76 kb of the chlorella virus PBCV-1 330-kb genome: map
3T positions 182 to 258.";
3U Virology 223:303-317(1996).
3V [2]
3W SEQUENCE FROM N.A.
3X MEDLINE=20013326; PubMed=10544099;
3Y Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., King W.,
3Z Lisee A.D., Nickerson K.W., Van Etten J.L.;
3A "Chlorella virus PBCV-1 encodes a functional homospesmidine
3B synthase.";
3C Virology 263:254-262(1999).
3D [3]
3E SEQUENCE FROM N.A.
3F MEDLINE=20478054; PubMed=11021991;
3G Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
3H "Characterization of a beta-1,3-glucanase encoded by chlorella virus
3I PBCV-1.";
3J Virology 276:27-36(2000).
3K [4]
3L SEQUENCE FROM N.A.
3M Van Etten J.L.;
3N Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
3O [5]
3P SEQUENCE FROM N.A.
3Q Van Etten J.L.;
3R Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
3S [6]

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RN [6] SEQUENCE FROM N.A.
 RP Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC96899.1; -.
 DR PIR; T18034; T18034.
 SQ SEQUENCE 79 AA; 8698 MW; B191C627F5D5C5A7 CRC64;

Query Match 95.0%; Score 19; DB 12; Length 79;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 49 VAEF 52

RESULT 28
 Q9KI36 PRELIMINARY; PRT; 80 AA.
 AC Q9KI36;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Yag.
 GN Yag.
 OS Agrobacterium tumefaciens.
 OG Plasmid Ti.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Winans S.C., Zhu J., Oger P.M., Schrammeyer B., Hooykaas P.J.,
 RA Farrand S.K.;
 RT "Octopine-type Ti plasmid sequence."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF242881; AAF77180.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 SQ SEQUENCE 80 AA; 8723 MW; 4B9379C1D907CABE CRC64;

Query Match 95.0%; Score 19; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 65 VAEF 68

RESULT 29
 Q89WL6 PRELIMINARY; PRT; 81 AA.
 AC Q89WL6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Bar0662 protein.
 GN BSR0662.
 OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RX MEDLINE=22484998; PubMed=12597275;
 RA Sasamoto S., Watanabe A., Ideawa K., Iiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005937; BAC45927.1; -.
 KW Complete proteome.
 SQ SEQUENCE 81 AA; 9235 MW; D512A9FFED0DA6C7 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 81;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 43 VAEF 46

RESULT 30
 Q9KAV4 PRELIMINARY; PRT; 84 AA.
 AC Q9KAV4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein BH2182.
 GN BH2182.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=66665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis."
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001514; BAB05901.1; -.
 DR PIR; F83922; F83922.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 84 AA; 9669 MW; 6CDE3768ED9F5D84 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 38 VAEF 41

RESULT 31
 Q821D2 PRELIMINARY; PRT; 84 AA.
 AC Q821D2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN CCA01010.
 OS Chlamydomonada caviae.

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XC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
XX NCBI_TaxID=83557;
XP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
XA MEDLINE=22569155; PubMed=12682364;
YA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
ZA Heidelberg J., Holtzaple E., Khouri H., Federova N.B., Carty H.A.,
UA Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
ZA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavol P.M.,
ZA Fraser C.M.;
XT "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
XT examining the role of niche-specific genes in the evolution of the
XT Chlamydiaceae.";
XL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016997; AAP05749.1; -.
DR TIGR; CCA01010; -.
GW Hypothetical protein; Complete proteome.
SQ SEQUENCE 84 AA; 9191 MW; 7DF609729C7093A CRC64;

Query Match 95.0%; Score 19; DB 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 2 VAEF 5
Zb 68 VAEF 71

RESULT 32
ZYVPV6 PRELIMINARY; PRT; 84 AA.
AC Q7VPV6;
JT 01-OCT-2003 (TrEMBLrel. 25, Created)
JT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
JT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ZE Hypothetical protein.
ZN CP80775.
XS Chlamydia pneumoniae (Chlamydophila pneumoniae).
XC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
XX NCBI_TaxID=83558;
XP SEQUENCE FROM N.A.
RC STRAIN=TW-183;
XA Geng M.M., Schuhmacher A., Muehldorfer I., Bersch K.W., Schaefer K.P.,
ZA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
XT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
XT other Chlamydia strains based on whole genome sequence analysis.";
XL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
XR EMBL; AE017159; AAP98704.1; -.
ZW Hypothetical protein.
SQ SEQUENCE 84 AA; 9260 MW; 7786DF8BDD7B3AB8 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZY 2 VAEF 5
Zb 68 VAEF 71

RESULT 33
ZY3116 PRELIMINARY; PRT; 85 AA.
AC O43116;
JT 01-JUN-1998 (TrEMBLrel. 06, Created)
JT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
JT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ZE Hypothetical protein (Fragment).
XS Colletotrichum gloeosporioides (Anthracoноse fungus) (Glomerella
XS cingulata).
XC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC Glomerella.
XX NCBI_TaxID=5457;
XP SEQUENCE FROM N.A.
RC STRAIN=U062;
RA Stephenson S.-A., Maclean D.J., Manners J.M.;
RT "Disruption of a novel pathogenicity gene of Colletotrichum
RT gloeosporioides results in a hypersensitive response in the host
RT Stylosanthes guianensis.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94183; AAB92222.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001387; HTH_3.
DR Pfam; PF01381; HTH_3; 1.
DR SMART; SMO0530; HTH_XRE; 1.
DR Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 85 AA; 9316 MW; BFB9A0E5F44B9CF2 CRC64;

Query Match 95.0%; Score 19; DB 3; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Qb 45 VAEF 48

RESULT 34
Q99149 PRELIMINARY; PRT; 87 AA.
AC Q99149;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transferrin (Fragments).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
XX NCBI_TaxID=9940;
XP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=91177867; PubMed=1849850;
RA Tu G.F., Achen M.G., Aldred A.R., Southwell B.R., Schreiber G.;
RT "The distribution of cerebral expression of the transferrin gene is
RT species specific.";
RL J. Biol. Chem. 266:6201-6208(1991).
CC -!- FUNCTION. TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CC CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
CC OF AN ANION, USUALLY BICARBONATE.
DR EMBL; M64691; AAA31585.1; -.
DR EMBL; M64692; AAA31586.1; -.
DR PIR; A38725; A38725.
DR HSSP; P19134; ITFD.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Transferrin.
DR SMART; SMO0094; TR_FER; 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR Iron transport; Metal-binding.
FT NON_TER 1
FT NON_TER 44
FT NON_TER 87
FT NON_TER 87
SQ SEQUENCE 87 AA; 9433 MW; AA464B2ABDC92FAB CRC64;

Query Match 95.0%; Score 19; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2 VAEF 5	13 VAEF 16	87 AA.	88 AA.	89 AA.
DB	13 VAEF 16				
RESULT 35					
Q7Y3Y9	PRELIMINARY;	PRT;	87 AA.		
ID	Q7Y3Y9				
AC	Q7Y3Y9				
DT	01-OCT-2003 (TrEMBLrel. 25, Created)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Bacteriophage PY54.				
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.				
OX	NCBI_TaxID=172667;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RA	Hertwig S.; Klein I., Schmidt V., Beck S., Hammerl J.A., Appel B.;				
RT	"Sequence analysis of the genome of the temperate <i>Versinia</i>				
RT	<i>enterocolitica</i> phage PY54.";				
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	Hertwig S.;				
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.				
DR	EMBL; AJ564013; CAD91786.1; --				
KW	Exonuclease; Hypothetical protein.				
SQ	SEQUENCE 87 AA; 8538 MW; D17D7A7B3075459B CRC64;				
Query Match	95.0%; Score 19; DB 9; Length 87;				
Best Local Similarity	100.0%; Pred. No. 1.3e+03;				
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	2 VAEF 5				
DB	31 VAEF 34				
RESULT 36					
Q8S590	PRELIMINARY;	PRT;	88 AA.		
ID	Q8S590				
AC	Q8S590				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)				
DE	Cytochrome P460 (Fragment).				
GN	CYP.				
OS	Nitrosomonas europaea.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;				
OC	Nitrosomonadaceae; Nitrosomonas.				
OX	NCBI_TaxID=915;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=IFO14299;				
RA	Iizumi T., Nakamura K.;				
RT	"Construction of tryptophan requiring-mutant of <i>Nitrosomonas europaea</i>				
RT	by inactivation of <i>trpC</i> gene using homologous recombination.";				
RT	Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.				
RL	EMBL; AB303031; BA83388.1; --				
DR	NON_TER 88				
FT	SEQUENCE 88 AA; 9765 MW; A59003348FAE280C CRC64;				
Query Match	95.0%; Score 19; DB 2; Length 88;				
Best Local Similarity	100.0%; Pred. No. 1.3e+03;				
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	2 VAEF 5				
DB	29 VAEF 32				
RESULT 37					
Q41185	PRELIMINARY;	PRT;	88 AA.		
ID	Q41185				
AC	Q41185				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)				
DE	Glyceraldehyde-3-phosphate-dehydrogenase subunit GapB (Fragment).				
GN	GAPB.				
OS	<i>Arabidopsis thaliana</i> (Mouse-ear cress).				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93013005; PubMed=1398114;				
RA	Shih M.C., Heinrich P., Goodman H.M.;				
RT	"Cloning and chromosomal mapping of nuclear genes encoding chloroplast				
RT	and cytosolic glyceraldehyde-3-phosphate-dehydrogenase from				
RT	<i>Arabidopsis thaliana</i> ;"				
RL	Gene 119:3317-319(1992).				
DR	EMBL; S45911; AB23533.1; --				
DR	GO; GO:0009507; C:chloroplast; IEA.				
KW	Chloroplast.				
FT	NON_TER 88				
SQ	SEQUENCE 88 AA; 9198 MW; FCDB6A7E37B6999D CRC64;				
Query Match	95.0%; Score 19; DB 10; Length 88;				

db 3 VAEF 6

RESULT 39

29CNX1 ID Q9CNX1 PRELIMINARY; PRT; 89 AA.
AC Q9CNX1.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RPS15
DE RPS15 OR PM0301.
DS Pasteurella multocida.
DC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
DC Pasteurellaceae; Pasteurella.
DX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of *Pasteurella multocida* Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006066; AAK02385.1; -;
DR HSSP; P80378; 1AB3.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR005589; Ribosomal_S15.
DR InterPro; IPR005290; Ribosomal_S15_b.
DR Pfam; PF00312; Ribosomal_S15; 1.
DR ProDom; PD157043; RS15_bact; 1.
DR TIGRFAMs; TIGR00952; S15_bact; 1.
DR PROSITE; PS00362; RIBOSOMAL_S15; 1.
KW Complete proteome.
SQ SEQUENCE 89 AA; 10184 MW; F796E0AB5283ED0E CRC64;

Query Match 95.0%; Score 19; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5

DB 12 VAEF 15

RESULT 40

Q9CFD1 ID Q9CFD1 PRELIMINARY; PRT; 89 AA.
AC Q9CFD1.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein YPJ6.
GN YPJ6 OR L1150.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malmgren K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
lactis ssp. lactis IL1403".
RL Genome Res. 11:751-753(2001).
DR EMBL; AE006385; AAK05648.1; -;
DR PIR; F86818; F86818.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 89 AA; 10403 MW; D90DF3CF71D1D2D06 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5

DB 68 VAEF 71

RESULT 41

Q81ZX3 ID Q81ZX3 PRELIMINARY; PRT; 90 AA.
AC Q81ZX3.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MAD2 mitotic arrest deficient-like 1 variant.
GN MAD2L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin F., Fan D.M.;
RT "Identifying a new variant of MAD2L1.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394735; AAN74648.1; -;
DR InterPro; IPR003511; DNABind_HORMA.
DR Pfam; PF02301; HORMA; 1.
DR PROSITE; PS0815; HORMA; 1.
SQ SEQUENCE 90 AA; 10335 MW; 8209F5A7A7D8D09B CRC64;

Query Match 95.0%; Score 19; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5

DB 20 VAEF 23

RESULT 42

Q98TB2 ID Q98TB2 PRELIMINARY; PRT; 91 AA.
AC Q98TB2.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Preproinsulin (Fragment).
OS Ambloplites rupestris (Rock bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centrarchidae; Ambloplites.
OX NCBI_TaxID=109273;
RN [1]
RP SEQUENCE FROM N.A.
RA Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
RT "Molecular cloning of preproinsulin cDNA from the rock bass.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
DR EMBL; AF19584; AAK28708.1; -;
DR HSSP; P01308; 1LPH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological processes; IEA.
DR InterPro; IPR004825; Ins/IGF/relax.
DR Pfam; PF00049; Insulin; 1.
DR PRINTS; PR00277; INSULINB.
DR SMART; SM00078; IIGF; 1.

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DR PROSITE; PS00262; INSULIN; 1.
FT NON TER 1 1
FT NON TER 91 91
SQ SEQUENCE 91 AA; 10100 MW; B86C9B256DC69D39 CRC64;

Query Match 95.0%; Score 19; DB 13; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 55 VAEF 58

RESULT 43
Q8KV12 PRELIMINARY; PRT; 94 AA.
AC Q8KV12
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative transcriptional regulator (Fragment).
OS Rhizobium etli.
OG Plasmid p42b.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE3;
PA Cervillos M.A., Izquierdo J., Porta H., Tun C., Davila G., Brom S.;
RT "Rhizobium etli CE3 contains at least three plasmids of the RepABC
family: A structural and an evolutionary analysis.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF313446; AN88940.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 94 AA; 10222 MW; C09D6EA3DFF1E2BA CRC64;

Query Match 95.0%; Score 19; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 38 VAEF 41

RESULT 44
O46425 PRELIMINARY; PRT; 94 AA.
AC O46425
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aquaporin 1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand;
PA Carter E.P., Umenishi F., Matthey M.A., Verkman A.S.;
RT "Increased water permeability across the blood-gas barrier in rabbit
lungs in the first 24 hours after birth.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
DR EMBL; AF000311; AAB94408.1; -.
DR HSP; P29972; 1FOY.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:005741; C:mitochondrial outer membrane; IEA.
DR GO; GO:001528; P:porin activity; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000425; MIP.
DR Pfam; PF00230; MIP; 1.
DR ProDom; PD000295; MIP_family; 1.
DR PROSITE; PS00221; MIP; 1.
KW Porin; Transmembrane; Transport.
FT NON TER 1 1
FT NON TER 94 94
SQ SEQUENCE 94 AA; 10057 MW; 963D5527631E8CDC CRC64;

Query Match 95.0%; Score 19; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 9 VAEF 12

RESULT 45
Q8U8Q1 PRELIMINARY; PRT; 96 AA.
AC Q8U8Q1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu4039.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323 (2001).
DR EMBL; AE009334; AAL44940.1; -.
DR PIR; AB3053; AB3053.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 11193 MW; FBD635894B46A8AE CRC64;

Query Match 95.0%; Score 19; DB 16; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 55 VAEF 58

RESULT 46
Q89WX7 PRELIMINARY; PRT; 96 AA.
AC Q89WX7
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bsl0551 protein.

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1N BSL0551.
 1S Bradyrhizobium japonicum.
 1C Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 1X Bradyrhizobiaceae; Bradyrhizobium.
 1Y NCBI_TaxID=375;
 1Z [1]
 2P SEQUENCE FROM N.A.
 2C STRAIN=USDA 110;
 2X MEDLINE=2484998; PubMed=12597275;
 2A Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 2S Sasamoto S., Watanabe A., Idesawa K., Iriyuchi M., Kawashima K.,
 2K Kohara M., Matsumoto M., Shingo S., Tsuruoka H., Wada T., Yamada M.,
 2A Tabata S.;
 2T "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 2T Bradyrhizobium japonicum USDA110.";
 2L DNA Res. 9:189-197(2002).
 2R EMBL; AF005936; BAC45816.1; -.
 2R GO; GO:0016020; C:membrane; IEA.
 2R InterPro; IPR003425; Unk_YGGT.
 2R Pfam; PF02325; YGGT; 1.
 2X Complete proteome.
 2Q SEQUENCE 96 AA; 10976 MW; A9E11F9AA4BC7734 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
 2b 44 VAEF 47
 RESULT 47
 3U0G9 PRELIMINARY; PRT; 96 AA.
 4C Q8U0G9;
 4T 01-JUN-2002 (TrEMBLrel. 21, Created)
 4T 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 4T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 4E Hypothetical protein PF1620.
 4N PF1620.
 4S Pyrococcus furiosus.
 4C Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 4X Pyrococcus.
 4Y NCBI_TaxID=2261;
 4Z [1]
 5P SEQUENCE FROM N.A.
 5C STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
 5A Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 5T "The complete sequence of the Pyrococcus furiosus genome.";
 5L Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 5R EMBL; AB010262; AAU81744.1; -.
 5W Hypothetical protein; Complete proteome.
 5Q SEQUENCE 96 AA; 10804 MW; D6DAE09D096D577A CRC64;

Query Match 95.0%; Score 19; DB 17; Length 96;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
 2b 24 VAEF 27
 RESULT 48
 3B6535 PRELIMINARY; PRT; 97 AA.
 4C Q86535;
 4T 01-NOV-1996 (TrEMBLrel. 01, Created)
 4T 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 4T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 4E 2C/3A (Fragment).
 4N 2C/3A.

OS Hepatitis A virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Hepatovirus.
 OX NCBI_TaxID=12092;
 ON [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSH/S;
 RX MEDLINE=92348853; PubMed=1668326;
 RA Fineschi N., Cavalieri F., Garelick H., Prugnola A., Pellegrini V.,
 RA Zuckerman A.J.;
 RT "Characterization of a hepatitis A virus strain suitable for vaccine
 RT production.";
 RL J. Hepatol. 13:S146-S151(1991).
 DR EMBL; S44109; AAB22740.2; -.
 FT NON_TER 1 1
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10614 MW; D207F7CB93110DDF CRC64;

Query Match 95.0%; Score 19; DB 12; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
 2b 44 VAEF 47
 RESULT 49
 Q8Y476 PRELIMINARY; PRT; 97 AA.
 AC Q8Y476;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DB Hypothetical protein lmo2579.
 GN LMO2579.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 ON [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679659;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitourman A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL; AL591983; CAD00657.1; -.
 DR PIR; AC1397; AC1397.
 DR Listlist; LMO2579; -.
 DR InterPro; IPR007138; ABM.
 DR Pfam; PF03992; ABM; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 97 AA; 10979 MW; 9E758586E94218E0 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
 2b 15 VAEF 18

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RESULT 50
Q9H238 O9H238 PRELIMINARY; PRT; 99 AA.
AC Q9H238;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PA3202.
GN PA3202.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Latbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004744; AAC06590.1; -.
DR PIR; E83244; E83244.
DR InterPro; IPR005545; YCII.
DR Pfam; PF03795; YCII; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 99 AA; 10609 MW; 3AD945F4D4D5A985C CRC64;

Query Match 95.0%; Score 19; DB 16; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 62 VAEF 65

RESULT 51
Q885M3 Q885M3 PRELIMINARY; PRT; 99 AA.
AC Q885M3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical protein.
GN P3PT01808.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Pedorova N., Tran B., Russell D.,
RA Barry K., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016862; AAC055328.1; -.
DR TIGR; P3PT01808; -.
DR InterPro; IPR005545; YCII.
DR Pfam; PF03795; YCII; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 99 AA; 10504 MW; 62836007E4849392 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 99;

QY 2 VAEF 5
DB 62 VAEF 65

RESULT 52
Q82UR2 Q82UR2 PRELIMINARY; PRT; 100 AA.
AC Q82UR2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN NE1419.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321861; CAD85330.1; -.
DR InterPro; IPR005545; YCII.
DR Pfam; PF03795; YCII; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 100 AA; 10936 MW; 82DC1153B8BFAE27 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 62 VAEF 65

RESULT 53
Q8VS54 Q8VS54 PRELIMINARY; PRT; 101 AA.
AC Q8VS54;
DT 01-VAR-2002 (TrEMBLrel. 20, Created)
DT 01-VAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Elongation factor TS (Fragment).
GN TSP.
OS Lactobacillus reuteri.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 55739;
RA Nam S.J., Kim J.K., Park J.Y., Ha Y.L., Kim J.H.;
RT "Cloning of UMP-kinase gene from Lactobacillus reuteri ATCC 55739."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401482; AAL60142.1; -.
DR GO; GO:003746; P:translational elongation factor activity; IEA.
DR GO; GO:006414; P:translational elongation; IEA.
DR InterPro; IPR001816; EF_TS.
DR Pfam; PF00889; EF_TS; 1.
KW NON TER
SQ SEQUENCE 101 AA; 11650 MW; B8CF30D941DB2B9B CRC64;
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Query Match 95.0%; Score 19; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 62 VAEF 65

RESULT 54

97YC2 Q97YC2 PRELIMINARY; PRT; 101 AA.
 C Q97YC2;
 T 01-OCT-2001 (TrEMBLrel. 18, Created)
 T 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 T 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein SSO1404.
 N SSO1404.
 S Sulfolobus solfataricus.
 C Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 C Sulfolobus.
 X NCBI_TaxID=2287;
 N [1]
 P SEQUENCE FROM N.A.
 C STRAIN=ATCC 35092 / DSM 1617 / P2;
 X MEDLINE=21332296; PubMed=11427726;
 A She Q., Singh R.K., Confalonieri P., Zivanovic Y., Allard G.,
 A Aweez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 A De Moors A., Etrauso G., Fletcher C.C., Gordon P.M.K.,
 A Heikamp-de Jong I., Jeffries A.C., Korera C.J., Medina N., Peng X.,
 A Thi-Ngoc H.P., Redder P., Schenck M.E., Theriault C., Tolstrup N.,
 A Garlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 A Charrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 A "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 L Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 R EMBL: AE006755; AK41639.1;
 R PIR: H90297; H90297.
 R InterPro: IPR003799; DUF196.
 R Pfam: PF02647; DUF196; 1.
 R TIGRFAMs: TIGR01573; cas2; 1.
 W Hypothetical protein; Complete proteome.
 I Q SEQUENCE 101 AA; 11936 MW; A7C338AD76202E17 CRC64;

Query Match 95.0%; Score 19; DB 17; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 20 VAEF 23

RESULT 55

81R27 Q81R27 PRELIMINARY; PRT; 102 AA.
 C Q81R27;
 T 01-JUN-2003 (TrEMBLrel. 24, Created)
 T 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 T 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 N BA2232.
 S Bacillus anthracis (strain Ames).
 C Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 X NCBI_TaxID=198094;
 N [1]
 P SEQUENCE FROM N.A.
 X MEDLINE=22608414; PubMed=12721629;
 A Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 A Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 A Holtzapple E.K., Ostlund O.A., Helgason E., Ristone J., Wu M.,
 A Kelonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
 A Debey R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 A Nelson W.C., Peterson J.D., Pop M., Kouri H.M., Radune D.,

RA Banton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nieman W.C.,
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
 RA Thomason B., Friedlander A.M., Koshler T.M., Hanna P.C., Koisto A.-B.,
 RA Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 DR EMBL: AE017031; AAP26109.1; -.
 DR TIGR; BA2232; -.
 KW Hypothetical protein; Complete proteome.
 S Q SEQUENCE 102 AA; 11925 MW; 13B8E296C8A341B1 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 54 VAEF 57

RESULT 56

Q7Z2N2 Q7Z2N2 PRELIMINARY; PRT; 103 AA.
 AC Q7Z2N2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BK150C2.6 (Putative novel protein similar to APOBEC1 (Apolipoprotein B
 DE mRNA editing protein) and Phorbollin) (Fragment).
 GN BK150C2.6.
 OS Homo sapiens (Human).
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL022318; CAB45276.1; -.
 KW Lipoprotein.
 FT NON_TER 1 103
 FT NON_TER 103 103
 S Q SEQUENCE 103 AA; 12146 MW; 5DC969AE3ED348D9 CRC64;

Query Match 95.0%; Score 19; DB 4; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 46 VAEF 49

RESULT 57

Q9F368 Q9F368 PRELIMINARY; PRT; 103 AA.
 AC Q9F368;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO4420.
 GN SCO4420 OR SC6F11.18.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 CX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.; and the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939120; CAC08429.1; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 103 AA; 11387 MW; 55C2B80589EB75B5 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 54 VAEF 57

RESULT 58

Q89MS9 PRELIMINARY; PRT; 103 AA.
 AC Q89MS9;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE BLr4113 protein.
 GN BLR4113.
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA 110;
 RC MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamiasawa K., Uchiyama T.,
 RA Sasamoto S., Watanabe A., Iidesawa K., Iiguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005950; BAC49378.1; --
 KW Complete proteome.
 SQ SEQUENCE 103 AA; 11104 MW; BF27CB9F90FB723 CRC64;

Query Match 95.0%; Score 19; DB 16; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 96 VAEF 99

RESULT 59

Q856B5 PRELIMINARY; PRT; 104 AA.
 AC Q856B5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE GP57.
 OS Mycobacteriophage Barnyard.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=205880;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22592660; PubMed=12705866;
 RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
 RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
 RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
 RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
 RA Hatfull G.F.;
 RA "Origins of highly mosaic mycobacteriophage genomes.";
 RT Cell 113:171-182(2003).
 RL EMBL; AY129339; AAN02111.1; --
 DR EMBL; AY129339; AAN02111.1; --
 SQ SEQUENCE 104 AA; 11074 MW; BB806EAC401B9FD0 CRC64;

Query Match 95.0%; Score 19; DB 9; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 59 VAEF 62

RESULT 60

Q8SVK0 PRELIMINARY; PRT; 105 AA.
 AC Q8SVK0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein ECU05_0770.
 GN ECU05_0770.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RC Genoscope;
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RC MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
 RA Delbac F., El Alsaoui H., Peyret F., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RA "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi.";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590445; CAD26596.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 105 AA; 11897 MW; 08059108C05D3BB9 CRC64;

Query Match 95.0%; Score 19; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 77 VAEF 80

RESULT 61

Q856U1 PRELIMINARY; PRT; 105 AA.
 AC Q856U1;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE GP3.
 OS Mycobacteriophage Corndog.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=205875;

3N SEQUENCE FROM N.A.
3P MEDLINE=22592660; PubMed=12705866;
3A Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
3A Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
3A Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
3A Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
3A Hafull G.F.,
3T "Origins of highly mosaic mycobacteriophage genomes.";
3L Cell 113:171-182(2003).
3R EMBL; AY129335; AAN01935.1; -
3Q SEQUENCE 105 AA; 11955 MW; 7D0EC09F5F2AF2DD CRC64;

Query Match 95.0%; Score 19; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
2b 41 VAEF 44

RESULT 62
296231 PRELIMINARY; PRT; 105 AA.
AC Q96Z31
AT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ST2000.
EN ST2000.
3S Sulfolobus tokodaii.
3C Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
3C Sulfolobus.
3X NCBI_TaxID=111955;
3N SEQUENCE FROM N.A.
3P STRAIN=JCM 10545 / 7;
3A MEDLINE=21456156; PubMed=11572479;
3A Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
3A Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
3A Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
3A Yoshikawa T., Tanaka T., Kudon Y., Yamazaki J., Kishida N., Oguchi A.,
3A Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
3A Oshima T., Kikuchi H.;
3T "Complete genome sequence of an aerobic thermoacidophilic
3T Crenarchaeon, Sulfolobus tokodaii strain7.";
3L DNA Res. 8:123-140(2001).
3R EMBL; AP000988; BAB67055.1; -
3R InterPro; IPR006783; Transposase_29.
3R Pfam; PF04693; Transposase_29; 2.
3Q SEQUENCE 105 AA; 11997 MW; AF6GABD4DF2DECOE CRC64;

Query Match 95.0%; Score 19; DB 17; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
2b 29 VAEF 32

RESULT 63
P71530 PRELIMINARY; PRT; 106 AA.
AC P71530;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NIFX.
3N NIFX.
3S Methanococcus maripaludis.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
3N SEQUENCE FROM N.A.
3P STRAIN=LL;
3A MEDLINE=96011360; PubMed=7592322;
3A Blank C.E., Kessler P.S., Leigh J.A.;
3T "Genetics in methanogens: transposon insertion mutagenesis of a
3T Methanococcus maripaludis nifH gene.";
3L J. Bacteriol. 177:5773-5777(1995).
3N SEQUENCE FROM N.A.
3P STRAIN=LL;
3A MEDLINE=97144542; PubMed=8990309;
3A Kessler P.S., McInarnan J., Leigh J.A.;
3T "Nitrogenase phylogeny and the molybdenum dependence of nitrogen
3T fixation in Methanococcus maripaludis.";
3L J. Bacteriol. 179:541-543(1997).
3R EMBL; U75887; AAC45519.1; -
3R PIR; T10097; T10097.
3R InterPro; IPR003731; DUF153.
3R Pfam; PF02579; Nitro_PeMo-Co; 1.
3Q SEQUENCE 106 AA; 11862 MW; 4734D89CFED33F3B CRC64;

Query Match 95.0%; Score 19; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
2b 35 VAEF 38

RESULT 64
Q9BGL5 PRELIMINARY; PRT; 106 AA.
AC Q9BGL5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Matrilysin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
3N SEQUENCE FROM N.A.
3P TISSUE=Endometrium;
3A Smith G.W., Riske W.A., Cassear C.A., Smith M.F.;
3R Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
3R EMBL; AF267158; AAG59846.1; -
3R HSPF; P09237; IMMQ.
3R MEROPS; M10.008; -
3R GO; GO:0005578; C:extracellular matrix; IEA.
3R GO; GO:0004222; F:metalloendopeptidase activity; IEA.
3R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
3R InterPro; IPR006026; Peptidase_M.
3R InterPro; IPR001818; Pept_M10A_M12B.
3R Pfam; PF00413; Peptidase_M10; 1.
3R PRINTS; PR00138; MATRIXIN.
3R SMART; SM00235; ZnMc; 1.
3R NON_TER 1
3R NON_TER 106
3R NON_TER 106
3Q SEQUENCE 106 AA; 11578 MW; EBD271054928018 CRC64;

Query Match 95.0%; Score 19; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 2 VAEF 5
2b 106

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Db          6 VAEF 9
Query Match 95.0%; Score 19; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 65
O23682
ID O23682 PRELIMINARY; PRT; 106 AA.
AC O23682;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cathepsin B-like cysteine proteinase (Fragment).
GN T7123.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Federspiel N.A., Conway A.B., Conway A.R., Davis K., Brendel V.,
RA Palm C.J., Au M., Araujo R., Chung E., Kurtz D.B., Buehler E.,
RA Dewar K., Feng J., Kim C., Li Y., Shinn P., Sun H., Oji O.,
RA Osborne B., Shen Y.K., Toriumi M., Vyotskaia V., Yu G., Theologis A.,
RA Ecker J., Davis R.W.;
RT "Genomic sequence of Arabidopsis BAC T7123."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U89595; AAC24377.1; -.
FT NON TER 106
SQ SEQUENCE 106 AA; 11743 MW; C5D5EA5897AD17AP CRC64;

Query Match 95.0%; Score 19; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 75 VAEF 78

RESULT 66
O9C1L1
ID O9C1L1 PRELIMINARY; PRT; 107 AA.
AC O9C1L1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative thioredoxin G6G8.7.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OC
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A;
RA MEDLINE=21135672; PubMed=11238395;
RA Bean L.E., Dvorachek W.H. Jr., Braun E.L., Errett A., Saenz G.S.,
RA Giles M.D., Werner-Washburne M., Nelson M.A., Natvig D.O.;
RT "Analysis of the pdx-1 (snz-1/sno-1) region of the Neurospora crassa
RT genome. Correlation of pyridoxine-requiring phenotypes with mutations
RT in two structural genes."
RL Genetics 157:1067-1075(2001).
DR EMBL: AF309689; AAK07845.1; -.
DR HSP; P80028; ITOF
DR GO: GO:0005489; P:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR Pfam; PF00085; ThioRedox_dom2.
DR PRINTS; PR00421; THIOREDOXIN.
DR Redox-active center.
KW SEQUENCE 107 AA; 11676 MW; CF456EAF85BE3776 CRC64;

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QY 2 VAEF 5
Db 9 VAEF 12

RESULT 67
O8IHV3
ID O8IHV3 PRELIMINARY; PRT; 107 AA.
AC O8IHV3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF11_0423
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Risen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow J.J., Suh B., Peterson J., Anguoli S.,
RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL: AE014842; AAN36006.1; -.
KW Hypothetical protein.
SQ SEQUENCE 107 AA; 12714 MW; CA351258EFC46E35 CRC64;

Query Match 95.0%; Score 19; DB 5; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 40 VAEF 43

RESULT 68
O8NEX6
ID O8NEX6 PRELIMINARY; PRT; 107 AA.
AC O8NEX6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Uncharacterized ACR.
GN CGL0915.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OC
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005276; BAB98308.1; -.
DR InterPro; IPR007138; ABM.
DR Pfam; PF03992; ABM; 1.
DR Complete proteome.
KW

```

IQ SEQUENCE 107 AA; 12373 MW; B5ACF23621078018 CRC64;
Query Match 95.0%; Score 19; DB 16; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RY 2 VAEF 5
b 22 VAEF 25

RESULT 69
9PUB2
D Q9PUB2 PRELIMINARY; PRT; 109 AA.
C O9PUB2;
U 01-MAY-2000 (TrEMBLrel. 13, Created)
YI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
YI 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Retinol binding protein (fragment).
S Crocodylus niloticus (Nile crocodile) (African crocodile).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Archosauria; Crocodylia; Crocodylinae; Crocodylus.
X NCBI_TaxID=8501;
X [1]
RP SEQUENCE FROM N.A.
C TISSUE=Liver;
X MEDLINE=20022983; PubMed=10555283;
X Hughes S., Zelus D., Mouchiroud D.;
X "Warm-blooded isochore structure in Nile crocodile and turtle.";
X Mol. Biol. Evol. 16:1521-1527(1999).
X EMBL; AJ011392; CAB56418.1; -.
X HSP; P02753; IRBP.
X GO; GO:0005215; P:transporter activity; IEA.
X GO; GO:0006810; P:transport; IEA.
X InterPro; IPR002345; Lipocalin.
X InterPro; IPR000566; Lipocln_cycPABP.
X Pfam; PF00061; lipocalin; 1.
X PRINTS; PR00179; LIPOCALIN.
X NON TER 1
FT NON TER 1
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12552 MW; 0DCAE93895B91A23 CRC64;

Query Match 95.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 25 VAEF 28

RESULT 70
O53333
ID O53333 PRELIMINARY; PRT; 109 AA.
AC O53333;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein RV3183.
GN RV3183 OR MTV014.27 OR MT3275.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence.";
RN Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RL laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021646; CAA16648.1; -.
DR EMBL; AE007140; AAK47615.1; -.
DR F1; E70949; E70949.
DR TIGR; MT3275; -.
DR TubercuList; RV3183; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001387; HTH_3.
DR Pfam; PF01381; HTH_3; 1.
DR SMART; SMO0530; HTH_XRE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 109 AA; 11802 MW; A6DBE160D79613A CRC64;

Query Match 95.0%; Score 19; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 97 VAEF 100

RESULT 71
Q7TX28
ID Q7TX28 PRELIMINARY; PRT; 109 AA.
AC Q7TX28;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible transcriptional regulatory protein.
GN M3209.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsepe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis";
RL proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248345; CAB95301.1; -.
KW Complete proteome.
SQ SEQUENCE 109 AA; 11802 MW; A6DBE160D79613A CRC64;

Query Match 95.0%; Score 19; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 97 VAEF 100

RESULT 72
 ID O11343 PRELIMINARY; PRT; 110 AA.
 AC O11343;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE XI-5 protein (fragment).
 GN XI-5.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Estebaranz J.L., Esteban M., Martin-Gallardo A.;
 RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
 of a Gene Map of Molluscum Contagiosum Virus.";
 RL Virus Genes 0:0-0(1997)
 DR EMBL; U86919; AB57977.1; -.
 FT NON_TER 1 1
 FT NON_TER 110 110
 SQ SEQUENCE 110 AA; 11856 MW; 6AE9CE25FC3DE780 CRC64;

Query Match 95.0%; Score 19; DB 12; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 9 VAEF 12

RESULT 73
 ID Q88EG3 PRELIMINARY; PRT; 110 AA.
 AC Q88EG3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE YCII-related domain protein.
 GN PF4502.
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22423080; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 RA Uterback T., Rizzo M., Lee K., Kosack D., Noestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hohnel J., Straetz M., Helm S.,
 RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 RA Fraser C.M.;
 RP "Complete genome sequence and comparative analysis of the
 metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AE016790; AAN70076.1; -.
 DR TIGR; PF4502; -.
 DR InterPro; IPR005545; YCII.
 DR Pfam; PF03795; YCII; 1.
 KW Complete proteome.
 SQ SEQUENCE 110 AA; 11775 MW; 774B31C0D925A01E CRC64;

Query Match 95.0%; Score 19; DB 16; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 73 VAEF 76

RESULT 74
 ID Q8U296 PRELIMINARY; PRT; 111 AA.
 AC Q8U296;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein PF0943.
 GN PF0943.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010208; AAL81067.1; -.
 DR InterPro; IPR007842; HEPN.
 DR Pfam; PF05168; DUF712; 1.
 DR PROSITE; PS0910; H3EN; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 111 AA; 13379 MW; C6A005AE82B6CA4E CRC64;

Query Match 95.0%; Score 19; DB 17; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 48 VAEF 51

RESULT 75
 ID Q86PL2 PRELIMINARY; PRT; 112 AA.
 AC Q86PL2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nuclear receptor NHR-1 (Fragment).
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodermata; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robinson-Rechavi M., Maina C.V., Gissendanner C.R., Laudet V.,
 RA Sluder A.;
 RT "Explosive lineage-specific expansion of the orphan nuclear receptor
 HNF4 in nematodes.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204162; AAO39166.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR008946; Str_ncl_receptor.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 112 AA; 12826 MW; 44FC60AE3744791 CRC64;

Query Match 95.0%; Score 19; DB 5; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 111

b 13 VAEF 16

earch completed: May 24, 2004, 17:41:03
ob time : 123.714 secs

GenCore version 5.1.6
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Y protein - protein search, using sw model

run on: May 24, 2004, 17:38:13 ; Search time 15 Seconds
(without alignments)
17.209 Million cells

itle: US-09-594-978A-1

effect score:

sequence: 1 XVAEF 5

coring table: BLOSUM62

COINTEGRATING VAR(1) ESTIMATES:

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total number of bits satisfying chosen parameters:

minimum DB sec length: 0

HHMM	DB seq	length:	0
xyjmm	DB seq	length:	200000000

cut-processing: Minimum Match 0%

зав-processing: minimum match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 1000 summaries

arabase : Issued Patents AA: *

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database : issued_patents_mh.
1: /cqn2 6/ptodata/2/iaa/5A COMB.pcp:*

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3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/pctus_COMB.pe

6: /cgn2_6/ptodata/2/iaa/backfiles1.pe

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query		DB	ID	Description
		Match	Length			
1	19	95.0	7	4	US-09-724-566A-78	Sequence 78, Appl
2	19	95.0	8	4	US-09-724-566A-81	Sequence 81, Appl
3	19	95.0	9	4	US-08-197-484-86	Sequence 86, Appl
4	19	95.0	9	4	US-08-197-484-145	Sequence 145, App
5	19	95.0	4	4	US-09-724-566A-73	Sequence 73, Appl
6	19	95.0	9	5	PCT-US95-02121-86	Sequence 86, Appl
7	19	95.0	9	5	PCT-US95-02121-145	Sequence 145, Appl
8	19	95.0	14	4	US-09-724-566A-72	Sequence 72, Appl
9	19	95.0	14	4	US-09-724-566A-97	Sequence 97, Appl
10	19	95.0	28	2	US-08-733-825-3	Sequence 3, Appl
11	19	95.0	35	1	US-08-487-890A-69	Sequence 69, Appl
12	19	95.0	35	1	US-08-468-763-1	Sequence 1, Appl
13	19	95.0	35	2	US-08-393-986A-1	Sequence 1, Appl
14	19	95.0	35	2	US-08-478-435-69	Sequence 69, Appl
15	19	95.0	35	2	US-08-337-483-69	Sequence 69, Appl
16	19	95.0	35	2	US-08-478-373-69	Sequence 69, Appl
17	19	95.0	35	3	US-08-474-671-69	Sequence 69, Appl
18	19	95.0	35	3	US-08-483-577A-69	Sequence 69, Appl
19	19	95.0	35	3	US-08-897-438-69	Sequence 69, Appl
20	19	95.0	35	3	US-08-637-654-69	Sequence 69, Appl
21	19	95.0	35	4	US-08-649-518-69	Sequence 69, Appl
22	19	95.0	68	4	US-09-393-634-80	Sequence 80, Appl
23	19	95.0	69	4	US-09-489-039A-13555	Sequence 13555, A
24	19	95.0	71	4	US-09-328-352-7111	Sequence 7111, Ap
25	19	95.0	73	1	US-08-321-071A-10	Sequence 10, Appl
26	19	95.0	74	4	US-08-894-139-10	Sequence 10, Appl
27	19	95.0	88	4	US-09-732-210-1412	Sequence 1412, Ap

101	19	95.0	241	4	US-09-134-001C-5598	Sequence 5598, Ap	174	19	95.0	337	4	US-09-371-671B-2	Sequence 2, Appli
102	19	95.0	241	4	US-09-489-039A-7795	Sequence 7795, Ap	175	19	95.0	338	4	US-09-328-352-7151	Sequence 7151, Ap
103	19	95.0	243	4	US-09-134-001C-3587	Sequence 3587, Ap	176	19	95.0	339	3	US-09-345-468-3	Sequence 3, Appli
104	19	95.0	246	4	US-09-252-991A-30976	Sequence 30976, A	177	19	95.0	339	4	US-09-414-453A-3	Sequence 3, Appli
105	19	95.0	247	4	US-09-230-136-16	Sequence 16, Appl	178	19	95.0	339	4	US-09-134-000C-5209	Sequence 5209, Ap
106	19	95.0	247	4	US-09-372-422A-48	Sequence 48, Appl	179	19	95.0	342	4	US-09-543-681A-4207	Sequence 4207, Ap
107	19	95.0	249	3	US-09-154-083-2	Sequence 2, Appli	180	19	95.0	345	4	US-09-107-532A-3849	Sequence 3849, Ap
108	19	95.0	249	3	US-09-345-468-9	Sequence 9, Appli	181	19	95.0	346	4	US-09-286-365-107	Sequence 107, App
109	19	95.0	249	4	US-09-372-422A-22	Sequence 22, Appl	182	19	95.0	347	4	US-09-134-001C-3298	Sequence 3298, Ap
110	19	95.0	249	4	US-09-414-453A-9	Sequence 9, Appli	183	19	95.0	350	4	US-09-655-270A-17	Sequence 17, Appl
111	19	95.0	249	4	US-09-252-991A-22610	Sequence 22610, A	184	19	95.0	350	4	US-09-651-941-21	Sequence 21, Appl
112	19	95.0	250	1	US-08-234-939-2	Sequence 2, Appli	185	19	95.0	350	4	US-09-955-597-21	Sequence 21, Appl
113	19	95.0	250	1	US-08-558-865-2	Sequence 2, Appli	186	19	95.0	353	4	US-09-252-991A-27528	Sequence 27528, A
114	19	95.0	250	3	US-08-654-025-2	Sequence 2, Appli	187	19	95.0	356	4	US-09-328-352-7671	Sequence 7671, Ap
115	19	95.0	250	3	US-08-654-025-7	Sequence 7, Appli	188	19	95.0	357	4	US-09-540-236-3808	Sequence 3808, Ap
116	19	95.0	251	4	US-09-252-991A-23816	Sequence 23816, A	189	19	95.0	363	4	US-09-252-991A-30015	Sequence 30015, A
117	19	95.0	253	4	US-09-252-991A-17352	Sequence 17352, A	190	19	95.0	364	4	US-09-543-681A-7525	Sequence 7525, Ap
118	19	95.0	253	4	US-09-107-532A-5072	Sequence 5072, Ap	191	19	95.0	368	4	US-09-252-991A-24621	Sequence 24621, A
119	19	95.0	254	4	US-09-372-422A-34	Sequence 34, Appl	192	19	95.0	368	4	US-09-489-039A-94561	Sequence 94561, Ap
120	19	95.0	257	2	US-08-506-340A-3	Sequence 3, Appli	193	19	95.0	370	4	US-09-540-224-4	Sequence 4, Appli
121	19	95.0	257	4	US-09-543-681A-6811	Sequence 6811, Ap	194	19	95.0	370	4	US-09-554-595D-53	Sequence 53, Appl
122	19	95.0	259	4	US-09-543-681A-6390	Sequence 6390, Ap	195	19	95.0	370	4	US-09-808-972-4	Sequence 4, Appli
123	19	95.0	259	4	US-09-489-039A-11936	Sequence 11936, A	196	19	95.0	371	2	US-08-837-593-6	Sequence 6, Appli
124	19	95.0	261	4	US-09-252-991A-23795	Sequence 23795, A	197	19	95.0	372	4	US-09-800-729-213	Sequence 213, App
125	19	95.0	262	4	US-09-252-991A-19738	Sequence 19738, A	198	19	95.0	374	4	US-09-489-039A-12678	Sequence 12678, A
126	19	95.0	263	4	US-09-800-729-88	Sequence 88, Appl	199	19	95.0	388	4	US-09-489-039A-8170	Sequence 8170, Ap
127	19	95.0	269	1	US-08-447-554-5	Sequence 5, Appli	200	19	95.0	390	4	US-09-933-313B-8	Sequence 8, Appli
128	19	95.0	269	1	US-08-468-763-17	Sequence 17, Appl	201	19	95.0	390	4	US-08-311-731A-332	Sequence 332, App
129	19	95.0	269	1	US-08-448-160-5	Sequence 5, Appli	202	19	95.0	390	4	US-09-543-681A-6415	Sequence 6415, Ap
130	19	95.0	269	2	US-08-393-986A-17	Sequence 17, Appl	203	19	95.0	390	4	US-09-489-039A-13547	Sequence 13547, A
131	19	95.0	270	4	US-09-252-991A-29192	Sequence 29192, A	204	19	95.0	391	2	US-08-928-692-26	Sequence 26, Appl
132	19	95.0	271	4	US-09-107-532A-5071	Sequence 5071, Ap	205	19	95.0	391	4	US-09-339-972-26	Sequence 26, Appl
133	19	95.0	273	4	US-09-489-039A-9190	Sequence 9190, Ap	206	19	95.0	394	4	US-09-934-903-4	Sequence 4, Appli
134	19	95.0	277	1	US-08-400-413-1	Sequence 1, Appli	207	19	95.0	397	4	US-09-252-991A-22235	Sequence 22235, A
135	19	95.0	280	1	US-08-595-559-3	Sequence 3, Appli	208	19	95.0	398	4	US-09-242-859A-8	Sequence 8, Appli
136	19	95.0	281	4	US-09-314-701-58	Sequence 58, Appl	209	19	95.0	398	4	US-09-242-859A-8	Sequence 8, Appli
137	19	95.0	282	4	US-09-134-000C-3572	Sequence 3572, Ap	210	19	95.0	398	4	US-09-252-991A-17379	Sequence 17379, A
138	19	95.0	283	4	US-08-956-171E-5203	Sequence 5203, Ap	211	19	95.0	400	2	US-08-733-825-2	Sequence 2, Appli
139	19	95.0	288	4	US-09-743-847-2	Sequence 18721, A	212	19	95.0	400	3	US-09-264-097-6	Sequence 6, Appli
140	19	95.0	290	4	US-09-743-847-2	Sequence 2, Appli	213	19	95.0	403	4	US-09-540-236-2573	Sequence 2573, Ap
141	19	95.0	291	4	US-09-252-991A-25517	Sequence 25517, A	214	19	95.0	405	3	US-09-232-200-63	Sequence 63, Appl
142	19	95.0	291	4	US-09-489-039A-9578	Sequence 9578, Ap	215	19	95.0	405	4	US-09-232-197-63	Sequence 63, Appl
143	19	95.0	294	4	US-09-523-263B-20	Sequence 20, Appl	216	19	95.0	405	4	US-09-231-023A-20	Sequence 20, Appl
144	19	95.0	295	4	US-09-543-681A-5660	Sequence 5660, Ap	217	19	95.0	405	4	US-09-232-201-63	Sequence 63, Appl
145	19	95.0	297	4	US-09-489-039A-9087	Sequence 9087, Ap	218	19	95.0	405	4	US-09-540-715A-20	Sequence 20, Appl
146	19	95.0	299	4	US-09-314-701-46	Sequence 46, Appl	219	19	95.0	405	4	US-09-232-195-63	Sequence 63, Appl
147	19	95.0	299	4	US-09-393-634-35	Sequence 35, Appl	220	19	95.0	406	4	US-09-543-681A-7962	Sequence 7962, Ap
148	19	95.0	301	4	US-09-489-039A-11964	Sequence 11964, A	221	19	95.0	410	2	US-08-723-415B-10	Sequence 10, Appl
149	19	95.0	311	4	US-09-614-912-198	Sequence 198, App	222	19	95.0	410	2	US-08-723-415B-11	Sequence 11, Appl
150	19	95.0	317	4	US-09-483-077A-17	Sequence 17, Appl	223	19	95.0	410	2	US-08-428-131-2	Sequence 2, Appli
151	19	95.0	318	2	US-08-872-719-2	Sequence 2, Appli	224	19	95.0	410	3	US-09-078-596-2	Sequence 2, Appli
152	19	95.0	318	3	US-08-957-302A-12	Sequence 12, Appl	225	19	95.0	410	3	US-09-189-627A-10	Sequence 10, Appl
153	19	95.0	318	3	US-09-336-890-2	Sequence 2, Appli	226	19	95.0	410	3	US-09-189-627A-11	Sequence 11, Appl
154	19	95.0	318	3	US-09-542-403-12	Sequence 12, Appl	227	19	95.0	410	4	US-09-710-861-10	Sequence 10, Appl
155	19	95.0	318	4	US-09-668-499-2	Sequence 2, Appli	228	19	95.0	410	4	US-09-710-861-11	Sequence 11, Appl
156	19	95.0	318	4	US-09-975-594-938	Sequence 938, App	229	19	95.0	410	4	US-09-252-991A-24839	Sequence 24839, A
157	19	95.0	319	2	US-08-795-927-4	Sequence 4, Appli	230	19	95.0	411	4	US-09-540-236-3549	Sequence 3549, Ap
158	19	95.0	319	3	US-09-345-468-5	Sequence 5, Appli	231	19	95.0	411	4	US-09-252-991A-17176	Sequence 17176, A
159	19	95.0	319	4	US-09-414-453A-5	Sequence 5, Appli	232	19	95.0	414	4	US-09-134-001C-5101	Sequence 5101, Ap
160	19	95.0	319	4	US-09-440-597-4	Sequence 4, Appli	233	19	95.0	415	4	US-09-252-991A-31684	Sequence 31684, A
161	19	95.0	321	4	US-09-252-991A-18807	Sequence 18807, A	234	19	95.0	415	4	US-09-252-991A-26713	Sequence 26713, A
162	19	95.0	323	4	US-09-543-681A-17111	Sequence 17111, A	235	19	95.0	416	4	US-09-328-352-4187	Sequence 4187, Ap
163	19	95.0	323	4	US-09-543-681A-6957	Sequence 6957, Ap	236	19	95.0	424	4	US-09-328-352-4187	Sequence 4187, Ap
164	19	95.0	323	4	US-09-489-039A-7408	Sequence 7408, Ap	237	19	95.0	424	4	US-09-489-039A-9628	Sequence 9628, Ap
165	19	95.0	324	4	US-09-328-352-4636	Sequence 4636, Ap	238	19	95.0	425	4	US-09-489-039A-8386	Sequence 8386, Ap
166	19	95.0	326	4	US-09-230-196-20	Sequence 20, Appl	239	19	95.0	431	4	US-09-134-001C-4357	Sequence 4357, Ap
167	19	95.0	326	4	US-09-489-039A-9512	Sequence 9512, Ap	240	19	95.0	431	4	US-09-252-991A-24878	Sequence 24878, A
168	19	95.0	327	4	US-09-252-991A-30065	Sequence 30065, A	241	19	95.0	432	1	US-08-522-166-8	Sequence 8, Appli
169	19	95.0	328	4	US-09-489-039A-9306	Sequence 9306, Ap	242	19	95.0	432	1	US-08-488-382A-8	Sequence 8, Appli
170	19	95.0	331	4	US-09-489-039A-9639	Sequence 9639, Ap	243	19	95.0	432	2	US-08-480-912-8	Sequence 8, Appli
171	19	95.0	335	1	US-08-202-054-2	Sequence 2, Appli	244	19	95.0	435	4	US-09-252-991A-30562	Sequence 30562, A
172	19	95.0	335	4	US-08-446-923-2	Sequence 2, Appli	245	19	95.0	436	4	US-09-151-984A-9	Sequence 9, Appli
173	19	95.0	335	4	US-09-482-273-118	Sequence 118, App	246	19	95.0	436	4	US-09-134-000C-3950	Sequence 3950, Ap

247	19	95.0	436	6	5405943-4	Patent No. 5405943	320	19	95.0	485	4	US-09-540-715A-18	Sequence 18, Appl
248	19	95.0	437	4	US-09-252-991A-25332	Sequence 25332, A	321	19	95.0	485	4	US-09-540-715A-19	Sequence 19, Appl
249	19	95.0	440	4	US-09-252-991A-22487	Sequence 22487, A	322	19	95.0	485	4	US-09-769-864-1	Sequence 1, Appl
250	19	95.0	444	4	US-09-252-991A-18256	Sequence 18256, A	323	19	95.0	485	4	US-09-769-864-2	Sequence 2, Appl
251	19	95.0	444	4	US-09-252-991A-19565	Sequence 19565, A	324	19	95.0	485	4	US-09-769-864-5	Sequence 6, Appl
252	19	95.0	445	4	US-09-252-991A-28986	Sequence 28986, A	325	19	95.0	485	4	US-09-769-864-8	Sequence 7, Appl
253	19	95.0	445	4	US-09-107-532A-7232	Sequence 7232, Ap	326	19	95.0	485	4	US-09-769-864-8	Sequence 8, Appl
254	19	95.0	446	4	US-09-328-352-6076	Sequence 6076, Ap	327	19	95.0	486	4	US-09-381-687-4	Sequence 4, Appl
255	19	95.0	449	4	US-09-134-000C-5444	Sequence 5444, Ap	328	19	95.0	493	3	US-08-996-441B-70	Sequence 70, Appl
256	19	95.0	450	4	US-09-543-681A-7260	Sequence 7260, Ap	329	19	95.0	493	3	US-08-993-722A-70	Sequence 70, Appl
257	19	95.0	451	4	US-09-134-000C-6421	Sequence 6421, Ap	330	19	95.0	493	3	US-08-993-170A-70	Sequence 70, Appl
258	19	95.0	455	4	US-09-252-991A-19936	Sequence 19936, A	331	19	95.0	493	3	US-08-993-775B-70	Sequence 70, Appl
259	19	95.0	456	4	US-09-252-991A-31884	Sequence 31884, A	332	19	95.0	493	3	US-08-177-349-5	Sequence 5, Appl
260	19	95.0	457	4	US-09-252-991A-28824	Sequence 28824, A	333	19	95.0	493	4	US-09-348-352-6753	Sequence 6753, Ap
261	19	95.0	467	4	US-09-543-681A-6871	Sequence 6871, Ap	334	19	95.0	493	4	US-09-427-770-70	Sequence 70, Appl
262	19	95.0	468	4	US-09-252-991A-18608	Sequence 18608, A	335	19	95.0	493	4	US-09-427-769-70	Sequence 2869, Ap
263	19	95.0	469	4	US-09-543-681A-5423	Sequence 5423, Ap	336	19	95.0	493	4	US-09-540-236-2869	Sequence 1, Appl
264	19	95.0	474	4	US-09-252-991A-7524	Sequence 7524, A	337	19	95.0	495	3	US-09-179-966-1	Sequence 1, Appl
265	19	95.0	475	4	US-09-252-991A-32806	Sequence 32806, A	338	19	95.0	495	3	US-08-980-984-1	Sequence 1, Appl
266	19	95.0	479	4	US-09-328-352-5396	Sequence 5396, Ap	339	19	95.0	504	4	US-08-252-991A-20317	Sequence 20317, A
267	19	95.0	485	2	US-08-446-803-1	Sequence 1, Appl	340	19	95.0	506	3	US-09-232-191-9	Sequence 9, Appl
268	19	95.0	485	2	US-08-446-803-2	Sequence 2, Appl	341	19	95.0	506	3	US-09-232-200-9	Sequence 9, Appl
269	19	95.0	485	2	US-08-861-837-1	Sequence 1, Appl	342	19	95.0	506	4	US-09-232-200-95	Sequence 9, Appl
270	19	95.0	485	2	US-08-861-837-2	Sequence 2, Appl	343	19	95.0	506	4	US-09-232-197-9	Sequence 9, Appl
271	19	95.0	485	2	US-08-600-908A-12	Sequence 12, Appl	344	19	95.0	506	4	US-09-232-201-9	Sequence 9, Appl
272	19	95.0	485	3	US-08-683-838A-12	Sequence 12, Appl	345	19	95.0	506	4	US-09-232-201-95	Sequence 9, Appl
273	19	95.0	485	3	US-08-600-656-1	Sequence 1, Appl	346	19	95.0	506	4	US-09-232-201-95	Sequence 9, Appl
274	19	95.0	485	3	US-08-600-656-2	Sequence 2, Appl	347	19	95.0	506	4	US-09-232-195-9	Sequence 9, Appl
275	19	95.0	485	3	US-08-600-656-7	Sequence 7, Appl	348	19	95.0	516	4	US-09-232-195-95	Sequence 9, Appl
276	19	95.0	485	3	US-09-170-670-1	Sequence 1, Appl	349	19	95.0	522	4	US-09-986-676A-2	Sequence 2, Appl
277	19	95.0	485	3	US-09-170-670-2	Sequence 2, Appl	350	19	95.0	522	4	US-09-252-991A-30451	Sequence 30451, A
278	19	95.0	485	3	US-09-170-670-6	Sequence 6, Appl	351	19	95.0	524	2	US-08-928-632-12	Sequence 12, Appl
279	19	95.0	485	3	US-09-170-670-7	Sequence 7, Appl	352	19	95.0	524	3	US-08-957-302A-2	Sequence 2, Appl
280	19	95.0	485	3	US-09-193-068-8	Sequence 8, Appl	353	19	95.0	524	3	US-09-542-403-2	Sequence 12, Appl
281	19	95.0	485	3	US-09-193-068-1	Sequence 1, Appl	354	19	95.0	524	4	US-09-339-972-12	Sequence 12, Appl
282	19	95.0	485	3	US-09-193-068-2	Sequence 2, Appl	355	19	95.0	532	4	US-09-252-991A-27288	Sequence 27288, A
283	19	95.0	485	3	US-09-193-068-6	Sequence 6, Appl	356	19	95.0	536	4	US-09-107-532A-6930	Sequence 6930, Ap
284	19	95.0	485	3	US-09-193-068-7	Sequence 7, Appl	357	19	95.0	538	4	US-09-489-039A-13518	Sequence 13518, A
285	19	95.0	485	3	US-09-193-068-8	Sequence 8, Appl	358	19	95.0	540	4	US-09-621-451-2	Sequence 2, Appl
286	19	95.0	485	3	US-09-183-412-1	Sequence 1, Appl	359	19	95.0	540	4	US-10-223-355-2	Sequence 2, Appl
287	19	95.0	485	3	US-09-183-412-2	Sequence 2, Appl	360	19	95.0	544	4	US-09-328-352-4446	Sequence 4446, Ap
288	19	95.0	485	3	US-09-183-412-6	Sequence 6, Appl	361	19	95.0	547	3	US-08-483-577A-149	Sequence 149, App
289	19	95.0	485	3	US-09-183-413-7	Sequence 7, Appl	362	19	95.0	547	3	US-08-897-438-149	Sequence 149, App
290	19	95.0	485	3	US-09-183-413-8	Sequence 8, Appl	363	19	95.0	547	4	US-08-649-518-149	Sequence 149, App
291	19	95.0	485	3	US-09-264-097-5	Sequence 5, Appl	364	19	95.0	550	4	US-09-396-478A-2	Sequence 2, Appl
292	19	95.0	485	3	US-09-264-097-7	Sequence 7, Appl	365	19	95.0	552	4	US-09-489-039A-13735	Sequence 13735, A
293	19	95.0	485	3	US-09-354-191A-1	Sequence 1, Appl	366	19	95.0	557	4	US-09-134-001C-5569	Sequence 5569, Ap
294	19	95.0	485	3	US-09-354-191A-2	Sequence 2, Appl	367	19	95.0	557	4	US-09-489-039A-13795	Sequence 13795, A
295	19	95.0	485	3	US-09-354-191A-7	Sequence 7, Appl	368	19	95.0	557	4	US-09-134-000C-4354	Sequence 4354, Ap
296	19	95.0	485	4	US-09-291-023A-13	Sequence 13, Appl	369	19	95.0	558	4	US-09-252-991A-27678	Sequence 27678, A
297	19	95.0	485	4	US-09-291-023A-18	Sequence 18, Appl	370	19	95.0	566	4	US-09-513-783A-142	Sequence 142, App
298	19	95.0	485	4	US-09-291-023A-19	Sequence 19, Appl	371	19	95.0	567	2	US-08-504-459-4	Sequence 4, Appl
299	19	95.0	485	4	US-09-290-734-1	Sequence 1, Appl	372	19	95.0	567	2	US-08-504-459-6	Sequence 6, Appl
300	19	95.0	485	4	US-09-290-734-2	Sequence 2, Appl	373	19	95.0	571	3	US-08-803-326A-6	Sequence 6, Appl
301	19	95.0	485	4	US-09-290-734-6	Sequence 6, Appl	374	19	95.0	571	4	US-09-689-913A-6	Sequence 6, Appl
302	19	95.0	485	4	US-09-290-734-7	Sequence 7, Appl	375	19	95.0	571	4	US-09-689-913A-6	Sequence 6, Appl
303	19	95.0	485	4	US-09-290-734-8	Sequence 8, Appl	376	19	95.0	571	4	US-09-689-916A-6	Sequence 6, Appl
304	19	95.0	485	4	US-09-290-734-24	Sequence 24, Appl	377	19	95.0	573	4	US-09-252-991A-18744	Sequence 18744, A
305	19	95.0	485	4	US-09-290-734-26	Sequence 26, Appl	378	19	95.0	573	4	US-09-328-352-4675	Sequence 4675, Ap
306	19	95.0	485	4	US-09-636-252A-12	Sequence 12, Appl	379	19	95.0	580	4	US-09-198-452A-332	Sequence 332, App
307	19	95.0	485	4	US-09-417-359A-5	Sequence 5, Appl	380	19	95.0	587	4	US-08-635-552A-3	Sequence 3, Appl
308	19	95.0	485	4	US-09-381-687-1	Sequence 1, Appl	381	19	95.0	587	4	US-08-675-499A-4	Sequence 4, Appl
309	19	95.0	485	4	US-09-381-687-2	Sequence 2, Appl	382	19	95.0	587	4	US-08-812-008-4	Sequence 4, Appl
310	19	95.0	485	4	US-09-381-687-3	Sequence 3, Appl	383	19	95.0	589	4	US-09-643-657-14	Sequence 14, Appl
311	19	95.0	485	4	US-09-545-586-1	Sequence 5, Appl	384	19	95.0	591	2	US-08-736-770-5	Sequence 5, Appl
312	19	95.0	485	4	US-09-545-586-2	Sequence 2, Appl	385	19	95.0	591	4	US-09-643-657-5	Sequence 5, Appl
313	19	95.0	485	4	US-09-545-586-6	Sequence 6, Appl	386	19	95.0	591	4	US-09-643-657-15	Sequence 15, Appl
314	19	95.0	485	4	US-09-545-586-7	Sequence 7, Appl	387	19	95.0	597	4	US-09-252-991A-23152	Sequence 23152, A
315	19	95.0	485	4	US-09-545-586-8	Sequence 8, Appl	388	19	95.0	597	4	US-09-540-236-2805	Sequence 2805, Ap
316	19	95.0	485	4	US-09-545-586-24	Sequence 24, Appl	389	19	95.0	607	2	US-08-472-534-5	Sequence 5, Appl
317	19	95.0	485	4	US-09-545-586-26	Sequence 26, Appl	390	19	95.0	608	2	US-08-736-770-1	Sequence 1, Appl
318	19	95.0	485	4	US-09-540-715A-13	Sequence 13, Appl	391	19	95.0	620	4	US-08-637-770-40	Sequence 40, Appl
319	19	95.0	485	4			392	19	95.0	623	3	US-09-041-991A-6	Sequence 6, Appl

393	19	95.0	623	4	US-08-608-533A-6	Sequence 6, Appl	466	19	95.0	651	3	US-08-993-170A-56	Sequence 56, Appl
394	19	95.0	625	4	US-08-661-322A-48	Sequence 48, Appl	467	19	95.0	651	3	US-08-993-170A-58	Sequence 58, Appl
395	19	95.0	626	4	US-08-232-891A-20268	Sequence 20268, A	468	19	95.0	651	3	US-08-993-775B-52	Sequence 52, Appl
396	19	95.0	631	1	US-08-478-890A-111	Sequence 111, Appl	469	19	95.0	651	3	US-08-993-775B-56	Sequence 56, Appl
397	19	95.0	631	2	US-08-478-435-111	Sequence 111, Appl	470	19	95.0	651	3	US-08-993-775B-58	Sequence 58, Appl
398	19	95.0	631	2	US-08-337-483-111	Sequence 111, Appl	471	19	95.0	651	4	US-09-427-770-52	Sequence 52, Appl
399	19	95.0	631	2	US-08-478-373-111	Sequence 111, Appl	472	19	95.0	651	4	US-09-427-770-56	Sequence 56, Appl
400	19	95.0	631	3	US-08-478-373-111	Sequence 111, Appl	473	19	95.0	651	4	US-09-427-770-58	Sequence 58, Appl
401	19	95.0	631	3	US-08-474-671-111	Sequence 111, Appl	474	19	95.0	651	4	US-09-427-769-52	Sequence 52, Appl
402	19	95.0	631	3	US-08-483-577A-111	Sequence 111, Appl	475	19	95.0	651	4	US-09-427-769-56	Sequence 56, Appl
403	19	95.0	631	3	US-08-897-438-111	Sequence 111, Appl	476	19	95.0	651	4	US-09-427-769-58	Sequence 58, Appl
404	19	95.0	631	4	US-08-637-654-111	Sequence 111, Appl	477	19	95.0	652	3	US-08-996-441B-2	Sequence 2, Appl
405	19	95.0	631	4	US-08-649-518-111	Sequence 111, Appl	478	19	95.0	652	3	US-08-996-441B-4	Sequence 4, Appl
406	19	95.0	632	3	US-09-232-200-34	Sequence 34, Appl	479	19	95.0	652	3	US-08-996-441B-6	Sequence 6, Appl
407	19	95.0	632	3	US-09-232-200-35	Sequence 35, Appl	480	19	95.0	652	3	US-08-996-441B-8	Sequence 8, Appl
408	19	95.0	632	3	US-09-232-200-39	Sequence 39, Appl	481	19	95.0	652	3	US-08-996-441B-10	Sequence 10, Appl
409	19	95.0	632	4	US-09-232-197-34	Sequence 34, Appl	482	19	95.0	652	3	US-08-996-441B-12	Sequence 12, Appl
410	19	95.0	632	4	US-09-232-197-35	Sequence 35, Appl	483	19	95.0	652	3	US-08-996-441B-14	Sequence 14, Appl
411	19	95.0	632	4	US-09-232-197-39	Sequence 39, Appl	484	19	95.0	652	3	US-08-996-441B-16	Sequence 16, Appl
412	19	95.0	632	4	US-09-232-201-35	Sequence 35, Appl	485	19	95.0	652	3	US-08-996-441B-18	Sequence 18, Appl
413	19	95.0	632	4	US-09-232-201-39	Sequence 39, Appl	486	19	95.0	652	3	US-08-996-441B-20	Sequence 20, Appl
414	19	95.0	632	4	US-09-232-195-34	Sequence 34, Appl	487	19	95.0	652	3	US-08-996-441B-22	Sequence 22, Appl
415	19	95.0	632	4	US-09-232-195-35	Sequence 35, Appl	488	19	95.0	652	3	US-08-996-441B-24	Sequence 24, Appl
416	19	95.0	632	4	US-09-232-195-39	Sequence 39, Appl	489	19	95.0	652	3	US-08-996-441B-26	Sequence 26, Appl
417	19	95.0	635	4	US-08-107-322A-7135	Sequence 7135, Ap	490	19	95.0	652	3	US-08-996-441B-28	Sequence 28, Appl
418	19	95.0	638	4	US-08-489-039A-8996	Sequence 8996, Ap	491	19	95.0	652	3	US-08-996-441B-30	Sequence 30, Appl
419	19	95.0	639	4	US-08-328-352-4979	Sequence 4979, Ap	492	19	95.0	652	3	US-08-996-441B-32	Sequence 32, Appl
420	19	95.0	640	4	US-09-252-991A-23007	Sequence 23007, A	493	19	95.0	652	3	US-08-996-441B-34	Sequence 34, Appl
421	19	95.0	641	3	US-09-543-681A-6258	Sequence 6258, Ap	494	19	95.0	652	3	US-08-996-441B-36	Sequence 36, Appl
422	19	95.0	641	3	US-09-232-200-27	Sequence 27, Appl	495	19	95.0	652	3	US-08-996-441B-38	Sequence 38, Appl
423	19	95.0	643	3	US-09-232-200-41	Sequence 41, Appl	496	19	95.0	652	3	US-08-996-441B-40	Sequence 40, Appl
424	19	95.0	643	3	US-09-232-200-42	Sequence 42, Appl	497	19	95.0	652	3	US-08-996-441B-42	Sequence 42, Appl
425	19	95.0	643	3	US-09-232-200-45	Sequence 45, Appl	498	19	95.0	652	3	US-08-996-441B-44	Sequence 44, Appl
426	19	95.0	643	3	US-09-232-200-53	Sequence 53, Appl	499	19	95.0	652	3	US-08-996-441B-46	Sequence 46, Appl
427	19	95.0	643	3	US-09-232-200-71	Sequence 71, Appl	500	19	95.0	652	3	US-08-996-441B-48	Sequence 48, Appl
428	19	95.0	643	4	US-09-232-197-27	Sequence 27, Appl	501	19	95.0	652	3	US-08-996-441B-50	Sequence 50, Appl
429	19	95.0	643	4	US-09-232-197-42	Sequence 42, Appl	502	19	95.0	652	3	US-08-996-441B-54	Sequence 54, Appl
430	19	95.0	643	4	US-09-232-197-45	Sequence 45, Appl	503	19	95.0	652	3	US-08-996-441B-60	Sequence 60, Appl
431	19	95.0	643	4	US-09-232-197-53	Sequence 53, Appl	504	19	95.0	652	3	US-08-996-441B-62	Sequence 62, Appl
432	19	95.0	643	4	US-09-232-197-71	Sequence 71, Appl	505	19	95.0	652	3	US-08-996-441B-64	Sequence 64, Appl
433	19	95.0	643	4	US-09-232-201-27	Sequence 27, Appl	506	19	95.0	652	3	US-08-996-441B-66	Sequence 66, Appl
434	19	95.0	643	4	US-09-232-201-41	Sequence 41, Appl	507	19	95.0	652	3	US-08-996-441B-68	Sequence 68, Appl
435	19	95.0	643	4	US-09-232-201-42	Sequence 42, Appl	508	19	95.0	652	3	US-08-996-441B-98	Sequence 98, Appl
436	19	95.0	643	4	US-09-232-201-45	Sequence 45, Appl	509	19	95.0	652	3	US-08-996-441B-108	Sequence 108, Appl
437	19	95.0	643	4	US-09-232-201-53	Sequence 53, Appl	510	19	95.0	652	3	US-08-996-441B-110	Sequence 110, Appl
438	19	95.0	643	4	US-08-232-201-71	Sequence 71, Appl	511	19	95.0	652	3	US-08-996-441B-111	Sequence 111, Appl
439	19	95.0	643	4	US-08-543-661A-6345	Sequence 6345, Ap	512	19	95.0	652	3	US-08-993-722A-2	Sequence 2, Appl
440	19	95.0	643	4	US-09-232-195-27	Sequence 27, Appl	513	19	95.0	652	3	US-08-993-722A-4	Sequence 4, Appl
441	19	95.0	643	4	US-09-232-195-41	Sequence 41, Appl	514	19	95.0	652	3	US-08-993-722A-6	Sequence 6, Appl
442	19	95.0	643	4	US-09-232-195-42	Sequence 42, Appl	515	19	95.0	652	3	US-08-993-722A-8	Sequence 8, Appl
443	19	95.0	643	4	US-09-232-195-45	Sequence 45, Appl	516	19	95.0	652	3	US-08-993-722A-10	Sequence 10, Appl
444	19	95.0	643	4	US-09-232-195-53	Sequence 53, Appl	517	19	95.0	652	3	US-08-993-722A-12	Sequence 12, Appl
445	19	95.0	643	4	US-08-232-195-71	Sequence 71, Appl	518	19	95.0	652	3	US-08-993-722A-14	Sequence 14, Appl
446	19	95.0	643	4	US-08-487-890A-6	Sequence 6, Appl	519	19	95.0	652	3	US-08-993-722A-16	Sequence 16, Appl
447	19	95.0	644	1	US-08-478-435-6	Sequence 6, Appl	520	19	95.0	652	3	US-08-993-722A-18	Sequence 18, Appl
448	19	95.0	644	2	US-08-337-483-6	Sequence 6, Appl	521	19	95.0	652	3	US-08-993-722A-20	Sequence 20, Appl
449	19	95.0	644	2	US-08-478-373-6	Sequence 6, Appl	522	19	95.0	652	3	US-08-993-722A-22	Sequence 22, Appl
450	19	95.0	644	2	US-08-474-671-6	Sequence 6, Appl	523	19	95.0	652	3	US-08-993-722A-24	Sequence 24, Appl
451	19	95.0	644	3	US-08-483-577A-6	Sequence 6, Appl	524	19	95.0	652	3	US-08-993-722A-26	Sequence 26, Appl
452	19	95.0	644	3	US-08-897-438-6	Sequence 6, Appl	525	19	95.0	652	3	US-08-993-722A-28	Sequence 28, Appl
453	19	95.0	644	4	US-08-637-654-6	Sequence 6, Appl	526	19	95.0	652	3	US-08-993-722A-30	Sequence 30, Appl
454	19	95.0	644	4	US-08-649-518-6	Sequence 6, Appl	527	19	95.0	652	3	US-08-993-722A-32	Sequence 32, Appl
455	19	95.0	644	4	US-08-487-890A-148	Sequence 148, App	528	19	95.0	652	3	US-08-993-722A-34	Sequence 34, Appl
456	19	95.0	647	3	US-08-483-577A-148	Sequence 148, App	529	19	95.0	652	3	US-08-993-722A-36	Sequence 36, Appl
457	19	95.0	647	3	US-08-478-435-148	Sequence 148, App	530	19	95.0	652	3	US-08-993-722A-38	Sequence 38, Appl
458	19	95.0	647	3	US-08-996-441B-52	Sequence 52, Appl	531	19	95.0	652	3	US-08-993-722A-40	Sequence 40, Appl
459	19	95.0	651	3	US-08-996-441B-56	Sequence 56, Appl	532	19	95.0	652	3	US-08-993-722A-42	Sequence 42, Appl
460	19	95.0	651	3	US-08-996-441B-58	Sequence 58, Appl	533	19	95.0	652	3	US-08-993-722A-44	Sequence 44, Appl
461	19	95.0	651	3	US-08-993-722A-52	Sequence 52, Appl	534	19	95.0	652	3	US-08-993-722A-46	Sequence 46, Appl
462	19	95.0	651	3	US-08-993-722A-56	Sequence 56, Appl	535	19	95.0	652	3	US-08-993-722A-48	Sequence 48, Appl
463	19	95.0	651	3	US-08-993-722A-58	Sequence 58, Appl	536	19	95.0	652	3	US-08-993-722A-50	Sequence 50, Appl
464	19	95.0	651	3	US-08-993-722A-54	Sequence 54, Appl	537	19	95.0	652	3	US-08-993-722A-54	Sequence 54, Appl
465	19	95.0	651	3	US-08-993-170A-52	Sequence 52, Appl	538	19	95.0	652	3	US-08-993-722A-60	Sequence 60, Appl

685	19	95.0	652	4	US-09-427-769-68	Sequence 58, Appl	758	19	95.0	736	4	US-09-252-991A-27827	Sequence 27827, A
686	19	95.0	652	4	US-09-427-769-98	Sequence 98, Appl	759	19	95.0	748	4	US-09-252-991A-28449	Sequence 28449, A
687	19	95.0	652	4	US-09-427-769-108	Sequence 108, Appl	760	19	95.0	749	4	US-09-562-737-100	Sequence 100, Appl
688	19	95.0	652	4	US-09-427-769-110	Sequence 110, Appl	761	19	95.0	749	4	US-09-252-991A-16877	Sequence 16877, A
689	19	95.0	652	4	US-09-427-769-111	Sequence 111, Appl	762	19	95.0	753	4	US-09-328-552-5412	Sequence 5412, Ap
690	19	95.0	652	5	PCT-US92-00040-2	Sequence 2, Appl	763	19	95.0	771	4	US-09-252-991A-17243	Sequence 17243, A
691	19	95.0	652	5	5187091-2	Patent No. 5187091	764	19	95.0	788	2	US-08-907-166-6	Sequence 6, Appl
692	19	95.0	652	3	US-08-936-441B-100	Sequence 100, Appl	765	19	95.0	788	4	US-09-391-340-6	Sequence 16, Appl
693	19	95.0	653	3	US-08-993-722A-100	Sequence 100, Appl	766	19	95.0	789	4	US-09-390-234-16	Sequence 16, Appl
694	19	95.0	653	3	US-08-993-170A-100	Sequence 100, Appl	767	19	95.0	789	4	US-09-603-311-16	Sequence 6065, Ap
695	19	95.0	653	3	US-08-993-775B-100	Sequence 100, Appl	768	19	95.0	791	4	US-09-107-532A-065	Sequence 4, Appl
696	19	95.0	653	4	US-09-377-466B-8	Sequence 8, Appl	769	19	95.0	812	4	US-09-513-783A-4	Sequence 4, Appl
697	19	95.0	653	4	US-09-377-466B-10	Sequence 10, Appl	770	19	95.0	812	4	US-09-513-783A-6	Sequence 10, Appl
698	19	95.0	653	4	US-09-377-466B-12	Sequence 12, Appl	771	19	95.0	816	4	US-09-489-038A-10520	Sequence 15, Appl
699	19	95.0	653	4	US-09-377-466B-14	Sequence 14, Appl	772	19	95.0	819	4	US-09-651-656-15	Sequence 20, Appl
700	19	95.0	653	4	US-09-377-466B-16	Sequence 16, Appl	773	19	95.0	819	4	US-09-650-855-15	Sequence 24, Appl
701	19	95.0	653	4	US-09-377-466B-18	Sequence 18, Appl	774	19	95.0	821	3	US-09-422-865-24	Sequence 20, Appl
702	19	95.0	653	4	US-09-377-466B-20	Sequence 20, Appl	775	19	95.0	844	3	US-09-029-267-20	Sequence 24, Appl
703	19	95.0	653	4	US-09-377-466B-22	Sequence 22, Appl	776	19	95.0	846	3	US-09-328-352-648	Sequence 6648, Ap
704	19	95.0	653	4	US-09-377-466B-24	Sequence 24, Appl	777	19	95.0	848	4	US-09-489-038A-13773	Sequence 13773, A
705	19	95.0	653	4	US-09-377-466B-37	Sequence 37, Appl	778	19	95.0	849	4	US-09-252-991A-17953	Sequence 17953, A
706	19	95.0	653	4	US-09-377-466B-39	Sequence 39, Appl	779	19	95.0	873	4	US-09-252-991A-30504	Sequence 30504, A
707	19	95.0	653	4	US-09-427-769-100	Sequence 100, Appl	780	19	95.0	925	4	US-09-252-991A-27057	Sequence 27057, A
708	19	95.0	653	4	US-09-427-769-100	Sequence 100, Appl	781	19	95.0	927	4	US-09-134-001C-4831	Sequence 4831, Ap
709	19	95.0	654	1	US-08-487-890A-12	Sequence 12, Appl	782	19	95.0	944	4	US-09-328-352-4401	Sequence 4401, Ap
710	19	95.0	654	2	US-08-478-435-12	Sequence 12, Appl	783	19	95.0	972	3	US-08-335-84A-24	Sequence 24, Appl
711	19	95.0	654	2	US-08-337-483-12	Sequence 12, Appl	784	19	95.0	972	4	US-09-129-366-24	Sequence 24, Appl
712	19	95.0	654	2	US-08-478-373-12	Sequence 12, Appl	785	19	95.0	975	4	US-09-543-681A-5755	Sequence 5755, Ap
713	19	95.0	654	3	US-08-474-671-12	Sequence 12, Appl	786	19	95.0	982	4	US-09-023-905A-7	Sequence 7, Appl
714	19	95.0	654	3	US-08-483-577A-12	Sequence 12, Appl	787	19	95.0	1074	3	US-09-252-991A-22792	Sequence 22792, A
715	19	95.0	654	3	US-08-897-438-12	Sequence 12, Appl	788	19	95.0	993	4	US-09-894-998A-50	Sequence 50, Appl
716	19	95.0	654	4	US-08-637-654-12	Sequence 12, Appl	789	19	95.0	1009	4	US-09-693-146-4	Sequence 4, Appl
717	19	95.0	654	4	US-08-649-518-12	Sequence 12, Appl	790	19	95.0	1037	4	US-09-894-998A-54	Sequence 54, Appl
718	19	95.0	657	3	US-08-613-009A-19	Sequence 19, Appl	791	19	95.0	1036	4	US-09-513-783A-32	Sequence 32, Appl
719	19	95.0	657	4	US-08-778-570B-25	Sequence 25, Appl	792	19	95.0	1061	4	US-09-252-991A-23691	Sequence 23691, A
720	19	95.0	657	4	US-08-093-584-25	Sequence 25, Appl	793	19	95.0	1074	3	US-08-470-058-2	Sequence 2, Appl
721	19	95.0	657	4	US-09-252-991A-27358	Sequence 27358, A	794	19	95.0	1074	3	US-09-037-188-2	Sequence 2, Appl
722	19	95.0	660	1	US-08-487-890A-8	Sequence 8, Appl	795	19	95.0	1074	3	US-09-285-310-2	Sequence 2, Appl
723	19	95.0	660	1	US-08-487-890A-10	Sequence 10, Appl	796	19	95.0	1113	4	US-09-894-998A-51	Sequence 51, Appl
724	19	95.0	660	2	US-08-478-435-8	Sequence 8, Appl	797	19	95.0	1114	4	US-08-975-413A-12	Sequence 12, Appl
725	19	95.0	660	2	US-08-478-435-10	Sequence 10, Appl	798	19	95.0	1125	4	US-09-513-783A-182	Sequence 182, Appl
726	19	95.0	660	2	US-08-337-483-8	Sequence 8, Appl	799	19	95.0	1128	4	US-09-252-991A-19672	Sequence 19672, A
727	19	95.0	660	2	US-08-337-483-10	Sequence 10, Appl	800	19	95.0	1155	4	US-09-543-681A-6286	Sequence 6286, Ap
728	19	95.0	660	2	US-08-478-373-8	Sequence 8, Appl	801	19	95.0	1410	2	US-08-470-058-4	Sequence 4, Appl
729	19	95.0	660	2	US-08-478-373-10	Sequence 10, Appl	802	19	95.0	1410	3	US-09-037-188-4	Sequence 4, Appl
730	19	95.0	660	3	US-08-474-671-8	Sequence 8, Appl	803	19	95.0	1410	3	US-09-285-310-4	Sequence 10, Appl
731	19	95.0	660	3	US-08-474-671-10	Sequence 10, Appl	804	19	95.0	1477	3	US-08-492-459-10	Sequence 10, Appl
732	19	95.0	660	3	US-08-483-577A-8	Sequence 8, Appl	805	19	95.0	1477	3	US-08-423-752-10	Sequence 3, Appl
733	19	95.0	660	3	US-08-483-577A-10	Sequence 10, Appl	806	19	95.0	1477	3	US-08-945-994-3	Sequence 24, Appl
734	19	95.0	660	3	US-08-897-438-8	Sequence 8, Appl	807	19	95.0	1477	3	US-08-716-873-24	Sequence 24, Appl
735	19	95.0	660	3	US-08-897-438-10	Sequence 10, Appl	808	19	95.0	1477	3	US-09-368-431-24	Sequence 10, Appl
736	19	95.0	660	4	US-08-637-654-8	Sequence 8, Appl	809	19	95.0	1477	4	US-09-414-006-10	Sequence 10, Appl
737	19	95.0	660	4	US-08-637-654-10	Sequence 10, Appl	810	19	95.0	1477	4	US-09-447-223-10	Sequence 28442, A
738	19	95.0	660	4	US-08-649-518-8	Sequence 8, Appl	811	19	95.0	1490	4	US-09-252-991A-28442	Sequence 22, Appl
739	19	95.0	660	4	US-08-649-518-10	Sequence 10, Appl	812	19	95.0	1610	4	US-09-513-783A-22	Sequence 2, Appl
740	19	95.0	678	1	US-08-282-141-2	Sequence 2, Appl	813	19	95.0	2165	1	US-08-514-975B-2	Sequence 2, Appl
741	19	95.0	678	1	US-08-435-434-2	Sequence 2, Appl	814	19	95.0	2165	5	PCT-US95-12507-2	Sequence 2, Appl
742	19	95.0	678	1	US-08-435-436-2	Sequence 2, Appl	815	19	95.0	2227	3	US-08-475-886-2	Sequence 2, Appl
743	19	95.0	678	2	US-08-438-436-2	Sequence 2, Appl	816	19	95.0	2227	3	US-08-475-886-4	Sequence 6, Appl
744	19	95.0	678	3	US-08-438-862-2	Sequence 2, Appl	817	19	95.0	2227	3	US-08-475-886-6	Sequence 4, Appl
745	19	95.0	678	3	US-08-438-864-2	Sequence 2, Appl	818	19	95.0	2227	3	US-08-397-232-4	Sequence 4, Appl
746	19	95.0	678	3	US-08-628-747-2	Sequence 2, Appl	819	19	95.0	2227	3	US-08-397-232-2	Sequence 2, Appl
747	19	95.0	678	3	US-08-402-253-2	Sequence 2, Appl	820	19	95.0	2227	3	US-09-171-387-2	Sequence 2, Appl
748	19	95.0	678	3	US-08-443-866B-2	Sequence 2, Appl	821	19	95.0	2227	4	US-09-653-499-2	Sequence 4, Appl
749	19	95.0	680	4	US-09-252-991A-26639	Sequence 26639, A	822	19	95.0	2227	4	US-09-653-499-6	Sequence 12, Appl
750	19	95.0	682	4	US-09-252-991A-24919	Sequence 24919, A	823	19	95.0	2227	4	US-10-104-966-12	Sequence 2, Appl
751	19	95.0	685	4	US-09-252-991A-26723	Sequence 26723, A	824	19	95.0	2227	4	US-10-135-988-2	Sequence 4, Appl
752	19	95.0	696	6	5262177-4	Patent No. 5262177	825	19	95.0	2227	4	US-10-135-988-6	Sequence 6, Appl
753	19	95.0	698	2	US-08-175-158A-2	Sequence 2, Appl	826	19	95.0	2227	4	US-10-135-988-8	Sequence 1, Appl
754	19	95.0	703	4	US-09-252-991A-23905	Sequence 23905, A	827	19	95.0	2227	4	US-08-015-973-1	Sequence 2, Appl
755	19	95.0	718	4	US-09-252-991A-33109	Sequence 33109, A	828	19	95.0	2308	1	US-08-448-164-1	Sequence 1, Appl
756	19	95.0	720	4	US-09-252-991A-18618	Sequence 18618, A	829	19	95.0	2308	1	US-08-448-164-1	Sequence 1, Appl
757	19	95.0	720	4	US-09-134-000C-5631	Sequence 5631, Ap	830	19	95.0	2308	3	US-08-081-929-2	Sequence 2, Appl

831	19	95.0	2314	4	US-09-816-703A-2	Sequence 2, Appli	904	18	90.0	149	1	US-08-100-874-2	Sequence 2, Appli
832	19	95.0	2629	2	US-08-751-189-4	Sequence 4, Appli	905	18	90.0	149	3	US-08-963-409-4	Sequence 4, Appli
833	19	95.0	2629	2	US-09-060-836-4	Sequence 4, Appli	906	18	90.0	149	3	US-08-641-873-20	Sequence 20, Appli
834	19	95.0	2629	3	US-09-184-445-4	Sequence 4, Appli	907	18	90.0	152	3	US-08-963-409-5	Sequence 5, Appli
835	19	95.0	5588	3	US-09-036-987A-6	Sequence 6, Appli	908	18	90.0	152	4	US-09-252-991A-18700	Sequence 18700, A
836	19	95.0	5588	3	US-09-370-700-6	Sequence 6, Appli	909	18	90.0	152	4	US-09-252-991A-31418	Sequence 31418, A
837	19	95.0	5588	3	US-09-603-207-6	Sequence 6, Appli	910	18	90.0	157	4	US-09-134-001C-2991	Sequence 2991, Ap
838	19	95.0	8991	4	US-08-714-741-32	Sequence 32, Appli	911	18	90.0	158	1	US-08-611-107-4	Sequence 4, Appli
839	18	90.0	9	4	US-09-372-338-6	Sequence 6, Appli	912	18	90.0	158	2	US-08-422-560A-4	Sequence 4, Appli
840	18	90.0	9	4	US-10-126-752-6	Sequence 6, Appli	913	18	90.0	158	3	US-08-468-793-4	Sequence 4, Appli
841	18	90.0	10	2	US-08-482-228-120	Sequence 120, App	914	18	90.0	160	2	US-08-602-941-1	Sequence 1, Appli
842	18	90.0	10	2	US-08-482-228-120	Sequence 120, App	915	18	90.0	160	3	US-08-961-264-1	Sequence 1, Appli
843	18	90.0	11	2	US-08-934-222-99	Sequence 99, Appli	916	18	90.0	160	4	US-09-442-098A-1	Sequence 1, Appli
844	18	90.0	11	2	US-08-934-222-99	Sequence 99, Appli	917	18	90.0	160	4	US-09-612-342-1	Sequence 1, Appli
845	18	90.0	11	2	US-08-333-402-99	Sequence 99, Appli	918	18	90.0	160	4	US-09-612-421A-1	Sequence 1, Appli
846	18	90.0	11	2	US-08-333-402-99	Sequence 99, Appli	919	18	90.0	160	4	US-09-734-401-1	Sequence 1, Appli
847	18	90.0	11	3	US-09-231-797-99	Sequence 99, Appli	920	18	90.0	162	3	US-09-108-020-50	Sequence 50, Appli
848	18	90.0	11	3	US-08-934-224-99	Sequence 99, Appli	921	18	90.0	172	4	US-09-107-532A-5847	Sequence 5847, Ap
849	18	90.0	11	3	US-08-934-224-99	Sequence 99, Appli	922	18	90.0	172	4	US-09-634-238-296	Sequence 296, App
850	18	90.0	11	3	US-08-934-224-99	Sequence 99, Appli	923	18	90.0	184	4	US-09-489-039A-11491	Sequence 11491, A
851	18	90.0	11	3	US-09-413-423-99	Sequence 99, Appli	924	18	90.0	185	1	US-07-741-940-6	Sequence 6, Appli
852	18	90.0	19	4	US-08-835-281-10	Sequence 10, Appli	925	18	90.0	185	1	US-08-289-548A-6	Sequence 6, Appli
853	18	90.0	20	1	US-08-558-130-1	Sequence 1, Appli	926	18	90.0	185	1	US-08-452-654-6	Sequence 6, Appli
854	18	90.0	20	2	US-08-799-825-22	Sequence 22, Appli	927	18	90.0	185	1	US-08-452-655B-6	Sequence 6, Appli
855	18	90.0	20	4	US-09-092-000-5	Sequence 5, Appli	928	18	90.0	185	2	US-08-865-336-3	Sequence 3, Appli
856	18	90.0	20	4	US-09-280-068-22	Sequence 22, Appli	929	18	90.0	185	2	US-08-865-336-4	Sequence 4, Appli
857	18	90.0	20	4	US-08-835-281-12	Sequence 12, Appli	930	18	90.0	185	3	US-08-450-582-6	Sequence 6, Appli
858	18	90.0	20	4	US-09-481-593-18	Sequence 18, Appli	931	18	90.0	185	4	US-08-449-731-6	Sequence 6, Appli
859	18	90.0	20	5	PCT-US96-08723-1	Sequence 1, Appli	932	18	90.0	185	4	US-09-198-452A-858	Sequence 858, App
860	18	90.0	22	2	US-08-907-673-1	Sequence 1, Appli	933	18	90.0	187	4	US-09-134-001C-3419	Sequence 3419, Ap
861	18	90.0	22	3	US-08-809-397-6	Sequence 6, Appli	934	18	90.0	189	4	US-09-134-000C-4845	Sequence 4845, Ap
862	18	90.0	22	4	US-09-425-597-6	Sequence 6, Appli	935	18	90.0	199	1	US-08-602-262-2	Sequence 2, Appli
863	18	90.0	22	5	PCT-US95-12502-6	Sequence 6, Appli	936	18	90.0	199	3	US-09-004-716-2	Sequence 2, Appli
864	18	90.0	27	4	US-09-039-780A-82	Sequence 82, Appli	937	18	90.0	199	4	US-09-477-510-2	Sequence 2, Appli
865	18	90.0	28	4	US-09-039-780A-81	Sequence 81, Appli	938	18	90.0	199	4	US-09-543-681A-5219	Sequence 5219, Ap
866	18	90.0	30	4	US-09-039-780A-104	Sequence 104, App	939	18	90.0	199	5	PCT-US94-02889-2	Sequence 2, Appli
867	18	90.0	30	4	US-09-039-780A-83	Sequence 83, Appli	940	18	90.0	201	1	US-07-929-580B-5	Sequence 5, Appli
868	18	90.0	38	4	US-09-039-780A-84	Sequence 84, Appli	941	18	90.0	205	4	US-09-107-532A-5214	Sequence 5214, Ap
869	18	90.0	39	2	US-08-889-291-15	Sequence 15, Appli	942	18	90.0	208	1	US-08-631-607-3	Sequence 3, Appli
870	18	90.0	39	3	US-09-098-244-15	Sequence 15, Appli	943	18	90.0	208	4	US-09-098-358B-3	Sequence 3, Appli
871	18	90.0	39	4	US-09-375-314-15	Sequence 15, Appli	944	18	90.0	210	1	US-07-741-940-4	Sequence 4, Appli
872	18	90.0	39	4	US-09-767-395-15	Sequence 15, Appli	945	18	90.0	210	1	US-08-289-548A-4	Sequence 4, Appli
873	18	90.0	43	4	US-09-039-780A-89	Sequence 89, Appli	946	18	90.0	210	1	US-08-452-654-4	Sequence 4, Appli
874	18	90.0	44	4	US-09-039-780A-88	Sequence 88, Appli	947	18	90.0	210	1	US-08-452-655B-4	Sequence 4, Appli
875	18	90.0	44	4	US-09-039-780A-90	Sequence 90, Appli	948	18	90.0	210	3	US-08-450-582-4	Sequence 4, Appli
876	18	90.0	54	4	US-09-039-780A-90	Sequence 90, Appli	949	18	90.0	210	4	US-08-449-731-4	Sequence 4, Appli
877	18	90.0	56	4	US-09-039-780A-93	Sequence 93, Appli	950	18	90.0	211	4	US-09-328-352-5256	Sequence 5256, Ap
878	18	90.0	60	4	US-09-134-000C-4258	Sequence 4258, Ap	951	18	90.0	214	4	US-09-795-926-16	Sequence 16, Appli
879	18	90.0	61	4	US-09-107-532A-4993	Sequence 4993, Ap	952	18	90.0	220	4	US-09-107-532A-6803	Sequence 6803, Ap
880	18	90.0	66	4	US-09-543-681A-5898	Sequence 5898, Ap	953	18	90.0	223	1	US-07-708-885B-3	Sequence 3, Appli
881	18	90.0	69	4	US-09-328-352-5719	Sequence 5719, Ap	954	18	90.0	223	1	US-07-714-386-3	Sequence 3, Appli
882	18	90.0	88	4	US-09-732-210-1423	Sequence 1423, Ap	955	18	90.0	223	1	US-07-708-888A-3	Sequence 3, Appli
883	18	90.0	88	4	US-09-393-634-76	Sequence 76, Appli	956	18	90.0	229	4	US-09-489-039A-9391	Sequence 9391, Ap
884	18	90.0	101	4	US-09-107-532A-6901	Sequence 6901, Ap	957	18	90.0	232	4	US-09-134-000C-3556	Sequence 3556, Ap
885	18	90.0	105	4	US-09-489-039A-10362	Sequence 10362, A	958	18	90.0	235	3	US-09-390-721-4	Sequence 4, Appli
886	18	90.0	113	4	US-09-614-913-186	Sequence 186, App	959	18	90.0	237	3	US-09-248-335-48	Sequence 48, Appli
887	18	90.0	116	4	US-09-489-039A-12512	Sequence 12512, A	960	18	90.0	243	4	US-09-134-000C-3753	Sequence 3753, Ap
888	18	90.0	118	4	US-09-540-236-3531	Sequence 3531, Ap	961	18	90.0	245	4	US-09-543-681A-5699	Sequence 5699, Ap
889	18	90.0	122	4	US-09-540-236-3530	Sequence 3230, Ap	962	18	90.0	247	4	US-09-328-352-7311	Sequence 7311, Ap
890	18	90.0	131	4	US-09-328-352-4806	Sequence 4806, Ap	963	18	90.0	249	4	US-09-252-991A-32233	Sequence 32233, A
891	18	90.0	132	4	US-09-134-000C-3642	Sequence 3642, Ap	964	18	90.0	251	4	US-09-648-004-20	Sequence 20, Appli
892	18	90.0	136	4	US-09-732-210-211	Sequence 211, App	965	18	90.0	251	4	US-09-286-981B-4	Sequence 4, Appli
893	18	90.0	142	1	US-07-951-715A-24	Sequence 24, Appli	966	18	90.0	252	4	US-09-489-039A-13690	Sequence 13690, A
894	18	90.0	142	2	US-08-459-448A-24	Sequence 24, Appli	967	18	90.0	254	4	US-09-198-452A-632	Sequence 632, App
895	18	90.0	142	3	US-08-459-595A-24	Sequence 24, Appli	968	18	90.0	257	2	US-08-637-759B-92	Sequence 92, Appli
896	18	90.0	142	3	US-08-459-504B-24	Sequence 24, Appli	969	18	90.0	257	3	US-08-871-355A-92	Sequence 92, Appli
897	18	90.0	142	3	US-08-459-444-24	Sequence 24, Appli	970	18	90.0	257	4	US-09-201-945-92	Sequence 92, Appli
898	18	90.0	143	3	US-09-547-422-24	Sequence 24, Appli	971	18	90.0	262	1	US-08-622-353-9	Sequence 9, Appli
899	18	90.0	143	3	US-08-946-329A-52	Sequence 52, Appli	972	18	90.0	262	2	US-08-622-352A-11	Sequence 11, Appli
900	18	90.0	143	4	US-09-328-352-7008	Sequence 7008, Ap	973	18	90.0	262	3	US-08-826-390-11	Sequence 11, Appli
901	18	90.0	143	4	US-09-328-352-7008	Sequence 7008, Ap	974	18	90.0	265	4	US-08-926-926-6	Sequence 6, Appli
902	18	90.0	144	4	US-09-543-681A-5427	Sequence 5444, Ap	975	18	90.0	265	4	US-09-134-000C-5370	Sequence 5370, Ap
903	18	90.0	145	3	US-08-720-625-5	Sequence 5, Appli	976	18	90.0	267	4	US-09-543-681A-6389	Sequence 6389, Ap

977 18 30.0 268 4 US-09-489-039A-7310 Sequence 7310, Ap
978 18 30.0 269 4 US-09-540-236-2149 Sequence 2149, Ap
979 18 30.0 270 4 US-09-489-039A-9313 Sequence 9313, Ap
980 18 30.0 273 4 US-09-489-039A-12815 Sequence 12815, A
981 18 30.0 280 4 US-09-252-991A-23529 Sequence 23529, A
982 18 30.0 281 3 US-09-053-703-2 Sequence 2, Appl
983 18 30.0 281 4 US-09-540-236-2349 Sequence 2349, Ap
984 18 30.0 282 4 US-09-372-422A-8 Sequence 8, Appl
985 18 30.0 284 4 US-09-372-422A-4 Sequence 4, Appl
986 18 30.0 285 4 US-09-314-701-30 Sequence 30, Appl
987 18 30.0 286 4 US-09-489-039A-13264 Sequence 13264, A
988 18 30.0 288 4 US-09-372-422A-12 Sequence 12, Appl
989 18 30.0 288 4 US-09-372-422A-16 Sequence 16, Appl
990 18 30.0 288 4 US-09-372-422A-18 Sequence 18, Appl
991 18 30.0 288 4 US-09-372-448A-2 Sequence 2, Appl
992 18 30.0 288 4 US-09-372-422A-2 Sequence 2, Appl
993 18 30.0 289 4 US-08-372-422A-14 Sequence 14, Appl
994 18 30.0 292 4 US-08-372-422A-4 Sequence 4, Appl
995 18 30.0 292 4 US-09-372-422A-10 Sequence 10, Appl
996 18 30.0 292 4 US-09-489-039A-9431 Sequence 9431, Ap
997 18 30.0 295 4 US-09-134-000C-3576 Sequence 3576, Ap
998 18 30.0 296 4 US-09-372-422A-20 Sequence 20, Appl
999 18 30.0 296 4 US-09-328-352-6427 Sequence 6427, Ap
1000 18 30.0 296 4 US-09-540-236-2843 Sequence 2843, Ap

ALIGNMENTS

RESULT 1
US-09-724-566A-78
; Sequence 78, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco

Query Match 95.0%; Score 19; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-09-724-566A-81
; Sequence 81, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; TITLE OF INVENTION: Xaa is hydroxyethylene or statine
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 4
; TITLE OF INVENTION: Xaa is hydroxyethylene or statine
; OTHER INFORMATION: Xaa is hydroxyethylene or statine
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 2000-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-02-10
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide inhibitor P3-P4' XD-V
; NAME/KEY: MOD_RES
; LOCATION: 3
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco

Query Match 95.0%; Score 19; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-08-197-484-86
; Sequence 86, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco

Query Match 95.0%; Score 19; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 29-JAN-1992
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 26-AUG-1991
 APPLICATION DATA:
 APPLICATION NUMBER: 14137-26-4
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4
 TELEPHONE: (206) 467-9600
 TELEFAX: (206) 623-6793
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 S-08-197-484-86

Query Match 95.0%; Score 19; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 2 VAEF 5

RESULT 4
 S-08-197-484-145
 Sequence 145, Application US/08197484
 Patent No. 6419931
 GENERAL INFORMATION:
 APPLICANT: VITIELLO, Maria A.
 APPLICANT: CHESTNUT, Robert W.
 APPLICANT: SETTE, Alessandro D.
 APPLICANT: CELIS, Esteban
 APPLICANT: GRAY, Howard
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend Kourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/197,484
 APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992
 APPLICATION DATA:
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991
 APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4
 TELEPHONE: (206) 467-9600
 TELEFAX: (206) 623-6793
 INFORMATION FOR SEQ ID NO: 145:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-197-484-145

Query Match 95.0%; Score 19; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
 DB 2 VAEF 5

RESULT 5
 US-09-724-566A-73
 Sequence 73, Application US/09724566A
 Patent No. 6627739
 GENERAL INFORMATION:
 APPLICANT: Anderson, John P.
 APPLICANT: Basi, Gurigbal
 APPLICANT: Doane, Minh Tam
 APPLICANT: Frigon, No. 6627739mand
 APPLICANT: John, Varghese
 APPLICANT: Power, Michael
 APPLICANT: Sinha, Sukanto
 APPLICANT: Tatsuno, Gwen
 APPLICANT: Tung, Jay
 APPLICANT: Wang, Shuwen
 APPLICANT: McConlogue, Lisa
 TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
 FILE REFERENCE: 228-US-NEWC2
 CURRENT APPLICATION NUMBER: US/09/724,566A
 CURRENT FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 09/501,708
 PRIOR FILING DATE: 2000-02-10
 PRIOR APPLICATION NUMBER: 60/119,571
 PRIOR FILING DATE: 1999-02-10
 PRIOR APPLICATION NUMBER: 60/139,172
 PRIOR FILING DATE: 1999-06-15
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 SEQ ID NO 73
 LENGTH: 9

Qy 2 VAEF 5

QY 2 VAEF 5

RESULT 8
US-09-724-566A-72
; Sequence 72, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Gurigbal
; APPLICANT: Doane, Mich Tam
; APPLICANT: Evigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen

APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P10-P4'staD-V peptide inhibitor
NAME/KEY: MOD_RES
LOCATION: 10_RES
OTHER INFORMATION: Xaa is statine moiety
S-09-724-566A-72

Query Match 95.0%; Score 19; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 11 VAEF 14

ESULT 9
S-09-724-566A-97
Sequence 97, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: APP-derived fragment P10-P4' (D-V)
S-09-724-566A-97

Query Match 95.0%; Score 19; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 11 VAEF 14

RESULT 10
US-08-733-825-3
Sequence 3, Application US/08733825
Patent No. 5837839
GENERAL INFORMATION:
APPLICANT: Toth, Matthew J.
APPLICANT: Huwyler, Leslie R.
TITLE OF INVENTION: Coding Sequences for Nevalonate
TITLE OF INVENTION: Pyrophosphate Decarboxylase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 5837839artis Patent and Trademark Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,825
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,652
FILING DATE: 18-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5837839ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-20615/P1/CGC 1834
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4606
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-825-3

Query Match 95.0%; Score 19; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 20 VAEF 23

RESULT 11
US-08-487-890A-69
Sequence 69, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mardin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-69

Query Match 95.0%; Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 14 VAEF 17

RESULT 12
US-08-468-763-1
Sequence 1, Application US/08468763
Patent No. 5741671
GENERAL INFORMATION:
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of
TITLE OF INVENTION: Transmembrane Water Channel Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: US
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,763
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,996
FILING DATE: 24-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9239
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-763-1

Query Match 95.0%; Score 19; DB 1; Length 35;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 14 VAEF 17

RESULT 13
US-08-393-996A-1
Sequence 1, Application US/08393996A
Patent No. 5858702
GENERAL INFORMATION:
APPLICANT: Agre, Peter C.
TITLE OF INVENTION: Isolation, Cloning and Expression of
TITLE OF INVENTION: Transmembrane Water Channel Proteins
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: US
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,996A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.48633
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9239
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-393-996A-1

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

2Y 2 VAEF 5
14 VAEF 17

RESULT 14

US-08-478-435-69
Sequence 69, Application US/08478435

Patent No. 5922323

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin

APPLICANT: Schryvers, Anthony

APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott

APPLICANT: Yang, Yan-Ping

APPLICANT: Murdin, Andrew

APPLICANT: Klein, Michel

TITLE OF INVENTION: Transferrin Receptor Genes

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,435

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,483

FILING DATE: 08-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-462 MIS:V5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-478-435-69

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

2Y 2 VAEF 5
14 VAEF 17

RESULT 15

US-08-337-483-69
Sequence 69, Application US/08337483

Patent No. 5922562

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin

APPLICANT: Schryvers, Anthony

APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott

APPLICANT: Yang, Yan-Ping

APPLICANT: Murdin, Andrew

APPLICANT: Klein, Michel

TITLE OF INVENTION: Transferrin Receptor Genes

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/337,483

FILING DATE: 08-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-337-483-69

Query Match 95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 VAEF 5
14 VAEF 17

RESULT 16

US-08-478-373-69
Sequence 69, Application US/08478373

Patent No. 5922841

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena

APPLICANT: Harkness, Robin

APPLICANT: Schryvers, Anthony

APPLICANT: Chong, Pele

APPLICANT: Gray-Owen, Scott

APPLICANT: Yang, Yan-Ping

APPLICANT: Murdin, Andrew

APPLICANT: Klein, Michel

TITLE OF INVENTION: Transferrin Receptor Genes

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

```

; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-463 MIS:VG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-478-373-69

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Query Match          95.0%; Score 19; DB 2; Length 35;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 VAEF 5
Db      14 VAEF 17

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RESULT 17
US-08-474-671-69
; Sequence 69, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,373
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,671
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-465 MIS:VG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-474-671-69

Query Match          95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
Db      14 VAEF 17

RESULT 18
US-08-483-577A-69
; Sequence 69, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483

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FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-577A-69

Query Match 95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 19
US-08-897-438-69
Sequence 69, Application US/08897438
Patent No. 6262016
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-720
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-897-438-69

Query Match 95.0%; Score 19; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 14 VAEF 17

RESULT 20
US-08-637-654-69
Sequence 69, Application US/08637654
Patent No. 6358727
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Harkness, Robin E
APPLICANT: Schryvers, Anthony B
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew D
APPLICANT: Klein, Michel H
TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-595
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-637-654-69

Query Match 95.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 14 VAEF 17

RESULT 21
US-08-649-518-69
; Sequence 69, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Mordin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-649-518-69

Query Match 95.0%; Score 19; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

Db 14 VAEF 17

RESULT 22
US-09-393-634-80
; Sequence 80, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 80
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR24
US-09-393-634-80

Query Match 95.0%; Score 19; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 14 VAEF 17

RESULT 23
US-09-489-039A-13555
; Sequence 13555, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13555
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13555

Query Match 95.0%; Score 19; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 5 VAEF 8

RESULT 24
US-09-328-352-7111
; Sequence 7111, Application US/09328352

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7111
LENGTH: 71
TYPE: PRT
ORGANISM: Acinetobacter baumannii
S-09-328-352-7111

Query Match 95.0%; Score 19; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 26 VAEF 29

RESULT 25
S-08-321-071A-10
Sequence 10, Application US/08321071A
Patent No. 5672686
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bcl-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,071A
FILING DATE: 11-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10103
FILING DATE: 09-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.121CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-321-071A-10

Query Match 95.0%; Score 19; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-594-978a-1.rai

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7111
LENGTH: 71
TYPE: PRT
ORGANISM: Acinetobacter baumannii
S-09-328-352-7111

Query Match 95.0%; Score 19; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 26 VAEF 29

RESULT 25
S-08-321-071A-10
Sequence 10, Application US/08321071A
Patent No. 5672686
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN Bcl-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,071A
FILING DATE: 11-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10103
FILING DATE: 09-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,427
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.121CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-321-071A-10

Query Match 95.0%; Score 19; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 47 VAEF 50

RESULT 26
US-08-894-139-10
Sequence 10, Application US/08894139
Patent No. 6448376
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMAN, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-894-139-10

Query Match 95.0%; Score 19; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 23 VAEF 26

RESULT 27
US-09-732-210-1412
Sequence 1412, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1412
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-732-210-1412

Query Match 95.0%; Score 19; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 11 VAEF 14

RESULT 28
US-07-612-674-12
; Sequence 12, Application US/07612674
; Patent No. 5658792
; GENERAL INFORMATION:
; APPLICANT: NUELLE, MARK J.
; APPLICANT: MCCLUNG, J. KEITH
; APPLICANT: STEWART, DAVID A.
; APPLICANT: DANNER, DAVID B.
; TITLE OF INVENTION: AN ANTIPROLIFERATIVE PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/612,674
; FILING DATE: 19901114
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 5683/82332
; TELEPHONE: 202-861-3027
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-612-674-12

Query Match 95.0%; Score 19; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 18 VAEF 21

RESULT 29
US-09-543-681A-5816

; Sequence 5816, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5816
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5816

Query Match 95.0%; Score 19; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 21 VAEF 24

RESULT 30
US-08-464-517-8
; Sequence 8, Application US/08464517
; Patent No. 5869840
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

S-08-464-517-8

Query Match 95.0%; Score 19; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 ||||
 b 13 VAEF 16

RESULT 31

S-08-246-361A-8
 Sequence 8, Application US/08246361A
 Patent No. 5998582

GENERAL INFORMATION:

APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/246,361A
 FILING DATE: 19-MAY-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MII-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 100 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-246-361A-8

Query Match 95.0%; Score 19; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 ||||
 Db 13 VAEF 16

RESULT 32

US-08-463-772-8

Sequence 8, Application US/08463772
 Patent No. 6066501

GENERAL INFORMATION:

APPLICANT: BEACH, David H.
 TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII(text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,772
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,308
 FILING DATE: 16-OCT-1992
 APPLICATION NUMBER: US 07/888,178
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/701,514
 FILING DATE: 16-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Matthew P. Vincent
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MII-004C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 100 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-463-772-8

Query Match 95.0%; Score 19; DB 3; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 ||||
 Db 13 VAEF 16

RESULT 33

PCT-US93-05000-8

Sequence 8, Application PC/TUS9305000

GENERAL INFORMATION:

APPLICANT: MITOTIX
 TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: US
 ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-8

Query Match 95.0%; Score 19; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 13 VAEF 16

RESULT 34
US-08-580-988A-21
Sequence 21, Application US/08580988A
Patent No. 5956161
GENERAL INFORMATION:
APPLICANT: Aggarwal et al.
TITLE OF INVENTION: Tumor Necrosis Factor
TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
TITLE OF INVENTION: For Its Use
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,988A
FILING DATE: January 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE:

DESCRIPTION: protein
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-580-988A-21

Query Match 95.0%; Score 19; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 70 VAEF 73

RESULT 35
US-09-540-236-3612
Sequence 3612, Application US/09540236
Patent No. 6573910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3612
LENGTH: 103
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-3612

Query Match 95.0%; Score 19; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 65 VAEF 68

RESULT 36
US-08-464-517-25
Sequence 25, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
3-08-464-517-25

Query Match 95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 2 VAEP 5
|||
3 66 VAEP 69

RESULT 37
3-08-246-361A-25
Sequence 25, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-246-361A-25

Query Match 95.0%; Score 19; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEP 5
|||
Db 66 VAEP 69

RESULT 38
US-08-463-772-25
Sequence 25, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-772-25

Query Match 95.0%; Score 19; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEP 5
|||
Db 66 VAEP 69

RESULT 39
US-09-489-039A-8721
Sequence 8721, Application US/09489039A
Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8721
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-8721

Query Match 95.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 43 VAEF 46

RESULT 40
PCT-US93-05000-25
; Sequence 25, Application PC/TUS9305000
; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL91-02A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 616-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US93-05000-25

Query Match 95.0%; Score 19; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 66 VAEF 69

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9915
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-9915

Query Match 95.0%; Score 19; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 50 VAEF 53

RESULT 42
US-09-252-991A-21614
; Sequence 21614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21614
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21614

Query Match 95.0%; Score 19; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 85 VAEF 88

RESULT 43
US-09-489-039A-7200
; Sequence 7200, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7200
LENGTH: 123
TYPE: PRT

ORGANISM: Klebsiella pneumoniae
S-09-489-039A-7200

Query Match 95.0%; Score 19; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 61 VAEF 64

RESULT 44

S-08-529-055-53
Sequence 53, Application US/08529055
Patent No. 6592876

GENERAL INFORMATION:

APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Wyther, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Thereof, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

S-08-529-055-53

Query Match 95.0%; Score 19; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 7 VAEF 10

RESULT 45

US-09-489-039A-12835
Sequence 12835, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12835
LENGTH: 143
TYPE: PRT

ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12835

Query Match 95.0%; Score 19; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 138 VAEF 141

RESULT 46

US-09-198-452A-167
Sequence 167, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:

APPLICANT: Griffois, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 167
LENGTH: 145
TYPE: PRT

ORGANISM: Chlamydia pneumoniae
US-09-198-452A-167

Query Match 95.0%; Score 19; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 31 VAEF 34

RESULT 47

US-09-134-000C-4292
Sequence 4292, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1

S-08-529-055-53

Query Match 95.0%; Score 19; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 7 VAEF 10

SEQ ID NO 4292
LENGTH: 145
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4292

Query Match 95.0%; Score 19; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 113 VAEF 116

RESULT 48
US-08-460-694-3

Sequence 3, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-694-3

Query Match 95.0%; Score 19; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 66 VAEF 69

RESULT 49
US-08-460-744-3

Sequence 3, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-3

Query Match 95.0%; Score 19; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 66 VAEF 69

RESULT 50

US-07-667-711B-3
Sequence 3, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:

APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

```
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
3-07-667-711B-3

Query Match          95.0%; Score 19; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      ||||
      66 VAEF 69

RESULT 51
3-08-679-493A-208
Sequence 208, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 208
LENGTH: 152
TYPE: PRT
ORGANISM: blueshark
3-08-679-493A-208

Query Match          95.0%; Score 19; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      ||||
      92 VAEF 95

RESULT 52
3-09-134-000C-4087
Sequence 4087, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4087
LENGTH: 153
TYPE: PRT
ORGANISM: Enterococcus faecalis
3-09-134-000C-4087

Query Match          95.0%; Score 19; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5

LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
3-07-667-711B-3

Query Match          95.0%; Score 19; DB 3; Length 150;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      ||||
      66 VAEF 69

RESULT 53
US-09-252-991A-20805
Sequence 20805, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20805
LENGTH: 156
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20805

Query Match          95.0%; Score 19; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
      84 VAEF 87

RESULT 54
US-09-370-838-203
Sequence 203, Application US/09370838
Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 203
LENGTH: 164
TYPE: PRT
ORGANISM: Homo sapien
US-09-370-838-203

Query Match          95.0%; Score 19; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY     2 VAEF 5
      ||||
      100 VAEF 103

RESULT 55
US-09-540-236-2222
Sequence 2222, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
```

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2222
LENGTH: 166
TYPE: PRT
ORGANISM: M. catarrhalis
US-09-540-236-2222

Query Match 95.0%; Score 19; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 97 VAEF 100

RESULT 56
US-08-471-058-16
Sequence 16, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-16

Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 122 VAEF 125

RESULT 57
US-08-690-095-3
Sequence 3, Application US/08690095
Patent No. 5792648
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 293274
US-08-690-095-3

Query Match 95.0%; Score 19; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 122 VAEF 125

RESULT 58
US-08-471-057-16
Sequence 16, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto

STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,057
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/320,157
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHNHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20007.20
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 S-08-471-057-16

Query Match 95.0%; Score 19; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred.No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
 b 122 VAEF 125

RESULT 59
 S-09-113-789-3
 Sequence 3, Application US/09113789
 Patent No. 6034219
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Au-Young, Janice
 APPLICANT: Goli, Surya K.
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113,789
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/690,095
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0110 US
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 293274
 US-09-113-789-3

Query Match 95.0%; Score 19; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred.No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 Db 122 VAEF 125

RESULT 60
 US-08-470-865-16
 ; Sequence 16, Application US/08470865
 ; Patent No. 6586395
 ; GENERAL INFORMATION:
 ; APPLICANT: KIEFER, MICHAEL C.
 ; APPLICANT: BARR, PHILIP J.
 ; TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ; TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,865
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/320,157
 FILING DATE: 07-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHNHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20007.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-470-865-16

Query Match 95.0%; Score 19; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred.No. 6.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5

DB 122 VAEF 125
|||||

RESULT 61
US-08-193-977-4
; Sequence 4, Application US/08193977
; Patent No. 5625031
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, KEVIN R.
; APPLICANT: COLEMAN, KEVIN G.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
; TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,977
; FILING DATE: 08-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
JS-08-193-977-4

Query Match 95.0%; Score 19; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 100 VAEF 103
|||||

RESULT 62
US-09-489-039A-9869
; Sequence 3869, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9869
; LENGTH: 174
; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9869

Query Match 95.0%; Score 19; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 77 VAEF 80
|||||

RESULT 63
US-08-737-980-2
; Sequence 2, Application US/08737980
; Patent No. 5843773
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Apoptosis Regulating Gene
; NUMBER OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,980
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 1995-6266
; FILING DATE: 24-MAR-1995
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-737-980-2

Query Match 95.0%; Score 19; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 122 VAEF 125
|||||

RESULT 64
US-09-328-352-6739
; Sequence 6739, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GFC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6739
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6739

Query Match 95.0%; Score 19; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 8 VAEF 11
|||||

RESULT 65
S-09-252-991A-24341
Sequence 24341, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24341
LENGTH: 185
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
S-09-252-991A-24341
Query Match 95.0%; Score 19; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
b 4 VAEF 7
RESULT 66
S-09-543-681A-7313
Sequence 7313, Application US/09543681A
Patent No. 6605703
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7313
LENGTH: 189
TYPE: PRT
ORGANISM: Proteus mirabilis
S-09-543-681A-7313
Query Match 95.0%; Score 19; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
b 73 VAEF 76
RESULT 67
S-08-816-241-1
Sequence 1, Application US/08816241
Patent No. 5804185
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,241
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0239 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1646823
US-08-816-241-1
Query Match 95.0%; Score 19; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
Db 104 VAEF 107
RESULT 68
US-09-128-395-1
Sequence 1, Application US/09128395
Patent No. 6087108
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL RNA EDITING ENZYME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,395
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,241
FILING DATE:
ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET INFORMATION: PF-0239 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT09
; CLONE: 1646823
US-09-128-395-1

Query Match 95.0%; Score 19; DB 3; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 104 VAEF 107

RESULT 69
US-09-134-000C-3800
; Sequence 3800, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3800
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3800

Query Match 95.0%; Score 19; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 115 VAEF 118

RESULT 70
US-09-232-200-85
; Sequence 85, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491

; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-232-200-85

Query Match 95.0%; Score 19; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 99 VAEF 102

RESULT 71
US-09-232-197-85
; Sequence 85, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-09-232-197-85

Query Match 95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 99 VAEF 102

RESULT 72
US-09-232-201-85
; Sequence 85, Application US/09232201A
; Patent No. 6348321
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MC
; CURRENT APPLICATION NUMBER: US/09/232,201A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15

EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
TYPE: PRT
ORGANISM: Aspergillus nidulans
3-09-232-201-85

Query Match 95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 99 VAEF 102

RESULT 73
3-09-232-195-85
Sequence 85, Application US/09232195A
Patent No. 6657049
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21P3MD
CURRENT APPLICATION NUMBER: US/09/232,195A
CURRENT FILING DATE: 1999-01-04
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 199
TYPE: PRT
ORGANISM: Aspergillus nidulans
3-09-232-195-85

Query Match 95.0%; Score 19; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 99 VAEF 102

RESULT 74
S-09-107-532A-4612
Sequence 4612, Application US/09107532A
Patent No. 6582275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA

ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4612:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (5) LOCATION 1...203
SEQUENCE DESCRIPTION: SEQ ID NO: 4612:
US-09-107-532A-4612

Query Match 95.0%; Score 19; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
Db 63 VAEF 66

RESULT 75
US-08-684-024-1
Sequence 1, Application US/08684024
Patent No. 5834298
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 205 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

IS-08-684-024-1

Query Match 95.0%; Score 19; DB 2; Length 205;

Best Local Similarity 100.0%; Pred. No. 8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2V 2 VAEF 5

2b 20 VAEF 23

Search completed: May 24, 2004, 17:43:20
Job time : 24 secs

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M protein - protein search, using sw model

run on: May 24, 2004, 17:34:23 ; Search time 39.6429 Seconds
(without alignments)
35.179 Million cell updates/sec

title: * US-09-594-978A-1

effect score: 20

sequence: 1 XVAEP 5

coreing table:

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Gapop 10.0 , Gapext 0.5

searched: 1149313 segs, 278921704 residues

total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:

1: /cgn2_6/prodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubaa/US03_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/prodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	19	95.0	9	14	US-10-128-711-86
5	19	95.0	9	14	US-10-128-711-145
6	19	95.0	10	12	US-09-908-943A-197
7	19	95.0	12	12	US-09-908-943A-196
8	19	95.0	12	14	US-10-032-818-34
9	19	95.0	13	14	US-10-239-313A-379
10	19	95.0	15	14	US-10-119-528-7
11	19	95.0	20	14	US-09-171-432A-62
12	19	95.0	20	10	US-09-171-432A-63
13	19	95.0	25	10	US-09-171-432A-65
14	19	95.0	28	9	US-09-864-761-47201
15	19	95.0	28	12	US-10-424-599-216297

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19	19	95.0	38	15	US-10-430-752A-45
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21	19	95.0	43	9	US-09-864-761-37202
22	19	95.0	43	12	US-10-424-599-183032
23	19	95.0	45	12	US-10-424-599-171318
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252	19	95.0	242	10	US-09-870-406A-44	Sequence 44, Appl	325	19	95.0	281	14	US-10-314-639-58	Sequence 9102, Ap
253	19	95.0	243	12	US-10-424-599-257488	Sequence 257488, A	326	19	95.0	281	14	US-10-156-761-9102	Sequence 1694, Ap
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256	19	95.0	244	12	US-10-424-599-158126	Sequence 158126, A	329	19	95.0	282	14	US-10-156-761-12355	Sequence 12355, A
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258	19	95.0	246	9	US-09-771-161A-129	Sequence 129, Ap	331	19	95.0	283	12	US-10-425-114-43968	Sequence 43988, A
259	19	95.0	246	14	US-10-156-761-13663	Sequence 13663, A	332	19	95.0	283	12	US-10-329-624-5203	Sequence 5203, Ap
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262	19	95.0	248	12	US-10-425-114-44065	Sequence 44065, A	335	19	95.0	285	12	US-10-282-122A-69922	Sequence 69922, A
263	19	95.0	249	9	US-09-832-312-9	Sequence 9, Appl	336	19	95.0	285	12	US-10-425-114-64235	Sequence 64235, A
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265	19	95.0	249	14	US-10-156-761-3204	Sequence 3204, Ap	338	19	95.0	286	12	US-10-262-511-144	Sequence 144, Appl
266	19	95.0	249	15	US-10-409-701-15	Sequence 15, Appl	339	19	95.0	287	12	US-10-424-599-147161	Sequence 147161, A
267	19	95.0	249	15	US-10-310-154-606	Sequence 606, Ap	340	19	95.0	287	15	US-10-369-493-20884	Sequence 20884, A
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269	19	95.0	253	15	US-10-369-493-23537	Sequence 23537, A	342	19	95.0	288	9	US-09-815-242-11193	Sequence 11193, A
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273	19	95.0	254	15	US-10-369-493-11429	Sequence 11429, A	346	19	95.0	290	15	US-10-262-511-146	Sequence 146, Appl
274	19	95.0	255	13	US-10-086-623-40	Sequence 40, Appl	347	19	95.0	290	15	US-10-369-493-15865	Sequence 15865, A
275	19	95.0	255	14	US-10-260-539-40	Sequence 40, Appl	348	19	95.0	291	12	US-10-041-018-27	Sequence 27, Appl
276	19	95.0	256	15	US-10-369-493-19054	Sequence 19054, A	349	19	95.0	291	14	US-10-017-161-2430	Sequence 2430, Ap
277	19	95.0	256	15	US-10-421-138A-312	Sequence 312, Appl	350	19	95.0	291	15	US-10-292-798-2070	Sequence 2070, Ap
278	19	95.0	256	15	US-10-374-780A-1247	Sequence 1247, Ap	351	19	95.0	291	15	US-10-264-237-2770	Sequence 2770, Ap
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294	19	95.0	263	11	US-09-833-245-2213	Sequence 2213, Ap	367	19	95.0	299	10	US-09-832-522-7	Sequence 7, Appl
295	19	95.0	263	14	US-10-182-447-1	Sequence 1, Appl	368	19	95.0	299	12	US-10-364-861-35	Sequence 35, Appl
296	19	95.0	264	12	US-10-282-122A-52414	Sequence 52414, A	369	19	95.0	299	13	US-10-059-964-46	Sequence 46, Appl
297	19	95.0	265	12	US-10-425-114-41437	Sequence 41437, A	370	19	95.0	299	14	US-10-314-639-46	Sequence 46, Appl
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587	19	95.0	379	14	US-10-137-223-6	Sequence 6, Appl	660	19	95.0	409	14	US-10-081-816-14	Sequence 14, Appl
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595	19	95.0	383	14	US-10-166-225A-76	Sequence 76, Appl	668	19	95.0	412	14	US-10-079-185-3	Sequence 3, Appl
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597	19	95.0	384	16	US-09-765-061B-72	Sequence 72, Appl	670	19	95.0	412	14	US-10-156-761-7850	Sequence 7850, Ap
598	19	95.0	384	10	US-09-765-061B-73	Sequence 73, Appl	671	19	95.0	412	14	US-10-156-761-7896	Sequence 7896, Ap
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679	19	95.0	415	12	US-10-282-122A-65787	Sequence 65787, A	752	19	95.0	441	12	US-10-282-122A-56949	Sequence 56949, A
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681	19	95.0	415	12	US-10-282-122A-68742	Sequence 68742, A	754	19	95.0	444	15	US-09-981-151A-73	Sequence 73, Appl
682	19	95.0	416	14	US-10-156-761-12502	Sequence 12502, A	755	19	95.0	445	12	US-10-282-122A-45092	Sequence 45092, A
683	19	95.0	416	15	US-10-369-493-4737	Sequence 4737, Ap	756	19	95.0	445	12	US-10-282-122A-74539	Sequence 74539, A
684	19	95.0	416	15	US-10-369-493-4737	Sequence 4737, Ap	757	19	95.0	446	9	US-09-798-029-17	Sequence 17, Appl
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686	19	95.0	417	12	US-10-424-599-274599	Sequence 274599, A	759	19	95.0	446	12	US-10-425-114-52177	Sequence 52177, A
687	19	95.0	417	12	US-10-425-114-56059	Sequence 56059, A	760	19	95.0	447	9	US-09-908-928-4	Sequence 4, Appl
688	19	95.0	417	14	US-10-128-714-8345	Sequence 8345, Ap	761	19	95.0	447	9	US-09-972-528-4	Sequence 4, Appl
689	19	95.0	417	14	US-10-128-714-8345	Sequence 8345, Ap	762	19	95.0	447	12	US-10-282-122A-72069	Sequence 72069, A
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706	19	95.0	424	15	US-10-369-493-5557	Sequence 5557, A	779	19	95.0	457	9	US-09-888-615-110	Sequence 110, Appl
707	19	95.0	424	12	US-10-282-122A-45014	Sequence 45014, A	780	19	95.0	457	11	US-09-981-151A-71	Sequence 71, Appl
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715	19	95.0	427	15	US-10-104-047-2362	Sequence 2362, Ap	788	19	95.0	460	12	US-10-108-260A-2540	Sequence 2540, Ap
716	19	95.0	428	12	US-10-403-571-110	Sequence 110, Appl	789	19	95.0	461	12	US-10-282-122A-50440	Sequence 50440, Ap
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724	19	95.0	432	12	US-10-425-114-72646	Sequence 72646, A	797	19	95.0	469	12	US-10-417-700A-65	Sequence 65, Appl
725	19	95.0	433	14	US-10-128-714-8545	Sequence 8545, Ap	798	19	95.0	469	12	US-10-417-700A-77	Sequence 77, Appl
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727	19	95.0	434	12	US-10-282-122A-66904	Sequence 66904, A	800	19	95.0	471	12	US-10-282-122A-76782	Sequence 76782, A
728	19	95.0	435	12	US-10-627-476-238	Sequence 238, App	801	19	95.0	471	12	US-10-425-114-72794	Sequence 72794, A
729	19	95.0	436	12	US-10-282-122A-50291	Sequence 50291, A	802	19	95.0	472	11	US-09-981-151A-27	Sequence 27, Appl
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732	19	95.0	436	15	US-10-369-493-21378	Sequence 21378, A	805	19	95.0	474	12	US-10-282-122A-62083	Sequence 62083, A
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739	19	95.0	437	15	US-10-177-293-457	Sequence 457, App	812	19	95.0	480	12	US-10-424-599-166523	Sequence 166523, A
740	19	95.0	437	15	US-10-295-027-1180	Sequence 1180, Ap	813	19	95.0	480	12	US-10-425-114-63937	Sequence 63937, A
741	19	95.0	438	12	US-10-282-122A-56153	Sequence 56153, A	814	19	95.0	480	12	US-10-607-565-108	Sequence 108, App
742	19	95.0	438	12	US-10-282-122A-56161	Sequence 56161, A	815	19	95.0	481	12	US-10-424-599-166520	Sequence 166520, A
743	19	95.0	438	12	US-10-282-122A-75202	Sequence 75202, A	816	19	95.0	481	12	US-10-424-599-166520	Sequence 166520, A
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821	19	95.0	485	9	US-09-769-864-6	Sequence 6, Appli	894	19	95.0	522	15	US-10-099-322-125	Sequence 125, App
822	19	95.0	485	9	US-09-769-864-7	Sequence 7, Appli	895	19	95.0	522	15	US-10-044-564-124	Sequence 124, App
823	19	95.0	485	9	US-09-769-864-8	Sequence 8, Appli	896	19	95.0	522	15	US-10-044-564-125	Sequence 125, App
824	19	95.0	485	9	US-09-854-346-2	Sequence 2, Appli	897	19	95.0	523	15	US-10-099-322-122	Sequence 122, App
825	19	95.0	485	9	US-09-854-346-4	Sequence 4, Appli	898	19	95.0	523	15	US-10-099-322-123	Sequence 123, App
826	19	95.0	485	9	US-09-854-346-12	Sequence 12, Appli	899	19	95.0	523	15	US-10-044-564-122	Sequence 122, App
827	19	95.0	485	9	US-09-854-346-13	Sequence 13, Appli	900	19	95.0	523	15	US-10-044-564-123	Sequence 123, App
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831	19	95.0	485	9	US-09-918-543-2	Sequence 2, Appli	904	19	95.0	524	12	US-10-403-161-40	Sequence 40, Appl
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833	19	95.0	485	9	US-09-918-543-12	Sequence 12, Appli	906	19	95.0	524	12	US-10-099-322-34	Sequence 34, Appl
834	19	95.0	485	9	US-09-918-543-12	Sequence 12, Appli	907	19	95.0	524	15	US-10-099-322-121	Sequence 121, App
835	19	95.0	485	9	US-09-795-211-1	Sequence 1, Appli	908	19	95.0	524	15	US-10-044-564-34	Sequence 34, Appl
836	19	95.0	485	10	US-09-795-211-2	Sequence 2, Appli	909	19	95.0	524	15	US-10-044-564-121	Sequence 121, App
837	19	95.0	485	10	US-09-925-576C-2	Sequence 2, Appli	910	19	95.0	526	9	US-09-815-242-13696	Sequence 13696, A
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839	19	95.0	485	10	US-09-925-576C-12	Sequence 12, Appli	912	19	95.0	526	12	US-10-282-122A-73677	Sequence 73677, A
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859	19	95.0	487	15	US-10-369-493-18040	Sequence 18040, A	932	19	95.0	539	12	US-10-282-122A-57265	Sequence 57265, A
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862	19	95.0	491	12	US-10-424-599-149190	Sequence 149190, A	935	19	95.0	539	14	US-10-230-026-34	Sequence 34, Appl
863	19	95.0	492	9	US-09-881-752A-142	Sequence 142, App	936	19	95.0	540	9	US-09-738-626-4450	Sequence 4450, Ap
864	19	95.0	492	12	US-10-282-122A-58846	Sequence 58846, A	937	19	95.0	540	15	US-10-369-493-3921	Sequence 3921, Ap
865	19	95.0	493	9	US-09-918-951-5	Sequence 5, Appli	938	19	95.0	543	12	US-10-282-122A-77151	Sequence 77151, A
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868	19	95.0	494	15	US-10-369-493-20452	Sequence 20452, A	941	19	95.0	546	12	US-10-282-122A-53681	Sequence 53681, A
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872	19	95.0	499	9	US-09-815-242-11035	Sequence 11035, A	945	19	95.0	548	15	US-10-369-493-6496	Sequence 6496, Ap
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877	19	95.0	501	12	US-10-425-114-56039	Sequence 56039, A	950	19	95.0	550	12	US-10-369-493-5478	Sequence 5478, Ap
878	19	95.0	504	9	US-09-738-626-7001	Sequence 7001, Ap	951	19	95.0	550	12	US-10-336-049-2	Sequence 2, Appli
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881	19	95.0	504	12	US-10-425-114-64036	Sequence 64036, A	954	19	95.0	552	12	US-10-282-122A-59108	Sequence 59108, A
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883	19	95.0	506	9	US-09-943-671-9	Sequence 9, Appli	956	19	95.0	553	12	US-10-282-122A-71716	Sequence 71716, A
884	19	95.0	506	15	US-10-405-877-95	Sequence 95, Appl	957	19	95.0	553	15	US-10-313-371A-2	Sequence 2, Appli
885	19	95.0	506	15	US-10-405-877-95	Sequence 95, Appl	958	19	95.0	553	15	US-10-313-371A-4	Sequence 4, Appli
886	19	95.0	515	9	US-09-925-300-1285	Sequence 925, Ap	959	19	95.0	556	15	US-10-369-493-5442	Sequence 5442, Ap
887	19	95.0	515	12	US-10-424-599-146129	Sequence 146129, A	960	19	95.0	556	15	US-10-369-493-11974	Sequence 11974, A
888	19	95.0	515	12	US-10-425-114-68917	Sequence 68917, A	961	19	95.0	558	12	US-10-363-616-374	Sequence 374, App
889	19	95.0	516	9	US-09-986-676A-2	Sequence 2, Appli	962	19	95.0	558	15	US-10-369-493-632	Sequence 632, Ap
890	19	95.0	516	9	US-09-971-611-2	Sequence 2, Appli	963	19	95.0	559	9	US-10-369-493-632	Sequence 632, Ap
891	19	95.0	516	16	US-10-399-161-8	Sequence 8, Appli	964	19	95.0	559	12	US-10-282-122A-1479	Sequence 1479, Ap
												US-10-282-122A-65056	Sequence 65056, A

965	19	95.0	559	12	US-10-282-122A-75373	Sequence 75373, A
966	19	95.0	559	12	US-10-282-122A-75352	Sequence 75352, A
967	19	95.0	561	12	US-10-282-122A-65931	Sequence 65931, A
968	19	95.0	561	12	US-10-369-493-21529	Sequence 21529, A
969	19	95.0	564	16	US-10-389-566-1369	Sequence 1369, Ap
970	19	95.0	565	12	US-10-380-565-34	Sequence 34, Appl
971	19	95.0	566	14	US-10-100-957A-142	Sequence 142, App
972	19	95.0	566	14	US-10-211-080-19	Sequence 19, Appl
973	19	95.0	567	12	US-10-425-114-45750	Sequence 45750, A
974	19	95.0	568	12	US-10-282-122A-65302	Sequence 65302, A
975	19	95.0	573	9	US-09-764-668-671	Sequence 671, App
976	19	95.0	573	11	US-09-764-875-1205	Sequence 1205, Ap
977	19	95.0	573	12	US-10-425-114-40721	Sequence 40721, A
978	19	95.0	574	12	US-10-425-114-42248	Sequence 42248, A
979	19	95.0	575	12	US-10-424-599-186118	Sequence 186118, A
980	19	95.0	575	12	US-10-312-352-8	Sequence 8, Appl
981	19	95.0	575	15	US-10-120-801-60	Sequence 60, Appl
982	19	95.0	576	12	US-10-335-977-7018	Sequence 7018, Ap
983	19	95.0	577	9	US-09-815-942-11305	Sequence 11305, A
984	19	95.0	577	12	US-10-282-122A-58657	Sequence 58657, A
985	19	95.0	577	12	US-10-335-977-7019	Sequence 7019, Ap
986	19	95.0	580	9	US-09-841-132-598	Sequence 598, App
987	19	95.0	580	12	US-10-282-122A-54815	Sequence 54815, A
988	19	95.0	580	15	US-10-289-763-332	Sequence 332, App
989	19	95.0	581	12	US-10-424-599-255268	Sequence 255268, A
990	19	95.0	584	15	US-10-108-260A-4380	Sequence 4380, Ap
991	19	95.0	585	12	US-10-431-449-2	Sequence 2, Appl
992	19	95.0	585	12	US-10-431-449-4	Sequence 4, Appl
993	19	95.0	585	12	US-10-431-449-6	Sequence 6, Appl
994	19	95.0	587	12	US-10-424-599-198064	Sequence 198064, A
995	19	95.0	587	13	US-10-042-523-3	Sequence 3, Appl
996	19	95.0	588	15	US-10-309-560-10	Sequence 10, Appl
997	19	95.0	590	12	US-10-282-122A-65911	Sequence 65911, A
998	19	95.0	592	12	US-10-424-599-214104	Sequence 214104, A
999	19	95.0	592	12	US-10-335-977-5869	Sequence 5869, Ap
1000	19	95.0	595	12	US-10-382-122A-44744	Sequence 44744, A

ALIGNMENTS

```

1  RESULT 1
2  JS-09-791-378-343
3  ; Sequence 343, Application US/09791378
4  ; Patent No. US20020142303A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Parekh, Rajesh
7  ; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
8  ; FILE OF INVENTION: SCHIZOPHRENIA
9  ; FILE REFERENCE: 9195-061-999
10 ; CURRENT APPLICATION NUMBER: US/09/791,378
11 ; CURRENT FILING DATE: 2001-02-23
12 ; PRIOR APPLICATION NUMBER: 09/750,395
13 ; PRIOR FILING DATE: 2000-12-28
14 ; NUMBER OF SEQ ID NOS: 677
15 ; SOFTWARE: Patent in version 3.0
16 ; SEQ ID NO 343
17 ; LENGTH: 8
18 ; TYPE: PRT
19 ; ORGANISM: Homo sapiens
20 ; JS-09-791-378-343

```

RESULT 2
JS-09-791-393-206

```

; Sequence 206, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohloff, Christian
; TITLE OF INVENTION: Proteins, Gense and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-206

Query Match          95.0%; Score 19; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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RESULT 3
US-09-791-389-206
; Sequence 206, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Farekka, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar
; TITLE OF INVENTION: and unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-206

```

Qy 2 VAEF 5
|||
Db 2 VAEF 5

SULT 4
 -10-128-711-86
 Sequence 86, Application US/10128711
 Publication No. US20030099634A1
 GENERAL INFORMATION:
 APPLICANT: VITIELLO, Maria A.
 CHESTNUT, Robert W.
 SETTE, Alessandro D.
 CELIS, Esteban
 GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 CYL IMMUNITY

NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/128,711
 FILING DATE: 22-Apr-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown

MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 86:
 -10-128-711-86

Query Match 95.0%; Score 19; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 2 VAEF 5

SULT 5
 -10-128-711-145
 Sequence 145, Application US/10128711
 Publication No. US20030099634A1
 GENERAL INFORMATION:
 APPLICANT: VITIELLO, Maria A.

CHESTNUT, Robert W.
 SETTE, Alessandro D.
 CELIS, Esteban
 GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
 CYL IMMUNITY

NUMBER OF SEQUENCES: 153
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: Steuart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/128,711
 FILING DATE: 22-Apr-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/197,484
 FILING DATE: 16-FEB-1994
 APPLICATION NUMBER: US 07/935,811
 FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: US 07/874,491
 FILING DATE: 27-APR-1992
 APPLICATION NUMBER: US 07/827,682
 FILING DATE: 29-JAN-1992
 APPLICATION NUMBER: US 07/749,568
 FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 145:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown

MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 145:
 US-10-128-711-145

Query Match 95.0%; Score 19; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
 ||||
 2 VAEF 5

RESULT 6
 US-09-508-943A-197
 ; Sequence 197, Application US/09908943A
 ; Publication No. US20030017991A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Van, Riqiang
 ; APPLICANT: Tomasselli, Alfredo G.
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Emmons, Thomas L.
 ; APPLICANT: Bienkowski, Mike J.
 ; APPLICANT: Heinrikson, Robert L.
 ; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
 ; FILE REFERENCE: 29915/00281A.US1

; CURRENT APPLICATION NUMBER: US/09/908,943A
 ; CURRENT FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: 60/219,795
 ; PRIOR FILING DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 197
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 197
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: synthetic peptide sequence
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
 ; NAME/KEY: SITE
 ; LOCATION: (10)..(10)
 ; OTHER INFORMATION: amino acid at position 10 has been derivatized with Bodipy FL
 JS-09-908-943A-197

Query Match 95.0%; Score 19; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8

RESULT 7

JS-09-908-943A-196
 ; Sequence 196, Application US/09/908943A
 ; Publication No. US20030017991A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yan, Riqiang
 ; APPLICANT: Tonasselli, Alfredo G.
 ; APPLICANT: Gurney, Mark E.
 ; APPLICANT: Emmons, Thomas L.
 ; APPLICANT: Bienkowski, Mike J.
 ; APPLICANT: Heinrikson, Robert L.
 ; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
 ; FILE REFERENCE: 29915/00281A.US1
 ; CURRENT APPLICATION NUMBER: US/09/908,943A
 ; CURRENT FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: 60/219,795
 ; PRIOR FILING DATE: 2000-07-19
 ; NUMBER OF SEQ ID NOS: 197
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 196
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence: synthetic peptide sequence
 ; NAME/KEY: SITE
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: amino acid at position 4 has been derivatized with a statine
 JS-09-908-943A-196

Query Match 95.0%; Score 19; DB 12; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8

RESULT 8

JS-10-032-818-34
 ; Sequence 34, Application US/10032818
 ; Publication No. US20030092629A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Jordan J.N.

; APPLICANT: Koelsch, Gerald
 ; APPLICANT: Grosh, Arun K.
 ; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
 ; FILE REFERENCE: 2932.1006-007
 ; CURRENT APPLICATION NUMBER: US/10/032,818
 ; CURRENT FILING DATE: 2001-12-28
 ; PRIOR APPLICATION NUMBER: US 60/275,756
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: US 60/258,705
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 34
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide
 US-10-032-818-34

Query Match 95.0%; Score 19; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 5 VAEF 8

RESULT 9

US-10-239-313A-379
 ; Sequence 379, Application US/10239313A
 ; Publication No. US20030175285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGUER - HAMOUR, Christine
 ; APPLICANT: CORVAIA, Nathalie
 ; APPLICANT: BECK, Alain
 ; APPLICANT: GOETSCH, Liliane
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
 ; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
 ; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
 ; FILE REFERENCE: 343 727 - US
 ; CURRENT APPLICATION NUMBER: US/10/239,313A
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: FR 00/03711
 ; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: PCT 01/70772
 ; PRIOR FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 697
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 379
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium leprae
 US-10-239-313A-379

Query Match 95.0%; Score 19; DB 14; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
 DB 4 VAEF 7

RESULT 10

US-10-119-528-7
 ; Sequence 7, Application US/10119528
 ; Publication No. US20030175722A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mann, M.
 ; APPLICANT: Mortensen, P.
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES

FILE REFERENCE: MDSP-P01-004
CURRENT APPLICATION NUMBER: US/10/119,528
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/282,551
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/285,362
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 15
TYPE: PRT
ORGANISM: Arabidopsis thaliana
S-10-119-528-7

Query Match 95.0%; Score 19; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 10 VAEF 13

RESULT 11
S-09-171-432A-62
Sequence 62, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Khudyakov, Yuri E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polyprotein
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /label= YK-1368
US-09-171-432A-62

US-09-171-432A-62

Query Match 95.0%; Score 19; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
Db 13 VAEF 16

RESULT 12
US-09-171-432A-63
Sequence 63, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.
TITLE OF INVENTION: Antigenically Reactive Regions of the
TITLE OF INVENTION: Hepatitis A Virus Polyprotein
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP
STREET: 3424 Peachtree Road, N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /label= YK-1369
US-09-171-432A-63

Query Match 95.0%; Score 19; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VAEF 5
Db 4 VAEF 7

RESULT 13
US-09-171-432A-65
Sequence 65, Application US/09171432A
Publication No. US20030187184A1
GENERAL INFORMATION:
APPLICANT: Fields, Howard A.

APPLICANT: Khudyakov, Yury E.
TITLE OF INVENTION: Antigenically Reactive Regions of the
Hepatitis A Virus Polypeptide
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: KILPATRICK STOCKTON LLP
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30326
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171.432A
FILING DATE: 23-NOV-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greene, Jamie L.
REGISTRATION NUMBER: 32,467
REFERENCE/DOCKET NUMBER: 03063-0231US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 949-2400
TELEFAX: (404) 949-2499
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /label= YK-1832
US-09-171-432A-65

Query Match 95.0%; Score 19; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 3 VAEF 6

RESULT 14
US-09-864-761-47201
Sequence 47201, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 47201
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005772.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
US-09-864-761-47201

Query Match 95.0%; Score 19; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
Db 4 VAEF 7

RESULT 15
US-10-424-599-216297
Sequence 216297, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285694
SEQ ID NO 216297
LENGTH: 28
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37345C.1.pep
US-10-424-599-216297

```
Query Match          95.0%; Score 19; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      10 VAEF 13

RESULT 16
;10-043-344-69
; Sequence 69, Application US/10043344
; Publication No. US2003008806A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518
; PRIOR FILING DATE: 1996-05-17
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 69
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
;10-043-344-69

Query Match          95.0%; Score 19; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      14 VAEF 17

RESULT 17
;10-242-355-570
; Sequence 570, Application US/10242355
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC003C1
; CURRENT APPLICATION NUMBER: US/10/242,355
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,897
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
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; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1267
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 570
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
;10-242-355-570

Query Match          95.0%; Score 19; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      14 VAEF 17

RESULT 18
;10-430-752A-49
; Sequence 49, Application US/10430752A
; Publication No. US20040005669A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Stefan
; APPLICANT: Jonasson, Per
; APPLICANT: Nygren, Per-Ake
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
; FILE REFERENCE: 11541-003001
; CURRENT APPLICATION NUMBER: US/10/430,752A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/485,286
; PRIOR FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: PCT/GB98/02382
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: GB 9716790.2
; PRIOR FILING DATE: 1997-08-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Verasper moseri
;10-430-752A-49

Query Match          95.0%; Score 19; DB 15; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      24 VAEF 27

RESULT 19
;10-430-752A-45
; Sequence 45, Application US/10430752A
; Publication No. US20040005669A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Stefan
; APPLICANT: Jonasson, Per
; APPLICANT: Nygren, Per-Ake
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
; FILE REFERENCE: 11541-003001
; CURRENT APPLICATION NUMBER: US/10/430,752A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/485,286
; PRIOR FILING DATE: 2000-02-07
```

PRIOR APPLICATION NUMBER: PCT/GB98/02382
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: GB 9716790.2
PRIOR FILING DATE: 1997-08-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 38
TYPE: PRT
ORGANISM: Lophius piscatorius
S-10-430-752A-45

Query Match 95.0%; Score 19; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
|||
b 25 VAEF 28

RESULT 20
S-10-372-003A-71
Sequence 71, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:

APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBIC40.001CPI
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 41
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic clone BGF13 with first open reading
OTHER INFORMATION: frame

S-10-372-003A-71
Query Match 95.0%; Score 19; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
|||
b 28 VAEF 31

RESULT 21
S-09-864-761-37202
Sequence 37202, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Reomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37202
LENGTH: 43
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035530.11
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.95
OTHER INFORMATION: SWISSPROT HIT: P33485, EVALUE 3.60e+00
OTHER INFORMATION: EST_HUMAN HIT: AI765888.1, EVALUE 3.00e-18
US-09-864-761-37202

Query Match 95.0%; Score 19; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|||
Db 40 VAEF 43

RESULT 22
US-10-424-599-183032
Sequence 183032, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
CURRENT FILING DATE: 2001-05-23
FILE REFERENCE: 38-21(53223)B

APPLICANT: CAO LONGWEL
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27713C.1.pep
S-10-424-599-205632

Query Match 95.0%; Score 19; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 26 VAEF 29

RESULT 26
S-10-424-599-192247
Sequence 192247, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192247
LENGTH: 55
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_1561C.1.pep
S-10-424-599-192247

Query Match 95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 2 VAEF 5
b 50 VAEF 53

RESULT 27
S-10-424-599-233502
Sequence 233502, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 233502
LENGTH: 55
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_52879C.1.pep
S-10-424-599-233502

Query Match 95.0%; Score 19; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 24 VAEF 27

RESULT 28
US-10-372-003A-63
Sequence 63, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Richard
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 55
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic clone BGF05 with first open reading
OTHER INFORMATION: frame
US-10-372-003A-63

Query Match 95.0%; Score 19; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 28 VAEF 31

RESULT 29
US-10-372-003A-67
Sequence 67, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBIC40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 55
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic clone BGF06 with first open reading
OTHER INFORMATION: frame
US-10-372-003A-67

Query Match 95.0%; Score 19; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.3e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
28 VAEF 31

SULT 30
-10-219-329-4
Sequence 4, Application US/10219329
Publication No. US20030096757A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035W01
CURRENT APPLICATION NUMBER: US/10/219,329
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
-10-219-329-4

Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
31 VAEF 34

SULT 31
-10-153-185-4
Sequence 4, Application US/10153185
Publication No. US20030148959A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.034U01
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
-10-153-185-4

Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||||
31 VAEF 34

SULT 32
-10-219-561-4

Sequence 4, Application US/10219561
Publication No. US20030166567A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
APPLICANT: Villanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.008US2
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/153,185
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-561-4

Query Match 95.0%; Score 19; DB 14; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||||
Db 31 VAEF 34

RESULT 33
US-10-424-599-215734
Sequence 215734, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Publication No. US20040031072A1
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 215734
LENGTH: 57
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_36836C.1.pap
US-10-424-599-215734

Query Match 95.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
|||||
Db 48 VAEF 51

RESULT 34
US-10-424-599-260762
Sequence 260762, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260762
LENGTH: 57
TYPE: PRT
ORGANISM: Glycine max

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27490C.1.pep
S-10-424-599-260762

Query Match 95.0%; Score 19; DB 12; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 4 VAEF 7

RESULT 35

S-10-372-003A-75
Sequence 75, Application US/10372003A
Publication No. US20030215846A1

GENERAL INFORMATION:

APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening
TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBIC40.001CPI

CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: US 60/132,711

PRIOR FILING DATE: 1999-05-05

NUMBER OF SEQ ID NOS: 81

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 75

LENGTH: 57

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic clone BGF24 with first open reading

OTHER INFORMATION: frame

S-10-372-003A-75

Query Match 95.0%; Score 19; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2 VAEF 5
b 28 VAEF 31

RESULT 36

S-10-424-599-214930

Sequence 214930, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 214930
LENGTH: 58
TYPE: PRT
ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_36107C.1.pep
US-10-424-599-214930

Query Match 95.0%; Score 19; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
Db 13 VAEF 16

RESULT 37

US-09-864-761-45291

Sequence 45291, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecmca-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 45291

```
LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009079.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.54
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: EST HUMAN HIT: AV756022.1, EVALUE 6.00e-28
OTHER INFORMATION: SWISSPROT HIT: P56315, EVALUE 2.00e+00
-09-864-761-45291

Query Match          95.0%; Score 19; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      8 VAEF 11

SULT 38
-09-393-634-80
Sequence 80, Application US/09393634
Patent No. US20020051997A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GR24
-09-393-634-80

Query Match          95.0%; Score 19; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      14 VAEF 17

SULT 39
-09-864-408A-40
Sequence 40, Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shmukets, Richard A.
TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24

; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-40

Query Match          95.0%; Score 19; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      3 VAEF 6

RESULT 40
US-10-364-861-80
; Sequence 80, Application US/10364861
; Publication No. US20040038312A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Hoon, Mark
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: T2R, a No. US20040038312A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098020US
; CURRENT APPLICATION NUMBER: US/10/364,861
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US 09/393,634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 80
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T2R24, GR24 or SF24
US-10-364-861-80

Query Match          95.0%; Score 19; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      14 VAEF 17

RESULT 41
US-10-383-982-80
; Sequence 80, Application US/10383982
; Publication No. US20030157568A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. US20030157568A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/10/383,982
```

CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GR24
S-10-383-982-80
Query Match 95.0%; Score 19; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
14 VAEF 17
b
RESULT 42
S-09-864-761-45716
Sequence 45716, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24253.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45716
LENGTH: 69
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL162171.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
OTHER INFORMATION: EST HUMAN HIT: BE559987.1, EVALUATE 2.00e-03
OTHER INFORMATION: SWISSPROT HIT: P56093, EVALUATE 2.00e+00
US-09-864-761-45716
Query Match 95.0%; Score 19; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
15 VAEF 18
Db
RESULT 43
US-09-738-626-5596
Sequence 5596, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5596
LENGTH: 69
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5596
Query Match 95.0%; Score 19; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
23 VAEF 26
Db
RESULT 44
US-10-424-599-185385
Sequence 185385, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 185385
LENGTH: 69
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_138417C.1.pep
US-10-424-599-185385

Query Match 95.0%; Score 19; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 24 VAEF 27

RESULT 45
US-10-029-386-28645
Sequence 28645, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 28645
LENGTH: 70
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR17.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7
OTHER INFORMATION: SWISSPROT HIT: P78716, EVALUATE 3.00e-04
US-10-029-386-28645

Query Match 95.0%; Score 19; DB 14; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 43 VAEF 46

RESULT 46
US-10-424-599-202605
Sequence 202605, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202605
LENGTH: 71
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_24978C.1.pep
US-10-424-599-202605

Query Match 95.0%; Score 19; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 17 VAEF 20

RESULT 47
US-10-424-599-274981
Sequence 274981, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274981
LENGTH: 71
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_90329C.1.pep
US-10-424-599-274981

Query Match 95.0%; Score 19; DB 12; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 39 VAEF 42

RESULT 48
US-10-029-386-30348
Sequence 30348, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2

```

CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30348
LENGTH: 71
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: SWISSPROT HIT: P21333, EVALUATE 5.00e-22
S-10-029-386-30348

Query Match          95.0%; Score 19; DB 14; Length 71;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      |||||
b      60 VAEF 63

RESULT 49
S-10-029-386-29320
Sequence 29320, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David X.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 29320
LENGTH: 72
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81
OTHER INFORMATION: SWISSPROT HIT: P14650, EVALUATE 6.00e-14
S-10-029-386-29320

Query Match          95.0%; Score 19; DB 14; Length 72;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
      |||||
b      45 VAEF 48

RESULT 50
S-10-214-188-10
Sequence 10, Application US/10214188
Publication No. US2003002260A1
GENERAL INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.

Bernards, Rene
Hijmans, Eleanor M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-214-188-10

Query Match          95.0%; Score 19; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
      |||||
Db      23 VAEF 26

RESULT 51
US-10-156-761-9071
Sequence 9071, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9071
LENGTH: 74
TYPE: PRT
```

ORGANISM: Streptomyces avermitilis
-10-156-761-9071

Query Match 95.0%; Score 19; DB 14; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
36 VAEF 39

SULT 52

-10-424-599-156128
Sequence 156128, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 156128
LENGTH: 75
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(75)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_112004C.1.pep
-10-424-599-156128

Query Match 95.0%; Score 19; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 VAEF 5
|||
2 VAEF 5

SULT 53

-10-424-599-261424
Sequence 261424, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 261424
LENGTH: 75
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(75)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_78089C.1.pep
-10-424-599-261424

Query Match 95.0%; Score 19; DB 12; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|||
Db 12 VAEF 15

RESULT 54

US-10-424-599-253204
Sequence 253204, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253204
LENGTH: 76
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(76)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_70669C.1.pep
US-10-424-599-253204

Query Match 95.0%; Score 19; DB 12; Length 76;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|||
Db 64 VAEF 67

RESULT 55

US-10-424-599-211908
Sequence 211908, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211908
LENGTH: 77
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(77)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_3337C.1.pep
US-10-424-599-211908

Query Match 95.0%; Score 19; DB 12; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VAEF 5
|||
Db 16 VAEF 19

RESULT 56
S-10-335-977-7493
Sequence 7493, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 7493:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...77
SEQUENCE DESCRIPTION: SEQ ID NO: 7493:
S-10-335-977-7493
Query Match 95.0%; Score 19; DB 12; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 2 VAEF 5
O 40 VAEF 43
RESULT 57
S-10-029-386-32709
Sequence 32709, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32709
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004186.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: P14373, EVALUE 7.50e+00
US-10-029-386-32709
Query Match 95.0%; Score 19; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 11 VAEF 14
RESULT 58
US-10-424-599-162039
; Sequence 162039, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162039
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_117339C.1.pap
US-10-424-599-162039
Query Match 95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VAEF 5
DB 28 VAEF 31
RESULT 59
US-10-424-599-262701
; Sequence 262701, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 262701
; LENGTH: 78

```
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_79240C.1.pap
-10-424-599-262701

Query Match          95.0%; Score 19; DB 12; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      5 VAEF 8

SULT 60
-10-363-616-368
Sequence 368, Application US/10363616
Publication No. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 368
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
-10-363-616-368

Query Match          95.0%; Score 19; DB 12; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      24 VAEF 27

SULT 61
-10-424-599-216097
Sequence 216097, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216097
LENGTH: 80
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_37165C.1.pap
-10-424-599-216097

Query Match          95.0%; Score 19; DB 12; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      2 VAEF 5
      ||||
      35 VAEF 38

RESULT 62
US-10-367-980A-14
; Sequence 14, Application US/10367980A
; Publication No. US20030228592A1
; GENERAL INFORMATION:
; APPLICANT: St Vincent's Institute of Medical Research
; APPLICANT: Rogers, Suzanne D
; APPLICANT: Best, James D
; TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8
; FILE REFERENCE: VS:AJH.FP17928
; CURRENT APPLICATION NUMBER: US/10/367,980A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 09/509,731
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: GLUT2
US-10-367-980A-14

Query Match          95.0%; Score 19; DB 15; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
DB      ||||
      13 VAEF 16

RESULT 63
US-09-864-408A-5282
; Sequence 5282, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encoc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5282
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5282

Query Match          95.0%; Score 19; DB 11; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VAEF 5
DB      ||||
      52 VAEF 55

RESULT 64
US-10-078-090-125
; Sequence 125, Application US/10078090
; Publication No. US20030044815A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
```

```
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Caffierkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
FILE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
TITLE REFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patent in version 3.1
SEQ ID NO 125
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapien
S-10-078-090-125

Query Match          95.0%; Score 19; DB 14; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      38 VAEF 41

RESULT 65
S-10-424-599-155636
Sequence 155636, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 155636
LENGTH: 85
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
S-10-424-599-155636

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      45 VAEF 49

RESULT 66
S-10-424-599-201853
Sequence 201853, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
```

```
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Caffierkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
FILE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
TITLE REFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patent in version 3.1
SEQ ID NO 125
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapien
S-10-078-090-125

Query Match          95.0%; Score 19; DB 14; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      38 VAEF 41

RESULT 65
S-10-424-599-155636
Sequence 155636, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 155636
LENGTH: 85
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
S-10-424-599-155636

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      45 VAEF 49

RESULT 66
S-10-424-599-201853
Sequence 201853, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
```

```
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Caffierkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
FILE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
TITLE REFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patent in version 3.1
SEQ ID NO 125
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapien
S-10-078-090-125

Query Match          95.0%; Score 19; DB 14; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      38 VAEF 41

RESULT 65
S-10-424-599-155636
Sequence 155636, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 155636
LENGTH: 85
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_11155C.1.pep
S-10-424-599-155636

Query Match          95.0%; Score 19; DB 12; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      2 VAEF 5
b      45 VAEF 49

RESULT 66
S-10-424-599-201853
Sequence 201853, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
```

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58530
LENGTH: 89

TYPE: PRT
ORGANISM: Haemophilus influenzae
3-10-282-122A-58530

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred.No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 12 VAEF 15

RESULT 71
3-10-282-122A-66960
Sequence 66960, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66960
LENGTH: 89

TYPE: PRT
ORGANISM: Pasteurella multocida

3-10-282-122A-66960

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred.No. 1.2e+03;

QY 2 VAEF 5
DB 12 VAEF 15

RESULT 72
US-10-282-122A-68774

Sequence 68774, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68774
LENGTH: 89

TYPE: PRT
ORGANISM: Proteus mirabilis
US-10-282-122A-68774

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred.No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAEF 5
DB 12 VAEF 15

RESULT 73

US-10-424-599-180307
Sequence 180307, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180307
LENGTH: 89
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_133832C.1.pep
-10-424-599-180307

Query Match 95.0%; Score 19; DB 12; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
11 VAEF 14
24 VAEF 27

SULT 74
-10-097-111-360
Sequence 360, Application US/10097111
Publication No. US20030138771A1
GENERAL INFORMATION:
APPLICANT: PELLETIER, JERRY
APPLICANT: GROS, PHILIPPE
APPLICANT: DUBOW, MICHAEL
TITLE OF INVENTION: DNA SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE BP1 THAT
TITLE OF INVENTION: ENCODE ANTI-MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0603
CURRENT APPLICATION NUMBER: US/10/097,111
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 09/676,412
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,218
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 360
LENGTH: 89
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
-10-097-111-360

Query Match 95.0%; Score 19; DB 14; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
11 VAEF 14

SULT 75
-10-424-599-245830
Sequence 245830, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245830
LENGTH: 90
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_64015C.1.pep
US-10-424-599-245830
Query Match 95.0%; Score 19; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 VAEF 5
60 VAEF 63
Search completed: May 24, 2004, 17:42:32
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